SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24845	55213	Α	24983	1	2180	METLNLYADLRSVTGEALLLL
						DEPGVGVDPISRRELWQMVHE
						LAGEGMLILWSTSYLDEAEQCR
						DVLLMNEGELLYQGEPKALTQ
						TMAGRSFLMTSPHEGNRKLLQ
						RALKLPQVSDGMIQGKSNIVGI
						KDTIDSVGHLRTMINTVKSVRP
						SFSVFCGYDDHLLNTMLLGGD
						GAITASANFAPELSVGIYRAWR
			<u> </u>			EGDLATAATLNKKLLQLPAIYA
						LETPFVSLIKYSMQCVGLPVET
						YCLPPILEASEEAKDKNRPLVD
						LEHAALQVGKGIIPPPLREYGAS
		l				EVRSVTRAFNHMAAGVKQLAD
						DRTLLMAGVSHDLRTPLTRIRL
						ATEMMSEQDGYLAESINKDIEE
						CNAIIEQFIDYLRTGQEMPMEM
		ĺ				ADLNAVLGEVIAAESGYEREIE
						TALYPGSIEVKMHPLSIKRAVA
						NMVVNAARYGNGWIKVSSGTE
						PNRAWFQVEDDGPGIAPEQRK
		1				HLFQPFVRGDSARTISGTGLGL
						AIVQRIGDNHNGMLELGTSERG
						GLSIRAWLPVPGTRAQGTTKE
						GAREDAVEFFAKLGFVNQGEIT
						TPTTTPIRHFLMIKPVATLDDIL
						HRGDWCAQLQQAWYEHIPLSE
						KMGVRIQQYTGQKFITTMPETG
						NQNPHHTLFAGSLFSLATLTGW GLIWLMLRERHLGGTIILADAHI
						RYSKPISGKPHAVADLGALSGD
						LDRLARGRKARVQMQVEIFGD
24846	55214	A	24984	875	1150	EBREARGICKARVQIMQVEITGB
24847	55215	A	24985	1507	1974	
24848	55216	A	24986	1	1006	
24849	55217	Α	24987	1491	1703	RECRYATNGKNNGCCRSAGSD
						FSSRLRYVR*PFIYTQ*SCGIGH
						CPGTDIRAKIRRTARFIKNYGTY
						CPS
24850	55218	Α	24988	1	1758	
24851	55219	Α	24989	1773	2165	PSRGVEVNSGWNWQATNRRVI
						RNFDDLDQLIIPGTARNAQTCIF
						NFVTVTMTLNNCRRIVQLANQ/
						DYRQPTGTAVAETHGTAEIALL
						ATNFNVAVFIAPLGNQRHNRVL
				1	1	TVWHKFRRVGVLHVGNMASVI
						И
24852	55220	Α	24990	1	141	SPGKIRPVIAAAMKQIKEFMSP
						DSDFFRYMKTPTSATR*YNDCG
						TGQ

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24853	55221	A	24991	1430	1933	PIIVCMGSLTMPDSACMAPFPPS
				ŀ		AVRRWNSSFPPTFSAHTSSPCA
						CYPRCYRTVKGVL**HHR*W/V
						LISTPGRGAYAASKYALEAWSD
						ALRMELRHSGIKVSLIEPGPIRT
						RFTDNVNQTQSDKPVENPGIAA
						RFTLGPEAVVDKVRHAFISEKP
						KMRYPVTHGDLWR
24854	55222	A	24992	1318	4265	LAIVALFLDLQNHIFSKGFWPS
						DKFYAAKVEEQNQRHQRYHGT
						SYNLEPDIKSSPGGLRDIHTLQ
						WVARRHFGATSLDEMVGFGFL
						TSAERAELNECLHILWRIRFAL
						HLVVSRYDNRLLCVHPTLLTTL
						DIHGEAQIWRREVSSRYGQYPK
		1				AQAAQPDQLMSDYFFRVSLAM
		1				QNKTLLFSLDDTLVNNALQTLN
						KTRPAMVDVIPTDGIVPLYINPQ
						GIAKLLRNETLTSLPKNLEPVFY
						NAAQTLLMPKLDAL
24855	55223	Α	24993	1	454	MGFDDTRDRALFEDSAMSQQP
						TVPDRLRWLLQTFKYQKNIRI*
						STPRKKPMRHSIWNIWGSRRC
						WSNPKRTFMSISVRGNMAAIM
						SFHTSAVMRSHCSILTTIKSRW
		l				ATLNTLILR
24856	55224	Α	24994	65	330	
24857	55225	В	24995	1	1998	
24858	55226	Α	24996	1175	1877	QQVPQKGPGRAKRHLHAAGW
						HWHQRDRCPEEKNVRQ*RRYR
						AVRFIII
24859	55227	В	24997	1	3117	
24860	55228	Α	24998	1888	2412	ARFKHVGDGTVTHRLFRRAAQ
						IVRVV*RAVSHRQHFTGVDIHQ
						HGATRFSLVKGHRIVQFAINQR
						LQAFINTQRQVVRSLAVSRRNI
						FNYATIAVFTHNALTRLPGKPFI
						ETLLNALNPLTEHAARDLEDSP
						VRITAYIEDVDALAQAGADIIAI
						DGTDRPRPVPVETLLARIHH
24861	55229	Α	24999	1	2457	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24862	55230	A	25000		3019	MAALRQSFWSQLFDRVHIGLD FFDASINRIAAWVIGTRNMKKA LLRALLEPTAELRNWKRRAITL RVWHCWKSRNRCRGRRSGKCI ANVTIRQQDHQIETVFINQRLH ERMFPPFVLFAERLSGDEDLGL KAPILEALNDLGYEKPSPIQAEC IPHLLNGRDVLGMAQTGSGKT AAFSLPLLQNLDPELKAPQILVL APTRELAVQVAEAMTDFSKHM RGVNVVALYGGQRYDVQLRA LRQGPQIVVGTPGRLLD
24863	55231	Α	25001	60	545	PSPFTAGASMAVERSTG\HEGE LVLETLVIDGDENT/CAGTRRSL RANA*CLFHPFRAGAEKLAEEV WFCRYPHCGCEQNTTTEEQRR TEWMVTESLADFLDPHDPGKT VEGYPAPKRARNRNRAEDHRQ RLRHRTRKKQTHGQRRRHRPE PAQRQPQTGTTD
24864	55232	Α	25002	1410	1575	
24865	55233	Α	25003	200	691	
24866	55234	Α	25004	1336	2028	
24867	55235	Α	25005	1	345	
24868	55236	A	25006	671	1204	RTSDKLPFCRRSRMENLARFLS TTLKQLRQQRGWSLSRLAEAT GVSKAMLGQIERNESSPTVATL WKIATGLNVPFSTFISPPQSAT/P SLFPYDPQLCFEHLAIQMASGAI SESTPHEKGVIEHVVVIDGQLD LCVDGEWHTLNCGEGVRFAAD VTHIYRNGGEQTVHFHSLIHYP RS
24869	55237	Α	25007	2251	2466	
24870	55238	A	25008	181	626	WQNFDTCGGDMLDKLDAALR FQQEALNLRAQRQEVLAANIA NADTPGYQARDIDFASELKKV MQRGRDATSVVALTMTSTQHI PAQALTPSTAELQYRI\PANPSL DGNTVDMDRERTQFADNSLQY QMSLSALSGQIKGMMNVLQSG N
24871	55239	Α	25009	57	278	
24872	55240	A	25010	171	532	KPVQFAIADGNNQPLALLNIHL PVMMLAIAHGPLLPAFPPELLV LFDDS/PLSSRVLLINAFSGGSDT AMRRAGKGAPAFLLPELPIITV VSPFLPQSSPRRKPIMSKRIPSAV NQRNPRQ
24873	55241	Α	25011	1	648	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	i i	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24874	55242	Α	25012	158	514	VLQLIKAVWTQRTQKPSWLHP
		l				VDSAPGLQMELPASPVPCTCTP
		1				QPLGGRWDWALWSRGWRLLR
						RLGPHRSPRRS*GSGLWPWPAQ
		l				KGAPIVQRWAKGLLKCHQSGS
		ļ				PGRGGAESERGL
24875	55243	Α	25013	1	693	
24876	55244	Α	25014	119	304	DRRRCAHKITVIPKRMTIAGIRL
						PPQTVNI*LGNFLRALIASTAGI
L						MTAQMVAHSPAPPIP
24877	55245	Α	25015	361	540	
24878	55246	Α	25016	191	446	AKRRLGVYDADCCSIDKTQSLS
		İ				ACTTRNCGAYSKCLCGKYAKP
						VGGIPQPLQESHVR*CCNVMEL
						SPCSDFT**HPPGAVSQPQT
24879	55247	Α	25017	1	2259	
24880	55248	Α	25018	1	1170	
24881	55249	Α	25019	3	1240	
24882	55250	Α	25020	1	1259	MAGPRYPVSVQGAALVQIKRL
						QTFAFSVRWSDGSDTFVRRSW
						DEFRQLKKTLKETFPVEAGLLR
						RSDRVLPKLLGQASLDAPLLGR
						VGRTSRGLARLQLLETYSRRLL
						ATAERVARSPTITGFFAPQPLDL
						EPALPPGSRVILPTPEEQPLSRA
						AGRLSIHSLEAQSLRCLQPFCTQ
		į				DTRDRPFQAQAQESLDVLLRHP
						SGWWLVENEDRQTAWFPAPYL
						EEAAPGQGREGGPSLGSSGPQF
1						CASRAYESSRADELSVPAGARV
						RVLETSDRGWWLCRYAGAGPE
						ELDTSARNAGALTRRREIRDAA
						TLLRLGLAYGPGGMSLREVTA
						WAQLHDVATLSDVALLKRLRN
						AADWFGILAAQTLAVRAAVTG
						CTSGK/QIASCRWNSNQCARGR
						QR*MATTYGI*SSYLSVH*F*AN
						RQQRR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24883	55251	A	25021	803	2061	AKPAARGGILAAPVRDTLFLYF
						RLKKNQRQEGFINTYPWPKKP
						GIFYMCVPIKGANAQDVAAFC
						VTARGRQNCLWESIARGPALIN
						NRGAARGRCNDRVVEVDHGFA
						VLTFNFQGVSPGEFTQTVDHFD
						FAAFRHTSQTTGQLIDHFLFPGT
]			!			NLVDIGFRFAEDDTVFSQRFGF
				1		FDNFCYVQQCFRRDTADVQAN
						TAKGVVTFYDYGFQTYWVKV
						LDPGSEVVAEAGDGASAIDLAH
						RLDIDVILLDLNMKGMSGLDTL
						NALRRDGVTAQIIILTVSDASSD
						VFALIDAGAAGYLLKDSDPEVL
						LEAIRAGAKGSKVFSERVNQYL
						REREMFGAEEDPFSVLTEREL\D
					İ	VLHELAQGLSNKQIASVLNISE
						QTVKVHIRNLLRKLNVRSRVA
						ATILFQSAAFRSRFRRATSDNV
24884	55252	Α	25022	1	1569	
24885	55253	Α	25023	2151	2709	YLREASETARRQFTLP\VILYNF
İ		l				RDLTGQDLTPETVTRLALQNEN
		1				IVGIKDTIDSVGHLRTMINTVKS
		1				VRPSFSVFCGYDDHLLNTMLLG
		ł				GDGAITASANFAPELSVGIYRA
1						WREGDLATAATLNKKLLQLPA
		I				IYALETPFVSLIKYSMQCVGLPV
						ETYCLPPILEASEEAKDKVHVL
			1			LTAQGILPV
24886	55254	В	25024	1	1201	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	tocation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24887	55255	A	25025	1	2209	MIGEIRDGETAEIAIKAAQTGHL
	ļ	ŀ				VLSTLHTNSTCETLVRLQQMG
	ŀ					VARWMLSSALTLVIAQRLVRK
						LCPHCRRQQGEPIHIPDNVWPSP
		ļ				LPHWQAPGCVHCYHGFYGRTA
	ļ					LFEVLPITPVIRQLISANTDVESL
				}		ETHARQAGMRTLFENGCLAVE
						QGLTTFEELIRVLGMPHGDGAA
						MDREENELGVSCIAVPVFDIHG
						RVPYAVSISLSTSRLKQLYAGLP
						VWCDGSRFFAQKARAİKCKQW
						GYVGAKSRQRWLFYAYDRLRK
					ł	TVVAHVFGERTMATLGRLMSL
						LSPFDVVIWMTDGWPLYESRL
						KGKLHVISKRYTQRIERYNLNL
		1				RQHLARLGRKSLSFSKSVELHD
1						KAAGGVPVLVRELLKAGLLHE
		İ				DVNTVAGFGLSRYTLEPWLNN
						GELDWREGAEKSLDSNVIASFE
						QPFSHHGGTKVLSGNLGRAVM
						KTSAVPVENQVIEAPAVVFESQ
						HDVMPAFEAGLLDRDCVVVVR
						HQGPKANGMPELHKLMPPLGV
						LLDRCFKIALVTDGRLSGASGK
						VPSAIHVTPEAYDGGLLAKVRD
						GDIIRVNGQTGELTLLVDEAEL
						AAREPHISELSAFTFGTGRGYSA
						AFGVKCPFRKRALSDPCYAMR
						EVADFLINKGVDGLFYLGTGGE
				}		FSQMNTAQRMALAEEAVTIVD
						GRVPVLIGVGSPSTDEAVKLAQ
						HAQAYGADGIVAINPYYWKVA
24888	55256	Α	25026	1	3395	MSELPFTIASKRIKYLGIQLTRD
						VKDLFKENYKPLLKEIKEDTNK
						WKYIPCSWLGRINIVKMAILAK
						VIYRFNAIPIKLPMTFFKELEKT
						TLKFIWNQKGAASRSNPEPKNK
		1		1		LEDHITNSTIYRLSTKSCSVSGL
	1					KQTLLAESEALTSYSHRVFSAW
						DFGLCGDVHVRLRQRIILYELK
						GQVPALLLDDGTLLTEGVAIM
						QYLADSVPDRQLLAPVNSISRY
	1				İ	KTIEWLNYIATELHKELKFSFH
						WSTTSHKGLGM
	1		L	I	1	" STISHINGESIVE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24889 55257	55257	A	25027	145	681	FNGATQRIFDARGKPSTYIGSIQ HVNADVDQRATTLQFFIGKDTP AGNAAATQGAGGGNVNLSQN AVGHLFTQLLRIERKTMVKVV
						GQHLAQFARGIDISRACYHMA ARFQCHQGMFVMKTVR*ADA NHIRFHCQQHGLRIVPHGCIPVF FCQRLPLGKAAVTDSYQFQIRC GCSSTKH
24890	55258	Α	25028	696	953	LSGLCSVRRAYPGGRSCPGVP* FVGLVARRPGGG*GSCFVLLHP QRSGTGGCL*QPPFPGAGAGRK IRECIRVGRSAGHAAGGET
24891	55259	A	25029	3	506	RGKPSTYIGSIQHVNADVDQRA TTLQFFIGKDTPAGNAAATQGA GGGNVNLSQNAVGHLFTQLLRI ERKTMVKVVGQHLAQFARGID ISRACYHMAARFQCHQGMFVM KTVR*ADANHIRFHCQQHGLRI VPHGCIPVFFCQRLPLGKAAVT DSYQFQIRCGCSSTKH
24892	55260	Α	25030	291	560	DSTQTQTREGESSTRIT
24893	55261	A	25031	63	404	
24894	55262	A	25032	660	1073	LSHECSFWLTNQLVSPRAQTVS GELQPAYAHGVLCRQYPSAFE KASETPQSSNPCPSSYTIHPTVE NFQTCRNQHLSKGCLINAGRA GPSPGTGGWGELEVAAAARLQ GAWKRHLQSSRPPGQALFASPP *WTGSVQ
24895	55263	A	25033	272	511	GSDTALPSAIAAPLLAAMAWLP PRERGTLAH/QVLEHYQLAQLP VSAL/QMPLHCPPQAIAHHQQL/ EQQALASLQNWGVFHV
24896	55264	Α	25034	1	3300	
24897	55265	A	25035	1117	1376	PPPIGLTYSSSASPLSLFCTVRKP FSRSCW*QTNSNPISSCPELVTP SE*L*PRRSIRLDSLSAVRGFAS RIWLSSAITFPSGSLA
24898	55266	A	25036	207	427	DEHLQQRKKPLFLNYGRTEQA SVK*RISWVQNPERSSLC*GILA A*NPMSVSGL*LT*HCLSARRY ELVCQPK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24899	55267	A	25037	2012	2547	LKFARPKLWGIFRNRQYHHML ER\RSQAIDAPALDRGAALGAL MRLEHPNASAEAALTMLAQLS PAQSGEALHGLLALARHQLAC QPAFIAGFSSHLNQLSEADFINA LPDLRAAMAWLPPRERGTLAH QVLEHYQLAQLPVSALQMPLH CPPQAIAHHQQLEQQALASLQN WGVFHV
24900	55268	A	25038	1	150	DKASRGRSRQQS/CAVLQPLLVI PRQT/WVWSGPPANSSRPGEEG PDC*KEN
24901	55269	A	25039	1	150	DEASRGRNRQQS/CAVLQPLLV IPRQT/WVWSGPPANSSRPAEEE PDC*KEN
24902	55270	A	25040	96	389	PCLSP*LYPSGVHKSTFIYGFYN T*PCTSQSLFWQHSC*GSITSSS YFYLLPEEGTGSNLCCSAASAG DTQANRVWSGPPANSSRPAAE GHDCWKEN
24903	55271	A	25041	1181	1364	VSLGNIKFRQTGAPLGQSFQRK EQSAIFAVLQPPLVIPRQI/WVW SGTPADSSRPAAEGPDC*KEN* RVNRQPTEWEKIFPIYPYDKGLI SRIYKELKQIYKKKIKPPHQKV GKGYVFSKEDIYAANRHMKKC SSSLAIREMQIKTTMRYHLTPA NRGIEIINCPFLDDAASCIDPTYS SNIFPPVNLSWGLPMKPKEVKI KRQKKEHLLKDRDFSFQEPIMA LRTVILEILMEKEMDNSQRECIK DILTKHLVELSILARTFKNTQLP ERAIFQIKQYNSVSCGVSEWQL EEAQVFWAKKEQSLALSILKQ MIKKLDASCAANNPSLKLTYTE CLRVCGNWLAETCLENPAVIM QTYLEKAVEVAGNYDGESSDE LRNGKMKAFLSLARFSDTQYQ RIENYMKSSEFENKQALLKRAK EEVGLLREHKIQTNRCPSGTKL PEEGTVSNLCCSAASTGDTQAN RVWSGTPADSSRPAAEGPDC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24904	55272	A	25042	42	963	VQEGCVRPFCCRSAGVCWRST
						PDSVCLGITSGGCRTAKTAACS
						FLWKLCPRGTPARCQVECSYTR
						CLS\SLLGGVSQAGGTRVRDPL
						EEEVCPLAELERCAGRSVAVFR
						ASRQEHLRLLKLTSQPPLPPGA
						LSQGDGSFIYKPLTGVAAFLSD
						ALPKRRNLERQSGYSTFEELCF
						QKRTWGRDAVRISDLLLGDHS
						HFGKCPISRLERAENMPVVSEL
						SAAGCSTEVNHVFVGIIWQKGK
						CSKYTAPSKSSVPVSSTRGHVHI
						TVQNPTLVPFVGKLNIDSPIGDR
						NIPVLTAGNCKTLGDLRSFPHN
24905	55273	A	25043	98	352	
24906	55274	Α	25044	3	414	PEEALCALAELERCAGRAAALF
						RAERQKRLRLLKLHPQPPLPPG
						ALSQRDGS\LSISP*LGL\RLSFR
						DALPREQFYRLFTDRSDRVPEN
						SVTDVCHIESKMEPLRLGP/SNV
						SIMRPSLVCSFTTLVFISSNAQSS
						LVA
24907	55275	Α	25045	2	1544	STTRGSPPQEARQYRHNQAYA
						YSIQGDGAEDDDERIVRFHTRL
						PVFMLPPTPRKTSWIVAPVLEV
						LARAIRHETEIQGIHTGTEDVPV
						SLFADDMIIYLDNLKDSSRKLL
						EVIRDFSKVSGYKINVHESVAL
						LYTNNDYAENHIKNSTPFTIGY
						VLAFVVMVIAVSCVRLLYAHN
						CTQHTSLKHKCQAWVVTTVDA
		ŀ				AAFMTQATREERRIAYSAPGGY
						FFHILEVLARTIRQEKEIQGIQTG
1						KEEVKVSLFADDMIIYLENLKD
						SSRKLLEVIKEFSKVSGYKINVD
						SRGSPTDLVIYKEEIVFLIVPKA
						KKSKIKVLASDPLCYAATTWR
						MTIIAGLPVEYNDRFIRGIAVFA
						PWRKTPGIYHQSHDPLCYAATT
1						WRMTIIAGLPVEYNDRFIRGIA
						VFAPWRKTPGIYHQSHGACLG
						RRSRTITVVDAQPQVMDMDPT
						CSLFTTGQCLGEPDLLASARRL
						QFFSHQYSIAVLMANARGNSA\
	<u> </u>					LW\DNYGGLIVRADRGSLLLVG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24908	55276	Α	25046	1	1228	MLQSNRTAASHSPSIQPAIQPAI
						QPASQLSIHNLWTQFRHSTKIPV
						EWVNGEWLNGRMPEDHHEWQ
						CNYQNVQQFIDEGNYTSGDNH
						TLRDPHYVEDKGHKYLVFEAN
						TGTENGYQGEESLFNKAYYGG
		1				GTNFFRKESQKLQQSAKKRDA
						ELANGALGIIELNNDYTLKKVM
						KPLITSNTRETVDFNGKHIHVR
						GAKLLFPAIQQPYPPLYFGGSSD
						VAQELAAEQVDLYLTWGEPPE
						LVKDFIEQVRAKAAAHGRKIRF
			ŀ			GIRLHVIVRETNDEAWQAAERL
						ISHLDDETIAKAQAAFARTDSV
						GQQRMAALHNGKRDNLEISPN
						LWAGVGLVRGGAGTALVGDG
						PTVAARINEYAALGIDSFVLSG
						YPHLEEAYRVGELLVPLLDVAI
		1				P\EIPQPQPLNPQGEALRKK
24909	55277	A	25047	1	1075	MTIKGEQAKKQLIAAALAQFGE
						YGMNATTREIAAQAGQNIAAIT
						YYFGSKEDLYLACAQWIADFIG
		•				EQFRPHAEEAERLFAQPQPDRA
ŀ			ļ			AIRELILRACRNMIKLLTQDDT
			l			VNLSKFISREQLSPTAAYHLVH
						EQEAEHRFAMGELPDEVLEICQ
						RLAKLTEMLRGLAELFLNDLSE
1						KTGSHDIVRLHRLILQMNRALG
1						MFEAQSKLWRLASLAQSSGAP
						VTKWATREEREGQLHLWFHCV
		İ				GIRVSDQLERLLWRSIPHIIVTS
		İ				ATLRSLNSFSRLQEMSGLKEKA
:						GDRFVA/SGFP/HLTTANRAKLL
						FPGCALSLPSTTKSSILPKWRPF
						SVSRWRAKNISVCWYCLPADG
						RCSAFSTM
24910	55278	A	25048	530	642	LKTLW/PAVQEPVPHRYHGATV
						FRIMQTIFIKQICRLLL*GTAGHF
						VCGITACHAAEAAHRLTVQPVP
						RILDQRRPAQLHSRQVTAAIRQ
		1				PLHRRQAVRRDAVCQPLLVVC
		1				VFRLMLPQQFPRLRVLHRLAFA
						GQAAFIVIAIVDGNTVAFAQVA
						DVCQPAVAIILPLLLCEFSGQVI
						MITLRPPVKAALLYQPVQRIVT
						EDAVAAVQEPVPHRYHGATVF
						RIMQTIFIKQICRLLL
24911	55279	Α	25049	1075	1479	<u> </u>

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NO.	sequence	nou	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24912	55280	A	25050	2	588	RWSSLTSSRYGFCRCPESADKE CLHVKSAAGKKATNVGHYAG WLRTYSPHLAAHRVNFFFGINA HMDQRGPGRLMISCNEACGSA CYSNHSYMRNDKHAVRRADSG RAEGGGPRVKSVIKAPVITPKK KPVVSTLKHWVLMLAWVTCSPLTVL\SPDGEMFDVMEKYAFSA WKWKRLRLAISQATFHALLPE KIG
24913	55281	Α	25051	912	1169	
24914	55282	В	25052	1	1665	
24915	55283	Α	25053	43	302	
24916	55284	В	25054	116	1534	
24917	55285	A	25055	1	1017	NVQQFIDEGNYTSGDNHTLRDP HYVEDKGHKYLVFEANTGTEN GYQGEESLFNKAYYGGGTNFF RKESQKLQQSAKKRDAELANG ALGIIELNNDYTLKKVMKPLITS NTRETVDFNGKHIHVRGAKLLF PAIQQPYPPLYFGGSSDVAQEL AAEQVDLYLTWGDPADL\VNEI VEQVRAKAAAHGRKIRFGIRLH VIVRETNDEAWQAAERLISHLD DETIAKAQAAF\ARTDSVGQQR MAALHNGKRDNLEISPNLWAG VGLVRGGAGTALVGDGPTVAA RINEYAALGIDSFVLSGYPHLEE AYRVGELLVPLLDVAIP\EIPQP QPLNPQGEALRKK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24918	55286	A	25056	1	2677	MVLNRLLTGLFFGSTPPRCHYD
		-				LIGADPDRTIRSVRLYWRHSLN
						ELISMLPKFNKELTRKLFKLQE
						MLPFLNLHMSPERMLQRMDSE
						KVVTFTTALMTGLSGAMASVL
						LLVMTVVFMLFEVRHVPYKMR
						FALNNPQIHIAGLHRALKGVSH
						YLALKTLLSLWTGVIVWLGLEL
						MGVQFALMWAVLAFLLNYVP
						NIGAVISAVPPMIQVLLFNGVY
				÷		ECILVGALFLVVHMVIGNILEPR
						MMGHRLGMSTMVDGVRVLKD
				ł		GTDLNQTGSFYLAARPYAEKN
				1		GAFIQGVLATFSEADALTRSQR
		-				EQSIALLAKTMGLPAPVIASLLE
						ISQPVSNHPIRTRLTAEVAALQQ
						QTADLFYENRLVPKKVDIRQRI
					,	WQPTRLEGKQFMSLNMFWFLP
		l				THGDGHYLGTEEGSRPVDHGY
		i				LQQIAQAADRLGYTGVLIPTGR
						SCEDAWLVAASMIPVTQR\LKF
						LVALRPSVTSPTVAARQAATLD
						RLSNGRALFNLVTGSDPQELAG
i						DGVFLDHSERYEASAEFTQVW
						RRLLQRETVDFNGKHIHVRGA
						KLLFPAIQQPYPALYFGGSSDV
						AQELAAEQVDLYLTWGEPPEL
						VKEKIEQVRAKAAAHGRKIRFG
						IRLHVIVRETNDEAWQAAERFV
					İ	LSGYPHLEEA/YRVGELLFPLLD
						VAIPE/IPQPQPLNPQGEAVAND
		l				LSPRRTVAASGDQLLAGAVGFS
24919	55287	Α_	25057	114	372	
24920	55288	Α	25058	2270	2760	TSPIPSQIRQYSIA/VGSTGNLGL
				1		SIGIMSARIGFKVTVHMSADAR
						AWKKAKLRSHGVTVVEYEQD
						YGVAVEEGRKAAQSDPNCFFID
		1		1		DENSRTLFLGYSV/AGQRLKAQ
		1				FAQQGRIVDADNPLFVYLPCGV
						GGGPGGVAFGLKLAFGDHVHC
						FFAEPTHSPCMLL
10.400:	55289	В	25059	1	2460	
24921	133209	טן	23037	1,	12400	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
l	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
ĺ				sequence		
24923	55291	Α	25061	332	1349	ILYDSDIYRFSCRSGGHIPAVIY
						HLSAKRRTMENAKMNSLIAQY
						PLVKDLVALKETT/WGFIPATL
						HGVKGLPYVGLTEQDVQDAH\
						ARLSRFAPYLAKAFPGKWLPTG
						GIIES\ELGAL\PAMQKRL\EKEY
			:			QQPISGQLLLKKDSHLPISGSIK
						ARGGIYEVLAHAEKLALEAGLL
ĺ						TLDDDYSKLLSPEFKQFFSQYSI
İ						AVGSTGNLGLSIGIMSARIGFKV
1						TVHMSADARAWKKAKLRSHG
						VTVVEYEQDYGVAVEEGRKAA
						QSDPNCFFIDDENSRTLFLGYSV
						AGQRLK\AQFAQQGRIVDADNP
						LFVYLPCGVGGGPGGVAFGLK
•						LAFGDRVHGLQA
24924	55292	Α	25062	284	1494	RLSLPDMFPPVQQFPVSLHRAF
						YRYDKSAYYALRIAGIASRLNP
						RRFSPSILTPERRCVVTLRNDIR
						RDVLRHNQPRSTASTRQARRR
						MKSSCWHMPTTSKPQALSHTS
		1				NSPTTSISRPNWSYSNVCNRSRT
						MANLSGYNFAYLDEQTKRMIR
						RAILKAVAIPGYQVPFGGREMP
						MPYG\WGTGGIQLTAS\VIGESD
						VLKVIDQGADDTTNAVSIRNFF
						KRVTGVNTTERTDDATVIQTRH
						RIPETPLTEDQIIIFQVPIPEPLRFI
						EPRETETRTMHALEEYGVMQV
-		1				KLYEDIARFGHIATTYAYPVKV
						NGRYVMDPSPIPKFDNPKMDM
						MPALQLFGAGREKRIYAVPPFT
						RVESLDFDDHPFTVQQWDEPC
						AICGSTHSYLDEVVLDDAGNR
}						MFVCSDTDY
24925	55293	Α	25063	1	333	

SEQ ID	SEQ ID NO:		I .		B:	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		02/340,217	sequence	or peptide sequence	detection, (-possible nucleotide insertion)
24926	55294	Α	25064	1368	2451	PAHAAPGGGC/VRSLACRFLWN
1						MRVTGKSYSTLRRVLSAIWNW
						RMMRCALTRALVAFRVR/SSVP
,						LAAVLAIYARENGAGTMFEPE
		l				AAYDEDTSIMNDEEASADNET
1						VMSVIDGDKPDHDDDTHPDDE
						PPQPPRGGRPGLRGLTLRWFSV
		ŀ				AAQRSDILDAVTLSLKVAALAT
						LIALVLGTLAAAALWRRDFFG
						KNAISLLLLLPIALPGIVTGLALL
						TAFKTINLEPGFFTIVVGHATFC
						VVVVFNNVIARFRRTSWSLVEA
		i				SMDLGANGWQTFRYVVLPNLS
						SALLAGGMLAFALSFDEIIVTTF
			•			TAGHERTLPLWLLNQLGRPRD
						VPVTNVVALLVMLVTTLPILGA
		1				WWLTAKATYLEKLKV
24927	55295	Α	25065	1	2072	MSEQLTDQVLVERVQKGDQKA
						FNLLVVRYQHKVASLVSRYVP
						SGDVPDVVQEAFIKAYRELTPR
						RPYLLRAFYEWLLDNQLTPHL
1						VVDVTLPGVQVPMEYARDGQI
						VLNIAPRAVGNLELANDEVRFN
						ARFGGIPRQVSVPLAAVLAIYA
						RENGAGTMFEPEAAYDEDTSI
						MNDEEASADNETVMSVIDGDK
			ŀ			PDHDDDTHPDDEPPQPPRGGRP
						ALRVVNVIVAIIFTTKPTAMGIA
						VRFTTAKGETPAIPDVTTTTAVI
			}			GETARASVVAKCIGIIITTAVPIV
ł						VKPFANISPATTSVPRFFGLPAS
						SSHTLIGAIIGIGLTNALLTGSSV
						MDALNLREVTKIFSSLIVSPIVG
ļ						LVIAGGLIFLLRRYWSGTKKRD
						RIHRIPEDRKKKKGKRKPPFWT
						RIALIVSAAGVAFSHGANDGQK
						GIGLVMLVLVGIAPAGFVVNM
						NASGYEITRTRDAVTNFAARES
						EASVIRHSNRFIETINGGRRCSR
						GITLTLHKLR\SAQPLL\AVLNR
				[LEQKKPVGLRYDPQAQSLVCLP
				1		TQTRTGWNLNGFEVGFRPCVR
						LMIYGRSLEAQATASLAAATG
						YDSHIFDLFPASASAQIDTDTAV
						ILLCHDLNRELPVLQAAREAKP
	•					FYLGALGSYRTHTLRLQKLHEL
						GWS\RQETTQIRAPVGIFPKARD
L	<u> </u>					AHTLALSVLAEVASVRLHQEE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24928	55296	A	25066	2	332	AGYSTRTALAIVNKPPSSAIPPT SGLASRKRNPASNDFNGCSRGC GGGGNAGRLNNGSKRSASTPP TIRPTNIAPP\AASPKAPPARWN VSSSGSAPAPRRRANPETQLR
24929	55297	A	25067		3192	MNKKFKYKKSLLAAILSATLLA GCDGGGSGSSSDTPPVDSGTGS LPEVKPDPTPNPEPTPEPTPDPE PTPEPIPDPEP/TPE/PEPTPEPTPD PEPTPEPIPDPEPNQNGAELSYN TEKTLTIRDSVFTYTENADGTIS LQDSNGRKATINLWQIDEANNT VALEGVSADGATKWQYNHNG ELVITGDNATVNNNGKTTVDG KDSTGTEINGNNGKVIQDGDLD VSGGGHGIDITGDSATVDNKGT MTVTDPESM
24930	55298	A	25068	1078	1317	
24931	55299	A	25069	135	361	SCSMLAGLCG*GSSSSVSITTCF ALSASTIA*PREPQQALPV*PLA LPNSSQDGTPMKATSIFSSPLCT RCTRPP
24932	55300	Α	25070	469	841	RWWKQYAAAGFQCMCATAVS NLTRPVAA*TAAIPESKSPVLPN SPASTVRRS*PVSTMPPIRPGDG DHDPRFKAPSGTPHQPPRAGHS L\RRHG*TENCTAA*GQLRTPG DNGTVMSADTITFP
24933	55301	В	25071	1	2922	
24934	55302	Α	25072	1	3849	
24935	55303	Α	25073	1	2280	
24936	55304	A	25074	672	1045	GAVLSINCRTLSPAAASGENVA TPP/VTSNNNTPIINKPKPLALAE ATGVIIAPKPPSSAAPMASPVTF CAVHKPLIRPNIASGVCVCSIVY CSNELTALNQPNSARQTTPKIHI GIRPNRPMARN
24937	55305	A	25075	650	1465	RKPICAADICQLSASAGYSTRT ALAIVSGLASRKRNPASNDFNG CSRGCGGGGNAGRLNNGSKVI NVPAAASP*FQATPPVASNKPPI MGEITDPRRTVNMVIAPACIKF SRPTSAGVAANSAVTPSDAKKP SHKPSK*IASNDGSGSSALRHSP MKPMPQVPRASKITFLRS*RSA STPPTIRPTNIAPPVSVTESPTCQ VECVIIWICTGTATPSKPRDTIE MKRARNTARNAGCVSAGSSGS SAEVGSSNSKTSGSIASARAIET RCC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24938	55306	A	25076	156	3092	LNRRWIANIAKLEAEQARKLK
24730	33300		23070	150	3072	KTEKDSLKDEVLHSLLPRAFSR
			}			FSQTMMWIDTVNGLIMVDCAS
						AKKAEDTLAVLRKSLGSLPVVP
			1			LSMENPIELTLTEWVRSGSAAQ
						GFQLLDEAELKSLLEDGGVIRA
İ						KKQDLTSEEITNHIEAGKVVTK
						LALDWQQRIQFVMCDDGSLKR
						LKFCDELRDQNEDIDREDFAQR
						FDADFILMTGELAALIQNLIEGL
						GGEAQHSGTGSLPEVKPDPTPN
						PEPTPEPTPDPEPTP
24939	55307	D	25077	61	2118	PEPIPEPIPDPEPIP
24939	55308	B A	25078	132	280	RRRAALPERSGPGLDHRRVRH/
24940	122300	A	23078	132	200	GCHVLPTPVTLVKRRKVSRVD
						AQWKSSV
24941	55309	A	25079	1	1449	AQWK33V
24941	55310	В	25080	110	550	
24942	55311	A	25081	657	805	RRRAALPERSGPGLDHRRVRH/
24943	33311	A	23001	037	1803	GCHVLPTPVTLVKRRKVSRVD
						AQWKSSV
24944	55312	A	25082	756	938	AQWK33V
24945	55313	A	25082	781	1257	
24946	55314	В	25083	1	2727	
24947	55315	A	25085	1	2286	
24948	55316	A	25085	1161	2024	VRSAVWPCLQRDPDCHHNRCG
24740	155510		23000	1101	2024	TGGTSRPGPARNPRIEPETCVG\
						RIRNLGVLLYDADAMERAAST
		İ				ENEKDLYQRQLDVFLDPNDPK
						VIEQAIKDGIPLSVIEAAQQSPV
						YKMAMEWKLALPLHPEYRTLP
						MVWYVPPLSPIQSAADAGELGS
						NGILPDVESLRIPVQYLANLLTA
						GDTKPVLRALKRMLAMRHYK
						RAETVDGKVDTRALEEVGLTE
						AQAQEMYRYLAIANYEDRFVV
						PSSHRELAREAFPEKNGCGLPF
						GDGCHGSDTKFNLFNSRRIDAI
						D\KTEPHP
24949	55317	A	25087	664	1065	VAPEPHHGRKQLCREGLGVFH
24747	ا ادودا	^	23001	1007	1003	PTHHITHHLGVSLSLLITIFDAQS
						VHGPDDGCQGLDSVAVDNRLV
						LFHVFSGEAIFMDDLHLLHNGA
						FS*FSSPEQE*F/PRLWRR*CHPL
	<u> </u>	<u></u>	<u> </u>		<u> </u>	*GFSQSPCSARGRLSPLRSEYIP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24950	55318	Α	25088	434	1663	PAGAFPDIANDFGEKSLLMPGG
1,753						AVINGDF\NNVLPVDLVDPQQV
						QEFVDHAWYRYPNDQVGRHPF
						DGITDPWYNPGDVKGSDTNIQ
						QLNEQERYSWIKAPRWRGNAM
		•				EVGPLARTLIAYHKGDAATVES
						VDRMMSALNLPLSGIQSTLGRI
						LCRAHEAQWAADAIENNYSRN
1						PSQGYSTVPRSPHPKVDPILTKP
						SGPAGPEMTRKQTQREDRPRSR
				•		PSMTTSPTSNLKPSVPAFKGVG
						YLDSLDRIGAADYQPTEQDILR
						TRVKTTGIVETHFTFKNLHFRT
						EQASVHACYCRLFDVEGQRSE
						RKKWIHCFEDVTAIIFCVALSG
						YDQVLHEDETTVLSTRIVDGHR
						YSDHSTIACPAFGTYTLLELKEL
						ALSCSTLLHIPHQRSPAGSFLAD
ļ						NLNCTQAAVIPEFGGF
24951	55319	Α	25089	1	1247	MTFGGDQIFESLVYRSAFRHVY
		1				SRGSPWYLHTNSDLSFVESKKE
						LIAEHILETFPWNLKGLTEIPWG
						DASGESGAVGLGVLAAVHYHP
						QRQSLMEKLALNKDAVVLVIS
						TEGDTDQVIERLESDAVLRYGI
						EDVVTNLDVLERMQPSESLLRA
		İ				VLHTKHLMNPEVLAAARRIVC
		İ				QVVEEIMARLAKEVRQAFSGV
						RDRRRRSFIPLARNFDFKSTLRA
						NLQHWHPQHGKLYIESPRFNSR
		1				IKRQSEQWQLVLLVDQSGSMV
						DSVIHSAVMAACLWQL\PGIRT
						HLVAFDTSVVDLTADVADPVE
						LLMKVQLGGGTNIASAGEYGR
1]			QLIEQPAKSVIILVSDFYEGGSSS
		1	1			LLTHQVKKCVQSGIKVLGLGA
						LDSTATPCYDRDTAQALGNVG
						AQI\AALMPGELGSLAWENLLA

SEQ ID		Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24952	55320	Α	25090	1	1691	MGAYLIRRLLLVIPTLWAIITINF
						FIVQIAPGGPVDQAIAAIEFGNA
						GVLPGAGGEGVRASHAQTGVG
						NISDSNYRGGRGLDPEVIAEITH
						RYGFDKPIHERYFKMLWDYIRF
						DFGDSLFRSASVLTLIKDSLPVS
						ITLGLCWYFVCRACVVTHALSL
			!			WQSASIEVPRTSATAKARKTEP
						GRQTKRKVRSSQTVAARQRIAT
						LPHSMTVCNPGLFHSQMADAL
						AHRYYGFNIAEPWDNGSEAML
						QRDIGLKSESRGLMAGKRCSCL
						KGECGWSLDMQARVSTCFYVR
						LLCGTELEDHRICHDTCDNKCG
						PQRRYVIKFRELCLVNSTVTLV
						DQEYELTVTDPELYDGSSQALA
						GISDLSSIYATCDPGYSCTDRVT
						LVDVRKRQSKTGPYKEIGRYGI
						DRNRSPLNPGFRGKPDLMPSQC
						IACGACACACPANALTIQTDDQ
						QNSRTWQLYMGRCIY/CDGRCE
						EVCPTRAIQ\LTNNFVLTVTNKA
						DLYTRATFHLQRCSRCERPFAP
						QKTIALAAELLAQQQNAPQNR
						EMLWAQASVCPECKQRATLIN
						DDTDVLLVAKEQL
24953	55321	A	25091	1	866	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		•		sequence		
24954	55322	A	25092	338	2388	CVQEPLITVSWRLFAIPAGMKF
						SLFLRCLFCFHLAARYLVLLCQ
						LH/SQGIKVLDFTGVQSGPSCTQ
}		ļ				MLAWFGADVIKIERPGVGDVT
						RHQLRDIPDIDALYFTMLNSNK
						RSIELNTKTAEGKEVMEKLIRE
ŀ]				ADILVENFHPGAIDHMGFTWEH
		1				IQEINPRLIFGSIKGFDECSPYVN
						VKAYENVAQAAGGAASTTGF
						WDGPPLVSAAALGDSNTGMHL
		ŀ				LIGLLAALLHRELNMTVAEIVE
						REEWAGFRARETAALEAVTAP
		ļ				STVIATGGGIILTEFNRHFMQNN
						GIVVYLCAPVSVLEDFRQRTME
						VLRLAFLSSGILEFFTSLSIALVA
						VYFGFSYLGELDFGHYDTGVTL
		l				AAGFLALILAPEFFQPLRDLGTF
		ŀ				YHAKAQAVGAADSLKTFMETP
						LAHPORGEAELASTDPVTIEAE
						ELFITSPEGKTLAGPLNFTLPAG
l						QRAVLVGRSGSGSRYCPYINHR
						NVRLGPIVTDVPWENSGDKSLP
						EATAQVISSGSGATKVEDGLGD
						LNKPVSNQNLVTGIDTPVYNAP
						SAGSAPFGVLADNMRYPILHKL
						KDRLNQTWYQIRIGDRLAYISA
						LDAQPDNGLSVLTYHHILRDEE
						NTRFRHTSTTTSVRAFNNOMA
						WLRDRGYATLSMVQLEGYVK
1						NKINLPARAVVITFDDGLKSVS
	i					RYAYPVLKQYGMKATAFIVTT
24955	55323	Α	25093	1810	2399	STFRNSDDEPYIVRPVAVAWRD
						YVPQPARNGLSNFTGNLEEPAV
						MVNYFLQGDPYQGMVHFTRFF
						HQHPSGLS*WVAGNIFQILCAN
						QPVRKRTRDNVQLLHSRGQRG
						VFRCSRRVLTGLVDRFGRTQTF
ļ						HREAAGEFSGEITGVTDGAWR
		l				HFRLVLTTQAQRAEEARQQAIS
						GGTEPSAFPDTLPVDTEYVMNF
24956	55324	A	25094	1	577	MPVSTAVATVIKTKQVEFQLQ
						VGVPLYFRLRANPIKTILDNQK
		1				RLDSKGNIKRCRVPLIKEAEQIA
			1			WLQRKLGNAARVEDVHPISER
						PQYFSGDGKSGKIQTVCFEVIG
						CREEPDAEECHGDREQRRVFIR
						EDGFFVTKDLYPNRRA\GIISTT
		1				AVISPSQPPIIAPRVAQSSEPRSA
						AHALARAIRQSTTV
L	<u> </u>		<u> </u>	11	L	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24957	55325	Α	25095	51	407	TCPIRAQRVETLYDRAYREVFG
				-		WNPRGPTGRPNARHTG*SKEG
		İ				GRTEADETDAADSGQRGMEQR
						SEMDRKPTGTTGQRSEKPRRTL
						ECLALHETRIFLPQRKETHSSDA
						HDMPGPPML
24958	55326	Ā	25096	3047	4131	AHSGQMYMPLSSCIRSCILGSV
		İ				VMTCGFPQKSAGQKRQKTADC
						RKRPQLYTKSLSLS/AVKAILAK
		l				GYDPVKWRKKDKVLDAVLKE
						LESGKYSDGDKHAFDQMLHSI
		l				GKQGGDPYLVMADFAAYVEA
						QKQVDVLYRDQEAWTRAAILN
		l				TARCGSSMESKRLDNAALAAGI
			1			SPNYINAHGKPQSISAETKRRLL
				•		DAMHQRTATKVAVTPVPNVM
						VYTSGKKMPMVVEGSGEYSW
						LLTTEEGTQYKGHVTGGKAFN
						LPTKLPEGYHTLTLTQDDQRAH
						CRVIVAPKRCYEPQALLNKPKL
	}	l				WGACVQLYTLRSEKNWGIGDF
	1	į				GDLKAMLVDVAKRGGSFIGLN
						PIHALYPAIRRAPAHTARLLAV
24959	55327	A	25097	524	697	AANWWWKSRRNWR*KMTAM
		\mathbf{I}				LDRIISHIIRTVRMSGSVAVTRAI
						AVPGLLLLIIATA
24960	55328	Α	25098	1	1938	
24961	55329	Α	25099	33	226	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24962	55330	A	25100		2314	MDRAGDGPIRPLSGPTDVYGDT VYLRDPGPNHGKTTNGPLRFVP LLPFGQQVFPRVTPNFWNPVSS AALPARYMQTIENAAVWAQIG DKMVTVGNIRAGQIIAVEPTAA SYYAFNCGFGKAFIDKGHLEPV QGRQKVEDGLGDLYKPLSNQN LVTWKDTPVYNAPSAGSAPFG VLADNLRYPILHKLKDRLNQT WYQIRIGDRLAYISALDAQPDN GLSVLTYHHILRDEENTRFRHT STTTSVRAFNNQMAWARVDRG YATLSMVQLEGYVKNKINNRA TEREELRVSKITVLILGVIAIILG VLFENQNIAFMVGLAFAIAASC NFPIILLSMYWSKLTTRGAMMG GWLGLITAVVLMILGPTIWVQI LGHEKAIFPYEYPALFSITVAFL GIWFFSATDNSAEGAHLRPIRR KKVYRFNYLRSDGPYQGWVSE RLLILRAISPGCSKLVHFPTLFDS LYRTLVKAGEKSGLLAPVLEKL ADYNENRQKIRSKLIQSLIYPC MLTTVAIGVVIILLTAVVPKITE QFVHMKQQLPLSTRILLGLSDT LQRTGPTLLATVFIVAVGFWL WLKRGNNRHRFHAMLLRVALI GPLICAINSARYLRTLSILQSSG VPLLDGMNLSTESLNNLEIRQR LANAAENVRQGNSIHLSLE/QT/ AIFPPMMLYMVASGEKSGQLG TLMGAQSHWECATVNAASRIR
24963	55331	A	25101	20	825	GFPRSRSCYASCTACRTHTYSA EK/QLTRALAKLARATSNEKLS QAFHAHLEETHGQIERIDQVVE SESNLKIKRMKCVAMEGLIEEA NEVIESTEKNEVRDAALIAAAQ KVEHYEIASYGTLATLAEQLGY RKAAKLLKETLEEEKATDIKLT DLAINNSFYKEDIFMNRIEHYH DWLRDAHAMEKQAESMLESM ASRIDNYPELRARIEQHLSETKN QIVQLETILDRNDISRSVIKDSM SKMAALGQSTADTTKNSTHRQ SNTRQGN
24964	55332	A	25102	2	269	GIIGLHLQQQEAVAVAIVRGAT RMLFATLVAVAAGERHYQRW ADC*CAAAG*NVVTVESRTAA ASSHYVGVSRQSHITAVISAPV DVPW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	1
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
24965	55333	Α	25103	607	727	RQAVYRG**TAGQRANLLLLR
						RHSACALAAGESQSSCPAG
24966	55334	Α	25104	465	574	
24967	55335	Α	25105	3	636	AHTSGFGDKESEKVSPQRKLHA
						MSRTFFWEN\LRCHGNLGSPTY
						AFQISAIDRVNFALVVGLHLRH
						DYRNEKLGRSGRHYQAPVGNR
						SSADGMHRDPCSQLDICCILLG
		1				AGSIYGLYRYIEPQLPDVATLK
				ļ		DVRLQIPMQIYSADGELIAQYG
		l				EKRRIPVTDGPVMWFPFMIITTC
						VKGNFALNNQFREDMLNYNTE
						GIYGKNVNFENNKQT
24968	55336	Α	25106	434	1205	
24969	55337	Α	25107	368	532	
24970	55338	Α	25108	722	934	
24971 55339	Α	25109	82	420	ARADPHRAHTAGVNGVNARLR	
					IFNADTCLRRHAQPCTGGEKDF	
		1				RVRFRVFKLGSIRAEGEKLAQL
						QRR*NRRRIQGDRSQPNRD/RA
						VPEDLPSKERMPGRTALTVNSR
						SEWT
24972	55340	Α	25110	618	788	WYPCCRNWRYLAGGDSGFCR
						GERA*R*IASQSGVT*AVATVV
						FPSVLAGLRITGHS
24973	55341	A	25111	186	1198	QKTAVSTSITALTRWGS/SRA/G
						KRGAVLRSRVTRGKYHYPSSW
	ļ	l				RETSSSVQNAPLMRQIKEVFLAI
						RIEQLLTKDEILELYLNKIYLGY
						RAYGVGAAAQVYFGKTVDQL
						TLNEMAVIAGLPKAPSTFNPLY
						SMDRAVARRNVVLSRMLDEG
						YITQQQFDQTRTEAINANYHAP
	İ	1				EIAFSAPYLSEMVRQEMYNRY
						GESAYEDGYRIYTTITRKVQQA
						AQQAVRNNVLDYDMRHAIAA
						RHYVLWKPTANIRARYKAQGI
1						ELPAVVPAGPDNPMGHHAIRL
						AAYGGVYLLHGTNADFGIGMR
						VSSGCIRLRDDDIKTLFSQVTPG
						TKVNIINTPIKVSAEPN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24974	55342	Α	25112	1087	3289	RLRSCGAQKNTFCNAAAGCRW
						RTTLSKMGGLLIAADLQDPVQ
						DMEMWQFHPTGIAC/AGVLVT
						E/GCRGEGGYLLNKHGERFMER
						YAPNAKDLAGRDVVARSIMIEI
						REGRGCDGPWGPHAKLKLDHL
						GKEVLESRLPGILELSRTFAHVD
						PVKEPIPVIPTCHYMMGGIPTKV
						TGQALTVNEKGEDVVVPGLFA
						VGEIACVSVHGANRLGGNSLL
						DLVVFGSARQVLHLQESIAEQG
						ALRDASESDVEASLDRLNRWN
						NNRNGEDPVAIRKALQECMQH
						NFSVFREGDAMAKGLEQLKVI
						RERLKNARLDATSSEFNTQRVE
		İ				CLELHNLMETAYATAVYATFR
	}					TERRGAHSR\FDFPDRDDENWL
	ŀ			1		CHSLYLPESESMTRRSDYTLEA
						DEGRDMMLLDALIQLKEKDPS
						LSFRRSCREGVCGSDGLNMNG
			:			KNGLACITPISALNQPGKKIVIR
						PLPGLPVIRDLVVDMGQFYAQ
						YEKIKPYLLNNGQNPPAREHLQ
	İ					MPEQREKLDGLYECILCACCST
						SCPSFWWNPDKFIGPGSLLAGY
						RSGLIAGIPKCSARYLSGEKRSV
						AWQQIAAEIGISIDAQFNESLKG
						ISRDESLRRILQHGGKEGDFNSQ
						ERAQLAYRKNLLYVHSLRELT
						VNAVLPGIRSLLADLRAQQISV
						GLASVSLNAPTILAALELREFFT
						FCADASQLKNSKPGPGIFLAGC
24975	55343	Α	25113	47	630	VGWETSFAQIRSRFLRIRFCRAY
						SSTLFVSAANPTT*G/QMVF*CG
						NGAQHKNILLLYRSIHGGFHFQ
						RGHHINTFNKRWRR**NRT*YQ
						RDVRATTGSGGGDRKTHLAGA
						VIRDITHRIERFTRRAGGNHNV
						QMFQVVDGRKCATAISTVLDM
		1				FGDHFGRQKIASCQRWLAKTIR
						TVQQPICKNIVRKPGCHSLA
24976	55344	Α	25114	731	829	
				·	J	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
24977	55345	A	25115	2	3744	RLPFKYPVKVKPLPAPFSKILLN
						SPAIPQLPITMNGSDFSLPEGPM
	1					NRWENIQLTPETRLAPRAYFFS
	1					YDSVAQARTFARETSSLFLPLS
						GQW\NFHFFDHPLQVPEAFTSE
		İ				LMADWGHITVPAMWQMEGHG
			ŀ			KLQYTDEGFPFPIDVPFVPSDNP
	Ì					TGAYQRIFTLSDGWQGKQTLIK
			ł			FDGVETYFEVYVNGQYVGFSK
						GSRLTAEFDISAMVKTGDNLLC
			ŀ			VRVMQWADSTYEKDQDMW.W
ŀ						SAGIFRDVYLVGKHLT
24978	55346	A	25116	1	2643	SAGII RBVI EVGRILLI
24979	55347	A	25117	2499	2935	RSGGVACNCAVSASCMLVTVL
24313	33347	Ι^	23117	2499	2733	PWLSLPV/SVFGLWDGFFASLG
						VTALLAATPA\W*GVKT*CRPG
						RSP/SLTVRLGSVISPMIGGLLLA
						TGGVALLPLLSLPALPPPPQPRE
						HPLKSLLAGFRFLLASPLVGGIA
						LLGGLLTMASAVRV
24980	55348	A	25118	676	1035	LEGGLETMASAVKV
24981	55349	A	25119	1	1842	
24982	55350	A	25120	1	1341	
24983	55351	A	25121	563	1360	PSVLRCRNWVI*SPYCISLPSRV
12.703						SSLPFLVWIPVAR/CTAIGASRE
						AMLGVLVEPMLLLGLWVAAQ
						VAGSTNISNITDTVYHWPLSQSI
						PLVLALCACAFATFIEMGKLPF
						DLAEAEQELQEGPLSEYSGSGF
						GVMKWGISLKQLVVLQMFVG
						VFIPWGQMETFTAGGLLLALVI
						AIVKLVVGVLVIALFENSMARL
		1				RLDITPRDMIRIELDSWEQNGE
		1				AIKRTGQPLLLSLLVRNLLDNA
		ł				VRYSPQGSVVDVTLNADNFIVR
24984	55352	A	25122	382	1424	VLLENLSEPPNQHDIIEILTVQR
21701	33332	1		502	1 2	KEEETALSCRLVLRKLTETEPVI
						IFEGIEAPATLPADEVPVGKDEN
						DNVEVSRWGTPREFDFEVRDH
						VTLGEMHSGLDFAAAVKLTGS
						RFVVMKGQIARMHRALSQFML
						DLHTEQHGYSENYVPYLVNQD
						TLYGTGQLPKFAGDLFHTRPRH
			1			ECFRHIGSLGLATPLVTECMQW
						LFGIPHTLQLDAIIITCWIILNAIC
						-
						VACGLQKGVRIASDVRSYLSFL
						MLGWVF\IVSGASFIMNYFTDS
		1				VGMLLMYLPRMLFYTDPIAKG
						GFPQGWTVFYWAWWVIYAIQ
		1				MSIFLARISRGRTVRELCFGMV
	<u> </u>	<u> </u>	L	<u>L</u>		QEFGCKSSTKIDNADFNQA

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24985	55353	Α	25123	416	610	
24986	55354	A	25124	662	811	AQQLPGMSDWQNSQEQHQMK N*VRLFMRTSRKLMDRLNVLIK LWSPNRT
24987	55355	В	25125	1	3264	
24988	55356	A	25126	489	3256	PRVFSSATRSLVAMRRWVYRV RRIQYRRTTQTAVFHSTHGNYR EGQPVGTLIDDRYKANENVEL VHYAQPLLNEADSLAKVMPSDI PLKQRRWLGLQMLEGDIYSRA YAGEASQHLDAALARLRNEMD DPALHIADARYQCIAAICDVVS NTLTAEPSRFTTAVDKIVLNRFL GLPIFLFVMYLMFLLAINIGGAL QPLFDVGSVALFVHGIQWIGYT LHFPDWLTIFLAQGLGGGINTV LPLVPQIGMMYLFLF
24989	55357	Α	25127	779	910	
24990	55358	A	25128	2203	2665	ACWARISAAVIQRSGMPGVRV CGRIKSCSKAVRCQRHVFATCV WNGRQVTSGAGTWSTIAWYSG VMSSAISSWSRPAIPFSAEA*TIG KSSC/YVGRVEVNEQIEYLIHNP IRTRARAVNFVDNNNRLQAVS KRFFGYEARLRHRAVKCVNHQ QH
24991	55359	Α	25129	241	918	
24992	55360	Α	25130	2142	2646	KGVCGTTNPAKI\QAILQAFHEI FGEGSCHIASVAVESGVPEQPF GSEETRAGARNRVANARRLLP EADFWVAIEAGIDGDSTFSWVV IENASQRGEARSATLPLPAVILE KVREGEALGPVMSRYTGIDEIG RKEGAIGVFTAGKLTRASVYH QAVILALSPFHNAVY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24993	55361	A	25131	473	1765	KAWLMTGIVRHWKGRAVPPA EQLLEHLGNGKSFDSVAQAWD AAMADAKAEDTVLWGVEAFRI NAAVAKDDTQIHTHMCYCEFT DIMDSIAALDADVITIETSRSDM ELLESFEEFDYPNEIGPGVYDIH SPNVPSVEWIEALLKKAAKRIP AERLWVNPDCGLKTRGWPETR AALANMVQAAQNLRRGARAG CAADFAASARLAVGEALTNIA ATQIGDIKRIKLSANWMAAAG HPGEDAGLYEAVKAVGEELCP ALGLTIPVGKDSMSMKTRWQE GNEEREMTSPLSLVISAFARVE DVRHTITPQLSTEDNALLLIDLG KGNNALGATALAQVYRQLGD KPADVRDVAQLKGFYDAIQAL VAQRKLLAYHDRSDGGLLVTL AEMAVLSSLGQGGYFGHMII/D
						SGQYPGKSKTGQSTPDVAAQA RQSWIP
24994	55362	A	25132	602	2563	VVTTLTLVLTAVGSVLLLFLV MKARMHAFLALMVVSMGAGL FSGMPLDKIAATMEKGMGGTL GFLAVVVALGAMFGEILHETG AVDQIAVKMLKSFGHSRAHYA IGLAGLVCALPLFFEVAIVLLIS VAFSMARHTGTNLVKLVIPLFA GVAAAAAFLVPGPAPMLLASQ MNADFGWMILIGLCAAIPGMII AGPLWGNFISRYVELHIPDDISE PHLGEGKMPSFGFSLSLILLPLV LVGLKTIAARFVPEGSTAYEWF EFIGHPFTAILVACLVAIYGLAM RQGMPKDKVMEICGHAL\QPA GIILLVIGAGGVFKQVLVDSGV GPALGEALTGMGLPIAITCFVL AAAVRIIQGSATVACLTAVGLV MPVIEQLNYSKRRGFTGRVEEN FGVCKGPSKYHSQHDAINRQG REASDAHGTLENLPLPLVPQPN AATALAALRASGLEVSENAIRD GIASAILPGRFQIVSESPRVIFDV AHNPHAAEYLTGRMKALPKNG RVLAVIGMLHDKDIAGTLAWL KSVVDDWYCAPLEGPRGATAE QLLEHLGNGKSFDSVAQAWDA AMADAKAEDTVLVCGSFHTVA HVMEVIDARRSGGKLCQMHVN VQDKIDEEINQVHICLCLVLVIV SGCKYVGYSLKCSEHYYSLVR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24995	55363	A	25133	518	1079	TQKETNKRCSPLVGWYPAFRM AHFLASERSCYQKLSN\RKSH\P AVAGMVSGMTVANLL/EHSAG NVFKSGI*LALHLFIDRCF*YCG DGIGLFLGARYSRRGERKSART ISLFAQPGPVVNFRRHDVWQRR CVCLVQLRKAIHDVYFRFFGNG DDLYYDVSWARDGAGKYAKW QDFRTLFTTAHCSSD
24996	55364	A	25134	322	798	AQRAHVVGTVGKFDEDDADIL HHRHNHLAKVFGLRLFLIAELE FIKFRHPLYQLGDAFTKKLFHIL ILVVGGSIFNHVMQQRRHQRFI VEFHLGQNAGN\ATGCVI*GSPL ERVCPS*ASRATRYACRRRLIW SIARPAAKVSACCSAIATSK*RS KGQRVLLGNCHVEVAIREFT
24997	55365	A	25135	440	906	CGFSSLSRLPHSSYSAHHAVAPS VLMSASGRPRWSQWYRWIFRA GVYTGSIWFFICSTVRPHDASQ RRLSSLT/QVSQDFTFQPVNHQL WAGGKPTAGITVGKQ*W*PFIK FTVPGDDSGDGRGQGFLQIAAG KCRAQTFFSFCRAGKHDPCRRT VS
24998	55366	A	25136	1059	1541	TAPLLRPGCRLS*SAAHPAAPA QSTNQCPGDRYAATLPAHHRH TNHG*IADVHQHISATPASAAS YAPGFLKDGAPASERHRETGC GRDRPH*PSLYKLSGILRPYQPA SFPG*QQRAVLSAR*LLPVQCSL HSQRCRRRPHRLHRSAPAPGIR ERRSRR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
24999	55367	A	25137	236	2211	QGALMSEDIFDAIIVGAGLAGS VAALVLAREGAQVLVIERGNS AGAKNVTGGRLYAHSLEHIIPG FADSAPVERLITHEKLAFMTEK SAMTMDYCNGDETSPSQRSYS VLRSKFDAWLMEQAEEAGAQL ITGIRVDNLVQRDGKVVGVEA DGDVIEAKTVILADGVNSILAE KLGMAKRVKPTDVAVGVKELI
						ELPKSVIEDRFQLQGNQGAACL FAGSPTDGLMGGGFLYTNENT LSLGLVCGLHHLHDAKKSVPQ MLEDFKQHPAV\APLIAGGKLV EYSAHVVPEAGINMLPELVGDL HERSLIFVASGPAGNSKETASD KLEEALPTKNWEVPGANWNTP
						GNGIPSVPEKLKGMLSAPNYRR MVLPAPLQILLLQNAKGGELLG AAGGQIAFNLGSAVGAYCGGM MLTLGLAYNYVALPAALLSFA AMSSLLLYGRYKRQQAADTPV LAKPLGQLDNAPFRCENVNLIR
						EEIGFNALDKFKRTTGALLQLQ QALHPALGADLCGSTGFAVLFI SPVRGNTHLRHLVHIFGTDLDL NRHSVRADHRGVQRLIAVRFW NGDIVFHAARTRLVQAVHLAQ HAITGVRIIDDHAESVDVHDRV KTLLFEHHFAVNRIKMLLPTTD
25000	55368	A	25138		1932	AARYSRFLQTPFDFRKNLLDHL
∠3000 <u> </u>	ومحجدا	I ^A	23130	11	1934	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ļ		sequence		
25001	55369	Α	25139	1	1200	MAIPAFGLGTFRLKDDVVISSVI
						TALELGYRAIDTAQIYDNEAAV
						GQAIAESGVPRHELYITTKIWIE
		1				NLSKDKLIPSLKESLQKLRTDY
1		ł				VDLTLIHWPSPNDEVSVEEFMQ
}						ALLEAKKQGLTREIGISNFTIPL
1		l				MEKAIAAVGAENIATNQIELSP
						YLQNRKVVAWAKQHGIHITSY
						MTLAYGKALKDEGIARIAAKH
						NATPAQVILAWAMGGGPVE\W
						RR*QIWRGFSSAS*RHELYITTK
		ŀ				IWIENLSKDKLIPSLKESLQKLR
						TDYVDLTLIHWPSPNDEVSVEE
						FMQALLEAKKQGLTREIGISNF
						TIPLMEKAIAAVGAENIATNQIE
						LSPYLQNRKVVAWAKQHGIHI
						TSYMTLAYGKALKDEGIARIAA
						KHNATPAQVILAWAMGGGPVE
						MAKVADMAGIFVSKLKTFNAG
			}			VKGSTLGASGPQYVMVPKKHA
						DQLRESLASGEIAAVQSTLVAD
						NTPLNSRVYTVRSGDTLSSIASR
						LGVSTKDLQQWNKLRGSKLKP
1						GQSLTIGAGSSAQRLANNSDSIT
						YRVRKGDSLSSIAKRHGVNIKD
ŀ						VMRWNSDTANLQPGDKLTLFV
						KNNNMPDS
25002	55370	A	25140	2237	2404	
25003	55371	Α	25141	307	642	
25004	55372	Α	25142	1449	2084	NAPRCAYY\VDVIAVTMPTTCC
						TLKISPLCRELILTLANRTTTQR
		1				AEPMTRRLIQVLFDELPQQPQQ
						QLHLPVSSHPKIRTMVEMMAK
						GPVEWGALGQWAGFFAMSER
		1				NLARLIVKETGLSFRQWRQQLQ
						LIMALQGLVKGDTVQKVAHTL
						GYDSTTA\FITMLRKPGKTAGTS
						LYHRRYGVSLLSSAWGQVGPP
						RYCRQANSVLSDRFCVLI
25005	55373	Α	25143	981	1103	
25006	55374	Α	25144	222	379	
25007	55375	Α	25145	1	1452	
25008	55376	Α	25146	500	854	
25009	55377	Α	25147	1	1374	
25010	55378	Α	25148	2	167	
25011	55379	Α	25149	781	1047	
25012	55380	Α	25150	1	783	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	İ			sequence		
25013	55381	IA	25151	442	857	LVKNPVKRMEIQQKNLTLFEYL
İ						DWWDVLFLLLESELLFANTWL
		1				AATSESVDDCSGVKPPSGKNGT
						*AMPSWAKASIIASSARCAMLY
						SFCTQTISAILRASATCVGVTLL
						RPICFTRPCCCISASTVRLASIDP
						SAGP
25014	55382	Α	25152	3	4105	
25015	55383	Α	25153	2	269	YKNPYIAAKIQPKTHDTLTPINP
						GRIKLWLMTKRPMWVVPERSN
						*IAARSLG*VGRM**P*QAGAE
						ATMYAGSTPIASATGTIAASAA
		1		1		A
25016	55384	A	25154	1	1370	MCPIEETASSFGGKPLSMVLVIQ
						MFMLLTGALIIILTKTNPASISK
						NEVFRSGMIAIVAVYGIAWMA
1						ETMFAPACYGYYILPTYPSDLA
	1					AIQFDRSGTTHIGRFVINHSFILP
						GLIGVSVSCVFGWIFAAIKRDA
						AAGRAKENVIFHHFPFQSVKAD
	}					IATNPFKRPGGAFIRITQTFRTV
		ŀ				QTFRLSAYRLDFAGDRLRISTPR
						AKMRTAFKKDHLRQRRRCIRQ
						RAPPARHNLVGAVALPATVAG
						VNFTFSNVPLDSSVLSSLLTDFS
						TAVGSIVMLAVIMGLMLAFDM
						GGPVNKVAYAFMLICVAQGVY
						TVVAIAAVGICIPPLGMGLATLI
						GRKNFSAEERETGKAALVMGC
		į				V\GVTEGAIPFAAADPLRVIPSI
						MVGSVGGAVTAALVGAQCYA
						GWGGLIVLPVVEGKLGYIAAV
		ì	Ì			AVGAVVTAVCVNVLKSLARKN
						GSSTDEKEDDLDLDFEIN
25017	55385	Α	25155	1	789	MKIIAGITPADSGTLEIEGNNYV
					ł	RLTPVHAHQLGIYLVPQEPLLFP
					•	SLSIKENILFGLAKKQLSMQKM
						KNLLAALGCQFDLHSLAGSLD
		1				VADRQMVEILRGLMRDSRILIL
						DEPTASLTPAETERLFSRLQELL
		1	1			ATGVGIVFISHKLPEIRQIADRIS
		1				VMRDGTIALSGKTSELSTDDIIQ
					1	AITPAVREKSLSASQKLWLELP
		1				GNRPQHAAGTPVLTLENLTGE
			1			GFRNVSLTLNAGEILGLAG/TEL
						AETLYGLRTLRGGRIML
25018	55386	A	25156	1	1332	
<u> </u>	1	1	1	1	1	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			•	sequence		
25019	55387	ĪA	25157	1594	2220	I MWVNPERGRAENTIIGGNATGI
20019				1.52		GTLNVQDQDSVITVRRLS*SAL
						KPGILVFKLTPAETERLFSRLQE
						LLATGVGIVFISHKLPEIRQIAD
					ļ	RISVMRDGTIAGTGFGDDFGFT
						HPLRQQRLPQHLVSFMRAAVQ
						QIFTLEIQRGVRPGCNVLAFGQ
				'		RGWTPGIVFQQVVELSLKFRIFL
			}			RTDKSFFQLAQSRHQDLWHVH
						AAKLTKIĞVK
25020	55388	A	25158	14	237	KTTSFPAKLFNACRISLLASAE/
						CQSEYFSIFSNMDLADTVMFL*
						GAIRFSDLVNEQIQHTFLIPGETI
						CRLSEVV
25021	55389	Α	25159	1	1506	
25022	55390	Α	25160	158	639	SGC*PGRPSLN/GRLDVLSAWS
	i					VSILRLGGMALEGSIAYIVINFC
						DVKPQRFRGLSVPAASITVVLIQ
						QFVLHRRELRRKLALPAHHLVT
						FTWGNVSAVDETRQWMVIKPS
	:					GVEYDVMTADD\RWWLR*PAV
						RWWKAAKNPLPIHQRIWRSTV
						AMPKLAVLC
25023	55391	Α	25161	2	2886	SVPTIIFFFLPVLRFWRPGIQQA
						KKCHLFATGTQSRRNTLRQRT
						AKGIPQQRMTAKREEISIGILHV
						TPQQRRECRGDNRFTARFRRTP
						WRLLGHCVSAAVTGVLPAVAG
		l				SPLAYSDTDEFYPVAGGTMSQ
						HLPLVAAQPGIWMAEKLSELPS
						AWSVAHYVELTGEVDSPLLAR AVVAGLAQADTLRMRFTEDNG
						EVWQWVDDALTFELPEIIDLRT
		ļ				NIDPHGTAQALMQADLPQDLR
					·	VDSGEPLVFHQTTLGFI
25024	55392	A	25162	1	1659	V D S O D I D V I I Q I I E G I I
25025	55393	В	25163	200	646	
25026	55394	Α	25164	1	3197	MPHRQHGPQMTPSHQRTTINR
						DQREQQPIGTAAPQTRPQSAPY
						CEPHTRRRTLQPHNRGFRTAKY
						TSTQARKYHMARPERSNDSDH
						PVHTRSRWNATQTERHTQHHV
		}				SPPSSLRTLRTNCTSHAHHRYH
						RHAQWHRVGLLDVKPTGVPSN
						TVFSPPKNALWADRVDTSRGR
						TTVEQDNHPNGGNVVGTPSDN
,						NFWLETTGGDPNKEYYHHHHY
						NEDYCRYYPLLIAEPLLFPSLSI
						KENILFGLAKKQLSMQKMK
25027	55395	В	25165	1	2505	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25028	55396	A	25166	159	11744	NSRISGLQQRYLMHIMVTQGGL
23028	33390	^	25100	139	11/44	MSLSIVHTRAALGVNAPPITVE
	ŀ					VHISKGLPGLTMVGLPETTVKE
]					ARDRV/RSAIINSGYEYPAKKITI
						NLAPADLPKEGGRYDLPIAIAL
	1					LAASEQLTANKLDEYELVGEL
	1				İ	ALTGALRGVPGAISSATEAIKSG
	1					RKIIVAKDNEDEVGLINGEGCLI
İ	1					ADHLQAVCAFLEGKHALERPK
	1	ĺ				PTDAVSRALQHDLSDVIGQ\EQ
						GKRVLEITAAAGHNLLLIGPPG
			}			TGKTMLASRINGLLPDLSNEEA
ŀ						LESAAILSLVNAESVQKLWRQR
ŀ			•			PFRSPHHSASLTAMVGGGAIPG
						PGEISLAHNGVLFLDELPEFERR
	1	ŀ				TLDALREPIESGQIHLSRTRAKI
						TYPARFQLVAAMNPSPTGHYQ
						GNHNRCTPEQTLRYLNRLSGPF
					ĺ	LDRFDLSLEIPLPPPGILSKTVVP
						GESSATVKQRVMAARERQFKR
						ONKLNAWLDSPEIROFCKLESE
	1					DAMWLEGTLIHLGLSIRAWOR
						LLKVARTIADIDQSDIITPTYCG
						KADARNSGNVCPSSRALVQR
25029	55397	A	25167	127	503	NRCLLLTLLRCKGRNREEENDA
		`				EAESEKLKNKFNRPSGRLSYGD
	1					RMFDIGVNLTSSQFAKTVMML
						*RARLGLR*TTGLELRELLPLIP
	1					AEKL*/YETDAPYLLPRDLSAKP
						STSRYHCVIEARAWFK
25020	55398	 	25168	3	406	515K11K VIEAKAWEK
25030	122240	Α	23108	J	400	

3331

NO: of p	eptide hod uence	t SEQ ID NO: in USSN 09/540,217	location of first codon for peptide	codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
sequ	uence	09/540,217	codon for peptide	lof peptide sequence	Idelation \=nossible nucleotide incertion)
		•			deterion, (-possible nucleotide miser non)
			sequence		
25031 553	399 A	25169	1	1252	MFDIGVNLTSSQFAKDRDDVV
23031	,,,	2310)		1232	ACAFDAGVNGLLITGTNLRESQ
					QAQKLARQYSSCWSTAGVHSH
					DSSQWQAATEEAIIELAAQPEV
					VAIGECGLDFNRNFSTPEEQER
					AFVAQLRIGADLNMPVFMHCR
i					DAHERFMTLLEPQMVENYETLI
					FEAHSTDYQTPQSLRQLVIDHF
		1			AILKVGPALTFALREALFSLAAI
		:			EEELVPAKACSGLRQVLEDVM
					LDRPEYWQSHYHGDGNARRLA
!		ļ			RGYSYSDRVRYYWPDSQIDDA
					FAHLVRNLADSPIPLPLISQYLP
					LQYVKVRSGELQPTPRELIINHI
					QDILAHTTQPVKANKQNKEEH
1					AMPNIVLSRIDERLIHGQVGVQ
					WVGFAGANLVLVANDEVAED
	ļ				PVQQNLMEMVLAEGIAVRFWT
					LQKVIDNIHRAADRQKILLVCK
					T*WKWYWQKGSPYVSGRCKK
	ļ				LSTTFIAPPIDRKSCWFVKHPPIS
25032 554	100 A	25170	2	319	YSSVFSLSASASFSSSRFRPLPT*
	,,,,	25170	[KREKKTPISNRQYIGIANSVCEK
	j				TSGGVSNIPTTNAPTSTYGRFLR
					KSSGEVIPIQHSSTIATGTSKETP
					NAINSAITKLK
25033 554	101 A	25171	1	1011	MIPHPKLEGDRSTQALPPTPVIR
					VTERRNLNWVGTTIGFVHTGK
		ľ			PLSFVYDMADIIKFDTVVPKAF
					EIARRNPGEPDREVRLACRDIFR
					SSKTLAKLIPLIEDVLAAGEIQPP
	İ				APPEDAQPVAIPLPVSLGDAGH
					RRRRSGRVSEVSWRSGVMSFR
					RASGDKPQPKPKVMPEHAECPP
					AARRGQMMSICPCFALKIDIAD
					NKFFNGETSPLFSQSQAKLARQ
					FHQKIAGYRPTPLCALDDLANL
		1			FGVKKILVKDESKRFGLNAFK
					MLGAPEKCHRRKNDF*RRSDRI
					VLIRL*REFSSHQKGLRDRPAH
					KAVLGDNQLFSGGTGAPVWPG
					FAKRAVMF/TPLKNLLSAISIFN
					AKHGHILIIWPRLAAGGHSACS
					GITFGFGCGLSPLARRKLMTPE
					RQLTSDTRPDRLLRWPASPSET
					GSGMATGCASSGGAGGCISPA
				·	ASTSSISGINLANVLLLRKISLH
]]					AKRTSRSGSPGLRRAISKAFGTT
		1			VSNLMMSAIS
	1	ŀ		l .	
25034 554	102 A	25172	1	510	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25036	55404	A	25174	704	1069	RLWQADCKENAG\GDYYWTFF PQPTFVSTQKYYCHVDNSCYM NFDFSAPEYHAHWRYGLLMVG ESQHGLGANAIQASQCFKAAN QPLGADATFLQQIKGEIICFGLFI TGVFSIDSAFCDIT
25037	55405	A	25175	1	639	MARVWLCDFIPYGYLPTLNAM PESTRKQIMPWTRLSGSLHTWN RTPNRRIGRYPSGLPPDSANRPR REPDACRSLHSPAKYRGNPNRD RLDHQQNGLPARGKDTPRSNK PSISQWTNTKPQPRHQPRGKKG HKSPAPEMPKPPQATSSTREQT KYGAAELWRSPWKTRYIELKA RGPMACVTISLNVCCAHLVRL VMVTLKQTDPIRNLGEMPSKSQ TKKAREVHLHSLHLQELAQEQ EPPARKRKTQWAVSERK
25038	55406	A	25176	82	356	AQCEEYRVPQTLKRNPKQCFDI SIRGGSQPCGIFSTPVRNTLQNM GQMGWLVAPG*WLWREIRKH NRWCACPRKPGRAGISMALRW GSGHA

NO: of peptide sequence hod in USSN location of first codon for last amino acid of peptide sequence sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25039 55407 A 25177 1 2635	MNKSGKYLVWTVLSIMGAFAL GYIALNRGEQINALWIVVASVC IYLIAYRFYGLYIAKNVLAVDP TRMTPAVRHNDGLDYVPTDKK VLFGHHFAAIAGAGPLVGPVLA AQMGYLPGMIWLLAGVVLAG AVQDFMVLFVSTRRDGRSLGE LVKEEMGPTAGVIALVACFMI MVIILAVLAMIVVKALTHSPWG TYTVAFTIPLALFMGIYLRYLRP GRIGEVSVIGLVFLIFAIISGGWV AESPTWAPYFDFTGVQLTWML RLINRSIMMDFSLTEEQELLLAS IRELITTNFPEEYFRTCDQNGTY PREFMRALADNGISMLGVPEEF GGIPADYVTQMLALMEVSKCG APAFLITNGQCIHSMRRFGSAE QLRKTAESTLETGDPAYALALT EPGAGSDNNSATTTYTRKNGK VYINGQKTFITGAKEYPYMLVL ARDPQPKDPKKAFTLWWVDSS KPGIKINPLHKIGWHMLSTCEV YLDNV*TSVWRTCACPALRRA TQRYRRQSRAGNLRTSGEAIRR DMEWTSLRSE\DWEKGDTIKQC ISAATSCVYGVTGEGILEGGDA QILREPLPGTKLGLLNWPVFDA LESRSTRERDGKPGGEICGETA NILIRGPENRPLRRDPPGKP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	<u> </u>
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25040	55408	A	25178	216	1829	TVCRCHFVTTKHIGRERNQRAR
						QCLVGKTTDTQQHNCDIRVGE
						QADHTRANHQHCTQRYDHLTG
		1				NDQVHTKPTLEQRRQVTTEDT
						TEVSKQHRHPGEHRDLFQRTLN
İ					·	ISADDORRLLLELQNDNLNHNR
		ļ				IWLRLAAQPEDHIYGCGEQFSY
						FDLRGKPFPLWTSEQGVGRNK
						QTYVTWQADCKENAGGDYYW
			}			TFFPQPTFVSTQKYYCHVDNSC
		İ				YMNFDFSAPEYHELALWEDKA
						TLRFECADTYISLLEKLTALLGR
						QPELPDWIYDGVTLGIQGGTEV
						CQKKLDTMRNAGVKVNGIWA
						QDWSGIRMTSFGKRVMWNWK
						WNSENYPQLDSRIKQWNQEGV
						QFLAYINPYVASDKDLCEEAAQ
		İ				HGYLAKDASGGDYLVEFGEFY
						GGVVDLTNPEAYAWFKEVIKK
						NMIELGCGGWMADFGEYLPTD
		1				TYLHNGVSAEIMHNAWPALW
						AKCNYEALEETGKLGEILFFMR
						AGST/GDIGG\YTTLFEMKRSKE
			1			LVLRWCDFSAFTPMMRTHEGN
						RPGEHWAF/DGDAKHRHLAVY
25041	55409	A	25179	277	488	
25042	55410	В	25180	260	1500	
25043	55411	Α	25181	1	764	MQEWGRYTILSGCCNSALKGD
						VCLLYGFRVAGRRQASE*TPGA
						YNRVPSSKK*GFQLVLLPFSAN
						GKSPAY*RFSKSFAEDGEKDAG
		1				FPHPYAEAGYDNGGRRSGAGT
						LLSR*I*TGAGRGAWRV*RLTG
						E*MAGKRT*VTASGYSQR*IMV
						FLWSLYRSYRL/GRVRQHNGPR
						YLPVLARNWKMSAWVAAAW
						QGLTDMKRKTMKIRSGS\IVILA
						SGYAATAA*PLSGDRIFLP*PGK
						TG*RHGGTPSCAGFTGDY
25044	55412	В	25182	1	3117	
25045	55413	В	25183	270	388	
25046	55414	A	25184	2154	2279	DDNGC AD # CD CD VD CT OC VD CT
25047	55415	Α	25185	614	623	RPNSGAR*GRGDKRSTQSVPET
		1				VRLLFCAGTFDQQPGNARWDD
						QYRCIRSGIVGVRAVLLGGDIL
L	<u> </u>	<u>l</u>		<u> </u>		DTQPLPVELAETLGKSAE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25048	55416	A	25186	1208	2813	CYGVAWPFDPTLKFEFWRYFT
1						HALMHFSLMHILFNLLWWWY
1						LGGAVEKRLGSGKLIVITLISAL
}		1				LSGYVQQKFSGPWFGGLSGVV
		ŀ				YALMGYVWLRGERDPQSGIYL
				ļ		RRGVIIFAPIWIVRRWFEMTPTQ
						WSNYFFENLFKYEWVQTRSPA
	1	ŀ				GAIQFEAVDAPEIIPDPFDPSKK
						RKPTMLVTDLTLRFDPEFEKISR
						RFLNDPQAFNEAFARAWFKLT
						HRDMGPKSRYIGPEVPKEDLIW
						QDPLPQPIYNPTEQDII\DLKFAI
						ADSGLSVSELVSVAWASASTFR
						GGDKRGGANGARLAL\MPQTR
						TGDVTRRQPIRAL\PVLE\KIQKE
						SGKASLADIIVLP\GLFVVEKSA
						SAAGLSIHVPFAPGRVDARQDQ
						\TAIGMFELLEPIADGFRNYRAR
						LDVSTTESLLIDKAQQLTLTAPE
•						MTALVGGMRVLGANFDGSKN
						GVFTDRVGVLSNDFFVNLLDM
						RYEWKATDESKELFEGRDRET
						GEVKFTASRADLVFGSNSVLRA
					ł	VAEVYASSDAHEKFVKDFVAA
						WVKVMNLDRFDLL
25049	55417	A	25187	1520	1960	PVPLNFGWQRSTEVLICHVNSP
						STAAMTISPWRR**RRRTKQLS
	1					APLLLGVSAIGW/LTIILVAFMA
						WLLAKT/AFGRSFYATGDNLQG
						AR/QLGVRTEAIRIVAFSLNAER
		1				DFDDLRDSGPLIAMILFIMPTLS
						SISSRRLNPGVPSEI
25050	55418	Α	25188	1155	1778	SASGGVMLKFIQNNREITALLA
		1				VVLLFVLPGFLDRQYLSVQTLT
						MVYSSAQILILLAMGATLVMLT
						RNIDVSVGSITGMCAVLLGMLL
						NAGYSLPVACVATLLLGLLAGF
						FNGVLVAWLK/IPAIVATLGT\L
						YRGLMSLWTGGHWFEGYPRIE
}						KPSPPVAGVHHWCVTQIGGLRP
						AVAKRVGPDLPGDNKGAKGVL
			1			NTLDNYGVDGKCV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25051	55419	A	25189	1	2227	I MVTIAGIILGGLALVGLITYFGK
25051	33419		2310)			WTYLWKEWLTSVDHKRLGIM
						YIIVAIVMLLRGFADAIMMRSQ
						QALASAGEAGFLPPHHYDQIFT
ļ						AHGVIMIFFVAMPFVIGLMNLV
						VPLQIGARDVAFPFLNNLSFWF
						TVVGVILVNVSLGVGEFAQTG
						WLAYPPLSGIEYSPGVGVDYWI
						WSLQLSGIAVAHIAAQNVAVLL
						ISSDLEEIELMADRVYVMHQGE
						ITHSALTERDINVETIMRVAFGD
						SQRGVMLKFIQNNREITALLAV
						VLLFVLPGFLDRQYLSVQTLTM
						VYSSAQILILLAMGATLVMLTR
						NIDVSVGSITGMCAVLLGMLLN
						AGYSLPVACVATLLLGLLAGFF
						NGVLVAWLKIPAIV\ATLGTLG\
						LYRSIMLLWTGGQWIEGLPAEL
						KQLSAPLLLGVSAIGWLTIILVA
						FMAWLLAKTAFGRSFYATGDN
						LQGARQLGVRTEAIRIVAFSLN
İ		İ				GCMAALAGIVFASQIGFIPNQT
						GTGLEMKAIAACVLGGISLLGG
						SGAIIGAVLGAWFLTQIDSVLV
						LLRIPAWWNDFIAGLVLLAVLV
						FDGRLRCALERNLRRQKYARF
						MTPPPSVKPASSATSDFICIGIVA
		l				LPLTMVIVSGGIDISFGSTIGLCA
						IALGVLFQSGVPMPLAILLTLLL
						GALCGLINAGLIIYTKVNPLVIT
						LGTLYLFAGSALMLSEEQKNTK
						KTRQREDKKKEKKKQRKREEK
25052	55420	Α	25190	1055	1206	SFALFSSSSPRSRP*FASTKS*TL
						TTGQVLPSTNVRFLTGNWGPPV
		<u>L</u>				VATG
25053	55421	В	25191	1	1386	
25054	55422	Α	25192	1	449	MQDPLLALLEDYNKGDLEKQV
						PPAQSGPQPGKAGRDRPIVIML
						DPGHGGEDSGAVGKYKTREKD
		l				VVLQIARRLRSLIEKEGNMKVY
						MTRNEDIFIPLQVRV/AKAQKQ
		1				RADLFVSIHADAFTSRQPSGSSV
		ļ	0.5100	1506	1041	FALSTKGGMCSYRGSGCLQ
25055	55423	Α	25193	1536	1941	STSNQNSTALCRRRGLVHCIDG
						ANDDDSVMVWPSGSGRPWSAE
						PGAPQR\YAQLVVEDVELDLLH
						FIVFGDDVMLNVVLQGQAFML
						ALGLVTNVGVLAHAHHHALVS
1						GVPNDGGGTWVGGRCVQQSQ
L	<u></u>	<u> </u>		<u> </u>	<u> </u>	LCTCWSHCQ

NO:				Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
1,.0.	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25056	55424	A	25194	240	855	SRAGYAPAAAQKVASPYVRRE
						R*NQSD\PAVLTGIGERGK*LLS
						RDFFIAPLAGMIVEKRGAVHLA
			}			RWSVPVERKGQWQPAGLWAQ
						FFLADIVCPAATALPDTTAEDQ
						HIDHPAVVHVHVIPVVNTCAED
						NHRAPMRFMGGIGKFTGDGFNI
		l				LARHPGNLLTPGWGVRFDFSVI
						FRTVFIFQPAIEAVIRQYQIINAD
						HRTGVAID
25057	55425	A	25195	840	1157	QYAPTAQPARPADPFALPTVQA
2000,	55 125	ļ · ·				RLTPFCYLVAKGDWCVYRRSY
						SLWHSVASPRVRQSPRLGY*GY
						TANSPGILLAPLSLRGEMFLPOD
		ŀ				APKSVPPYKRGKSVAIN
25058	55426	A	25196	1076	1339	LVCVASMPVEISTDASASSGVI
23030	33 120	l'`	23170	10,0		VISSAMSGSWSAETKRRLAMV*
						PEPLHLWAISIPTTSGRFTSSLIS
						PFPAR*YSPARYIPRVWRV
25059	55427	A	25197	2	118	THE TOTAL CONTROL OF THE TOTAL
	55428	Α	25198	1809	3145	ARHKQHAYGYRYRQSPRCYGV
25000	33 120	1	23170	1005		SGKKRGLRYYGSWLAISGSSRI
						TR/LLCMYLRRFFIGVIGADIAN
						MGISAGAMWLLSVSQVSLAAV
		l				SQVVAVRVWPASSYTRVTVES
						NRQLKYKQFALSNPERVVVDIE
						DVNLNSVLKGMAAQIRADDPFI
						KSARVGQFDPQTVRMVFELKP
						NVKPQLFALAPVAGFKERLVM
						DLYPANAQDMQDPLLALLEDY
						NKGDLEKQVPPAQSGPQPGKA
						GRDRPIVIMLDPGHGGEDSGAV
		l				GKYKTREKDVVLQIARRLRSLI
		l				EKEGNMKVYMTRNEDIFIPLQV
		l				RVAKAQKQRADLFVSIHADAF
		l				TSRQPSGSSVFALSIQRGARPVG
						DRYVDHTMFDMVQSLTIADSL
						KFGKAVLNKLGKINKLHKNQV
						EQAGFAVLKAPDIPSILVETAFI
						SNVEEERPNGQPGHPLDPATTM
						GTLIDCAHADSVQ
25061	55429	A	25199	1	277	G I BIDCAHAD3 VQ
	55430	A	25200	902	1006	
	55431	A	25201	2	1265	
	55432	A	25202	409	525	
	55433	A	25203	91	431	NHKPGNIDVARRIQRGFAGDQI
			•			GHLRPVERQCSPDKRRFIAADG
						REIRGKQRAGHIFQLLSRCLLQI
						LNHCQRRAAHFRFQLSNQRHQ
						QLLPV/HYHAAEREYPAGACLV
						RWLL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25066	55434	Α	25204	3	71	
25067	55435	A	25205	1	1212	
25068	55436	A	25206	1	2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVWDIVWNATAAFIAVIII SLLLDESGFFEWAALHVLRWG YGPGRLPFNRIGLIRRITRRIRQR LLFGLVTFILLLNRSQNPAQDIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQGQCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQSGLKRVYHSPG
25069	55437	A	25207	5	402	APDIREFTRDAIP EIFSVVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF /RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI
25070	55438	A	25208	48	219	PETCGHLWAYVWPSCAAV\GL YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25071	55439	A	25209	1	912	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25072	55440	A	25210	<u>I</u>	1857	MRVCARACVRTRTRMCVYAH
23012	33440	^	23210	1	1657	TCVCVRTYAYVRVRVRVHVRA
						RVRVCAYARTRVRNSLSILPFIQ
						LTLATPIHHIHQEEFNIRGIVPVL
						RRVKPDLAIGIDITPSCDTPDLH
						DYSEVRINQGVGITCLNYHGRG
						TLAGLITPPRLIRMLEQTALEHN
						IPVQREVAPGVITETGYIQLFLP
						GWEIGFSPLALLLAFLCSTSPGF
						GDPDGLGVIAYQDTVRPNAAT
						AISELNALAVKGVILTGDNPRA
						AAAIAGELGLEFKAGLLPEDKV
						KAVTELNQHAPLAMVGDGIND
						APAMKAAAIGIAMGSGTDVAL
						ETADAALTHNHLRGLVQMIEL
						ARATHANIRQNITIALGLKGIFL
						VTTLDDRVVAGSAGRYGGDGA
						GDSECVKIVAQEIRQTDRNIER
						DRSPRPSGERVRVRGKGGIEAN
						QPLSTAFTNQITIRQSIRLFSNQF
						VFHKGISRVVAGSSAIISNVSPG
					}	CILRTPNCRRGFPISCTGEGKAA
					Ì	YGWQRDGGHAEYLLAEEKDLI
						LLPDALSYEDGAFISCGVGTAY
	1					EGILRGEVSGSDNVLVVGLGPV
						GMMAMMLAKGRGAKRIIGVD
						MLPERLAMAKQLGVMDHGY*I
1						LPDVY/V*IGVARVSWMNGRID
						SELRTRVRAYAHTRTRARTCTR
			ľ			TRTRTYAYVRTHTHVCAYTHM
						RVRVRTHARAHTR
25073	55441	A	25211	3	1180	SKLGTRRSVVWA*SPSTSPTLW
23073	33	ĺ`.				CSTFSAAGHSSMKRMNEFVDL
		ł				LPAQQRMKGENWYRGTADAV
						TQNLDIIRRYKAEYVVILAGDHI
		İ				YKQDYSRMLIDHVEKGARCTV
		1				ACMPVPIEEASAFGVMAVDEN
						DKIIEFVEKPANPPSMPNDPSKS
						LASMGIYVFDADYLYELLEEDD
						RDENSSHDFGKDLIPKITEAGLA
		ļ				YAHPFPLSCVQSDPDAEPYLAR
						CGYAGNFMESEPRSGLIRVSCM
		1				PAGPPLPLPAARSEAPKAAGTV
				1		ASVPSIAPARLRPVPDPVELVLV
		1				AAEFITPGDPTPRLHGSGFIDIR
		ĺ				QIHHQTRSHLEGVKTGIRFLNH
						FSGNPQGGIAHVNGVARFQVK
						QCHQAWGQQYAARLRFQARGI
						SLQIAIHRVDIIHRFDVRQL
25074	55442	Α	25212	16	543	
25075	55443	Α	25213	1	3387	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25076	55444	A	25214	11688	2234	LSVGKTFPVLVPAAFRKVSATG
25070				1.000		AAVPGTPSILALPSYSTTPFGVC
						TSASMNVPVLTLRIRTRVTGEV
			i			AAIKPFSMANAPTPDSILPQLGV
						VSTRCS*TITCANR*STSARGSL
		1				ERLIMATLL/WVAGTFD*SVWF
						GHDTDVVTLYRFHEALCYSVT
						LRTPHRRVLRFKSQHPGELACFI
						SPVA
25077	55445	A	25215	905	4761	PPHNWMPSNATPGIAFVWCAY
						GAI/LPGDAPVPVVDDYRKVVR
						KDTKGLIARWKYFWMSVIALG
			.			VAFALYLAGKDTPATQLVVPFF
İ						KDVMPQLGLFYILLAYFVIVGT
						GNAVNLTDGLDGLAIMPTVFV
						AGGFALVAWATGNMNFASYL
						HIPYLRHAGELVIVCTAIVGAG
						LGFLWFNTYPAQVFMGDVGSL
		E				ALGGALGIIAVLLRQEFLLVIM
		ŀ				GGVFVVETLSVILQVGSFKLRG
						QRIFRMAPIHHHYELKGWP
25078	55446	Α	25216	269	1219	QTRTRRVQLQDLIEYVAIHQW/
						FSDKHPVPFYSCIFDDSITNCYS
						WSISKDGYFIFGGAYPMKDGQT
						RFLTMKDKMSAFQFQFGKTVK
					ł	SEKCTVLFPSRGQDFVCGKDNA
		:				FLIGEAAGFISASSLEGIIYALYS
						TDIPRSVLLKQPDKLNPAYWRA
					:	TRLVCITLFGQIVNTICMAAPDL
		İ				RKWIMLSPVAHKGHHLEWVLH
		1				DMQILPVPRPSGCICSGSSTFFC
						NWGCPYDRPQWQLYPSMCLC
						VHIGPAPVRSEKVESKRAISKV
		l				DQD\$AFRGCCRSGNRNGGRKI
						VAVSLKKVSGAAKPCGHFRST
						RYRVAYSTIIN
25079	55447	Α	25217	l .	1158	
25080	55448	Α	25218	1156	1899	LKLGIRYPQCQRLVTHSLDGISL
						PLHTAH*SQSNSAENTHRAISLK
						AVPPFFTAERRGVNAEEHRNGR
						LINGECRQRFNVLRVANGVRN
						VQFAKARDRNDIASFRQIGFDT
						FQTEVAQHFTDFRVAGFAFAID
						DSDLLVRLHFTALDAANADNA
						NIAVVIELRNLHLERTVKVNVR
						RRNVVNNRLVQRGHVFRHIFV
						VQTRDTVQRRSVNDREVQLLV
						GRVEVNEQIEYYADAFVIMLER
		<u> </u>				LCKVLCCR
25081	55449	Α	25219	1	2583	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25082	55450	A	25220	278	787	TLLSATRQVYALLSTKPAFFSS HSSFSTSSRLISSRAASSMDVAF PIAFSASKTVSIKFFSR*KLLRNS HRPPFMVMRSIIRSPSNVFMAS* FRFVSIPTLRIDAVRRSTIWCSTT ARFSSRADAKFIKNVFQQAIPDS AAKWFFPVPGFPLNAKFVHPVI SSSAMDFA
25083	55451	A	25221	866	1144	
25084	55452	A	25222	19	1203	NWNLTPYASLTGFTADNPEYH LSNGMKSKSVDTRSIYRELGAT LSYNMRLGNGMEVEPWLKAA VRKEFVDDNRVKVNSDGNFVN YLSGRRGIYQAGKDLDRFKNL VLVHAARYAADLSYLPLMQEL EKRYEGKLRIQTVVSRETAAGS LTGRIPALIESGELESTIGLPMN KETSHVMLCGNPQMTRRLIPAS VEVYHDSLC\RKIWHGWEQHIT ARYLVGADGANSMVRRHLYP DHQIRKYVAIQQWFAEKHPVPF YSCIFDNSITNCYSWSISKDGYF IFCGAYPMKDGQTRFTTLKEK MSAFQFQFGKTVKSEKCTVLFP SRWQDFVCGKDNAFLIGEAAG FISASSLEGISYALDSTDILRSAL RKPIRTEQGANGAIRELEKFRPA
25085	55453	В	25223	58	359	
25086	55454	Α	25224	4	329	
25087	55455	Α	25225	1	1008	
25088	55456	A	25226	1	1335	

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25089	55457	A	25227	3	1886	HRLNITAENDCRRLHCSLRDLS
						SLLQAVGRLAEYFIGDVFAARF
						NDALTVVERLVKVTLYGSQIKL
		İ				YNIETAVPSVLKPDLIDVHAQS
						LAGGCRLSAHWLAQYCSEIHR
						QNTQQFVTLISTTMDAITPLIST
						KVQDKLLLSACHLLVSLATTVR
						PVFLISIPAVQKVFNRITDASAL
						RLVDKAQVLVCRALSNILLLPW
						PNLPENEQQWPVRSINHASLISA
						LSRDYRNLK\PSAGAPQRKMPL
						DDTKLIIHQTLQRLRKILWENIS
						G\ESTKSSTDFAYQFGCRESV\Q
						VSLGLFPAF\IHQSDVTDEMLSF
						FLTLFRGLRVQMGVPFTEQIIQT
						FLNMFTREQLAESILHEGSTGC
						RVVEKFLKILQVVVQEPGQVFK
						PFLPSIIALCMEQVYPIIAERPSP
						DVKAELFELLFRTLHHNWRYFF
						KSTVLASVQRGIA\EEQMENEP
						QFSAIMQAFGQSFLQPDIHLFK
	ŀ					QNLF\YL\ETLNTKQKL\YHKK\I
						FR\TAM\LFQFVNVLLQ\VL\VH
						KSHDLL\QE\EIGHRHSYNMASV
						DF\DGFFAAFLPEFL\TSC\DGV\
						DANQKSVLGRNF\KMDRLCPCL
1						PGPAPHSPRMCTGWSTTCGLLT
						DSGNDSLAPWGLWKLLGPCLL
}						PGGTRDFLLVAT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25090	55458	Α	25228	689	3053	VDCRMS/FSYIEKFTDFLRLFVS
		•				VHLRRIESYSQFPVVEFLTLLFK
		l				YTFHQPTHEGYFSCLDIWTLFL
}						DYLTSKIKSRLGDKEAVLNRYE
						DALVLLLTEVLNRIQFRYNQAQ
						\LEEL\DDETLDDDQQTEWQRY
						LRHSLEVVAKVMELLPTHAFST
						LFPVLQDNL\EVYLGLQQFIVTS
	,			}		GSGHRLNITAENDCRRLHCSLR
						DLSSLLQAVGRLAEYFIGDVFA
						AR\FNDALTVVERLVKVTLYGS
1						QIKLYNIETAVPSVLKPDLIDVH
						AQSLAALQAYSHWLAQYCSEV
						HRQNTQQFVTLISTTMDAITPLI
						STKVQDKLLLSACHLLVSLATT
						VRPVFLISIPAVQKVFNRITDAS
						ALRLVDKAQVLVCRALSNILLL
						PWPNLPENEQQWPVRSINHASL
						ISALSRDYRNLKPSAVAPQRKM
						PLDDTKLIIHQTLSVLEDIVENIS
						GESTKSRQICYQSLQESVQVSL
						ALFPAFIHQSDVTDEMLSFFLTL
						FRGLRVQMGVPFTEQIIQTFLN
			ŀ			MFTREQLAESILHEGSTGCRVV
						EKFLKILQVVVQEPGQVFKPFL
						PSIIALCMEQVYPIIAERPSPDVK
						AELFELLFRTLHHNWRYFFKST
						VLASVQRGIAEEQMENEPQFSA
						IMQAFGQSFLQPDIHLFKQNLF
		I				YLETLNTKQKLYHKKIFRTAML
1						FQFVNVLLQVLVHKSHDLLQE
						EIGIAIYNMASVDFDGFFAAFLP
25091	55459	Α	25229	1	853	MISVANEIAEAGFDPQGRTSED
						LLDLAESRVFKIAESRANKDEG
						PKNIADVLDATVARIEQLFQQP
						HDGVTGVNTGYDDLNKKTAG
						LQPSDLIIVAARPSMGKTTFAM
						TLVENAGR\MLQDKP\VLIFSLE
						MPSEQIMMRSLASLSRVDQTKI
						RTGQLDDEDWARISGTMGILLE
						KRNIYIDDSSGLTPTEVRSRARR
ļ		1				I\AREHGGIGLIMIDYLPLMRVP
						ALFDNRTLEIAEISRSLKALAKE
						LNVPVVALSHLNRSLEQRAEER
						PGNSDLGESGSIEQDADLIL
<u> </u>			1	<u> </u>	L	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25092	55460	A	25230	206	1073	VKITSWLMSNSALPGTLKLLAL
23092	33400	^	23230	200	1075	ILKCSTCVRVLPRSELRNLER/Q
						GQLDSVGGFA/YLAEL/SKNTPS
		1				AANISA/YADIVRERAVVREMIS
1					,	V/ANEIAEAGFDPQGRTS/EDLL
		1				DLAESRVFKIAES/RANKDEGR
						NPMFDDRGKRGEPSDLIIVAAR
						PS/MGKTTFAMNLVENAAML/Q
		1				DKPVLIFSQTKI/RTGQLDDEDW
						ARISGT/MGILLEKRNIYIDDSSG
						L/TPTEVRSRARRIAREH/GGIGL
		l				!
						IMIDYLQLMRVP/ALSDNRTLEI
	ì					AEISRSLKHFEKLALICGCRNNG
			2 - 2 2 1		100	TTRYCKSLLA
25093	55461	В	25231	287	483 635	
25094	55462	В	25232	· · · · · · · · · · · · · · · · · · ·	2469	MPSDISLASCRLRATSRLFTDHR
25095	55463	A	25233	1	2409	RQSDCMTAINRIPIVDDEDNVR
						RETHCANNVRTALHLEADIHP
i						DVVLMDIRMPEMDGIKALKEM
						RSHETRTPVILMTAYAEVETAV
						EALRCGAFDYVIKPFDLDELNLI
]		l				
					;	VQRALQLQSMKKEIRHLHQAL
·						STSWQWGHILTNSPAMMDICK
						DTAKIALSQASVLISGESGTGKE
						LIARAIHYNSRRAKGAFIKVNC
						AALRESLLESELFGHEKGLFER
1	İ					ANEGTLLLDEIGRM/PLVLQAIL
						RILQEREFERIG/GHQTIK/VDIAS
						LLAPTRLQAMVKEGTFREDLFY
						RLNVIHLILPPLRDRREDISLLA
						NHFLQKFSSENQRDIIDIDPMA
	}					MSLLTA WSWPGNIRELSNVIER
						AVVMNSGPIIFSEDLPPQIRQPV CNAGEVKTAPVGERNLKEEIKR
						VEKRIIMEVLEQQEGNRTRTAL
						MLGISRRALMYKLQEYDATGF
						FRDGMTIMVGGFMGIGTPSRLV
						EALLESGVRDLTLIANDTAFVD
						TGIGPLIVNGRVRKVIASHIGTN
						PETGRRMISGEMDVVLVPQGTL
						IEQIRCGGAGLGGFLNPTGVGT
						VVEERQTSIDTSTRKRPFELGRP
						SRNNDKGIRPRSGAGSEEYPRT
						LHDSLKRLQTDYLDLYQVHWP
		-				LRPFYCFGKLGYSWTDSAPAVS
						QLDTLDALAEYQRAGKIRYIGV
						SNETAFGVMRYLHLADKHDLP
25096	55464	Α	25234	1	891	
25097	55465	Α	25235	1	1614	
25098	55466	Α	25236	1	946	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25099	55467	Α	25237	1055	1474	NGVKSKPPPNHQTGSAPGFSAI
						KNRTFAWPTLPNTSCWANTML
		ļ				IGSRELGIRSSQSGPLLGVRVWC
	1	l				/CRCRGTQG/HSQGKDG/IPENGI
						RAYKFTSS*ASFRNSACFRQPSR
						IKPLRKATWLLCGLSTRHLITK
						RLSSPDWA
25100	55468	Α	25238	2036	2743	DLLIRQMPLLSRRVIPVIRVPVT
						GVLWKSFTPRITIFGH/ALIDQH
						SMIVAAQGLTPDHQLLLQIYDR
	1					ARVSASRIVHQAQIYGDAVVR
						YAFIEHRAEVFDFASIEGNEENN
			ļ			VWLCDCAKVYGHAQVKAGIEE
						DAIPTIHYSSQVAEYAIVEGNCV
ŀ						LKHHVLVGGNAVVRGGPILLD
						EHVVIQGESRITGAVIIENHVEL
						TDHAVVEAFDGDTVHVRGPKV
						INGEERITRTPLAGLL
25101	55469	Α	25239	2234	2571	IMSSVDSSLVLPLKAMVPSRITL
						IRSAIWRISG/RLMRDKNNTHAS
		l				SKQLLQATKQAFGFRRGKRGG
		ł			[RFIEDQNPRVAHQPAEDFHHLA
		Ì				IGDIQRSCQTMQIKLAAQRRQQ
	<u> </u>	ļ				VLH
25102	55470	Α	25240	659	1206	WKSTSNTAKAKPGSVMAVDLR
						IPIRFGVMLSAA/FGDDVVDLIA
						QVDLVTTAVGPVVLERIAPAIA
					-	KGQVKRKEQGHESPLNIIACEN
						MVRGTTQLKGHVMNALPEDA
						KAWVEEHVGFVDSAVDRIVPP
						SASATNDPLEVTVETFSEWIVD
						KTQFKGALPNIPGMELTDNLM AFVERKLFTLKH
25103	55471	A	25241	332	683	ALPGR*RHVHLPGSAYEWNDA
23103	334/1	A	23241	332	083	EPAQESDELSLKMLTAICWLTA
						TA/STSLKI*R*KVALRCLVGRIR
						RLRRIRQQCQLLMRRSRVLSGR
						LSSV
25104	55472	A	25242	1	841	MVKVAGECRVRASAHLPGLNR
23104	33472	^	23242	1	041	STKNTEDRGANNQEGTNTQKT
1		l				RGETNERLKKNEHRDLRLARY
1						PAKENNKQGDKNKPRTYEKLT
						GTVTHQEPPHHADQSPGLCLFR
						TSRAQVERGPTVLLLISQENQIE
						RYDSDNHSQLNLCLRVPTVTTQ
				1		RRDYDIAERYRQKGIKLPARKE
						RLMTIAERLRQEGHQIGWQEG
						KLEGLHEQAIKIALRMLEQGFD
						RDQGIA/RRASCQRQQRQSSLPT
						P/EHCCAISGATARKPAALPAAR
						IRRILVSIIRCTSGCPALSG
L	<u> </u>	<u> </u>	<u> </u>	<u> </u>	l	INGL VOINCEDUCE ALSO

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
İ		ł		sequence		
25105	55473	Α	25243	240	651	RCPPQSCLLAEGRWCG*K/CRK
	1	ŀ				VSV*SNRYR*SRLSLGELLRAYS
		ł				RNRDLPGF/SSGSARVLVATDV
						AARGLDIKSLELVVNFELAWEP
						EVNVHRIGRTARAGNSGLAISF
						CAPEEAQRANITSRPPHPAHIAS
						DHQSTP
25106	55474	Α	25244	1455	1643	RDPHQICVAESVYLAAFVLLCA
						GLCVRRRSTTGARNAAAAC*N
						GLW*AEAQCPAYYVCPVVG
25107	55475	Α	25245	549	641	
25108	55476	Α	25246	1378	2084	PNFGYSPPASSCGQVSQNSS*LQ
İ						CSVSGRDKMLRTGPCARTVSSS
						YLMGVSFSRDA**DAR*VCACH
						NTIAALSASAERFTSCERASHSE
						ARSGCCNSVRVMSNNPCCPRSL
						IGVYDILFFQESTAKRCKRSLSG
						SGSACGKSRVRFTPYRPARRTP
						LRSTTSPISAASFPSGWECNAAS
		l				TCSAALRSTAITSLPSLAKFRAS
						SPSNSQTPRTAGLTGSAASESSI
						PQPQAAANS
25109	55477	Α	25247	1134	1428	GPCGCCSSNVARCASQTSSRFA
						AV/WHGAIGAR*LNADNRPLWI
						EITREHAELPGKTGRRMETKQR
						RAITFTQRQNGFESHTPGAVFFS
						INNRCQFGDR
25110	55478	Α	25248	96	535	RPQTTVQPALYVAEQSICSQPC*
						*FSTKCDRKPAAVLAPAGYAAL
		ł				PVLFSSAKLDGSWLRWNSASG
						RRQNGSFSCAALASKRPASASS
		İ				KLNSA**SLPSAVFAAPVRVAA
						SMIISGFCALASIRPSASTRRPSA
						SVFITSTFLPLR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25111	55479	A	25249	1471	3026	SPLRSSVACRGWHRKNNRRGW CPRRGDPARPVRDSLQ\HATAIII VATPGRLLDHLQKGTVSLDAL NTLVMDEADRMLDMGFSDAID DVIRFAPASRQTLLFSATWPEAI AAISGRVQRDPLAIEIDSTDALP PIEQQFYETSSKGKIPLLQRTLV RFANGSARVLVATDVAARGLD IKSLELVVNFELAWDPEVHVHR IGRTARAGNSGLAISFCAPEEAQ RANIISDMLQIKLNWQTPPANS SIATLEAEMATLCIDGGKKAKM RPGDVLGALTGDIGLDGADIGK IAVHPAHVYVAVRQAVAHKA WKQLQGGKIKGKTCRRCYPLA APYVRHCSLVGRAASHQALWH VAGFGLYALFRTGGCRLRCR YSGGLRLIRPTVAAGICRPDKT RKRRIRHRAPFPDAARAPYPAY RSQYNQFFFTNSDFSFIGPKPSM LQSMLCAPCNQADVFHFGANV SASKSYLFTFRSLMMVTLSPCS QQIAVSIFNDQLVAFLCRFCVV
						PLRRHIHGQMYMPLSS
25112	55480	Α	25250	196	330	
25113	55481	A	25251	62	617	NRRLPSGGDEMSAQVSLELHH RI\SQF\LVQESSCWTDW\KFRD GVAQLRPKEVRF\TMRTTVNGQ TRVPRKGVQPPTTWIFNDTKDQ LERRIARLETGMAWAEEPPSRT RHLISNCQISETDIPNVFAVRVN YLLYRAQK\ERDETFYVGTRFD KVPPSE\DTTWRCLKRDIVLDQ AVITSHNLSVLF
25114	55482	Α	25252	1	318	
25115	55483	A	25253	1	510	
25116	55484	A	25254	9	79	
25117 25118	55485	A	25255 25256	863	1245	FSQIYLARSALSSAHSSRSPWQH SVWTLVRSVTNLETSANSALG NLWLRRATAHALKALSPNFWR LAHLSLCLADEAFPSSRS/IIELW QQAGSFISSLATFCKSSFIPFSKE KEFRGIKVRMSSGNFI
25119	55487	A	25257	909	1069	GILSPFLVFVRFVKDQIVVDVW YYF*GLCSVPLVDISVLVPVPCC FGYCSLVV
25120	55488	В	25258	1	1878	
25121	55489	A	25259	778	990	
25122	55490	Α	25260	312	635	
25123	55491	Α	25261	4047	4276	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25124	55492	A	25262	1599	1776	WFPASSMSQPKKAQDQTDSQP
25121	331,72	`	20202	1.577		NSTRGTERSWYHSF*NGSKQ*K
						KSNSSPTHFMRPASS
25125	55493	A	25263	1	162	
25126	55494	Α	25264	1	3370	MNRAPIPKQSKDKTSRETKNTS
						RSKTRERTDELEGLSTDNHAET
						QHAETNTDMTHERYTQIRNHT
						YKTTHQMEDKRTKPKREKEIH
						NRPDDMAKAGIPRSILNTGHPG
						KLMQTEVHHVRTLKIMLKVYS
		l				RALQEELQFSSKAIGRLFPCAD
! !						DLLETHSHFLAQTHERSGYVPL
						CVCATHTKFYEFMEDVNTAYT
		ĺ				KRHTMFRSLSMVSECLFSLING
						DDMFVTFAAMQAQQGRSSLV
						WLFSQLYLYSFISLFIYMV
25127	55495	В	25265	44	238	
25128	55496	Α	25266	1	444	MPAEFITG\ERS\SEGFF\RIHAGI
						EQAISRGLAYAPYADLKNLDD
						KTIASFQQQLSDMGYKFQFITL
						AGIHSMWFNMFDLANAYAQG
						EGMKHYVEKVQQPEFAAKKD
						GYTFVSHQQEVGTGYFDKVTTI
						IQGGTSSVTALTGSTEESQF
25129	55497	A	25267	710	1395	DLPGISSKWVIAVIFGHLIVGIFI
		1	ŀ			PPAIIVRAGIT*RQVR/WIAAHE
						GKAPQQIIIMAHLDTYAPLSDA
		1	į			DADANLGGLTLQGMDDNAAG
						LGVTLQLAERLKNTPTEYGIRF
						VATSGEEEGKLGAENLLKRMS
						DTEKKNTLLVINLDNLIVGDKL
						YFNSGVQTLEARHQRSFNTVKP
						WPDSVISNRPFAGNTGSVDDND
						EIQRNLNDTNYNRMWEYNNRG
						VGSKVVAEAKK
25130	55498	Α	25268	2	2105	
25131	55499	Α	25269	754	1133	RAANQHQTVDLTRLQTRIAQR
	-					LFNRHSQAIEQRQPQIFQFVLVK
1		1				FAFPRFFLILPANVQWRLIATFC
						RFHTGVQGCQFTLVKRGPGDIR
					ŀ	DYQQTNLDWYNSRNTTKLDES
						VNRV/HAAIQS*RQNGL
25132	55500	В	25270	1	1275	
25133	55501	С	25271	1	1167	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25134	55502	Α	25272	275	2424	SPAMHFQSFT/WQNNLDDNTIA
						SFQQHLSDMGYKFQFITLAGIH
		Ì				SMWFNMFDLANAYAQGEGMK
						HYVEKVQQPEFAAAKDGYTFV
		İ				SHQQEVGTGVYAASGNSLLLM
		ŀ				RALNAAWPGIIDCSNHFARLRC
		ľ				SVWSIPRSDLRCAAAFRTGRLA
		ŀ				CCPAGDEKPYPSLRSSRWSGRG
		İ				ATALHYYTAKRCRPDKTRQRRI
		ļ				RQPARALDVGCGVTALSDLPG
						CRTSQRCRPDKTRQRRIRQPAR
						ALDVGCGVTALSDLRGAALHG
						SLANYRVVNFLFRLPDAMILSV
						LLRSCPFVFPLLRRLRAGAPVGP
						YCTGTPITPLPSTRLFAPLPNRC
						SMAGMYGGLQPVPHPAIGARC
	:					LMRCLTHLIRPTMGTGSMAEE
						ALGTSFKRLCAHYSRMRCWRIL
						SGLRGARPNKIVCRIRRLRRIRPI
ĺ						LRLRFPRHSRVVFIFGGGNPRR
			į			AKQRQTGEEVEKCHQPQHGTK
			ļ			CCARGGFAACLVFEYVVVFWT
1						SLPDSFCRKSFPTRIRGSMVPSL
						WDFPPGVDGRKGKTSWNGVPG
						PCVTCGLGLTCPESPCCPGLSLG
						DGYPEKVSVGPPIPLKFQAILQA
						FHEIFGEGSCHIASVAVESGVPE
						QPFGSEETRAGARNRVANARR
						LLPEADFWVAIEAGIDGDSTFS
						WVVIENASQRGEARSATLPLPA
						VILEKVREGEALGPVMSRYTGI
						DEIGRKEGAIGVFTAGKLTRAS
25135	55503	Α	25273	1	441	
25136	55504	Α	25274	3	2919	AVSNCSEGLSKEWGPRPCRHR
ĺ						GMEKLPLGGKFWPTQ/EAVRT
						VRARLQAD/VTGVPTVLVARTD
						ADASDLITSDCDPYDSEFMTGE
						RTSEGFFRTHAGIEQAISRGLAY
						APYADLVWCETSTPDLELARRF
						AQAIHAKYPGKLLAYNCSPSFN
						WQKNLDDKTIASFQQQLSDMG
						YKFQFITLAGIHSMWFNMFDLA
						NAYAQGEGMKHYVEKVQQPE
		•				FAAAKDGYTFVSHQQEVGTGY
_						FDKVTTIIQGGTPDKAFT
25137	55505	A	25275	432	549	

SEQ ID NO:	SEQ ID NO: of peptide sequence	•	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25138	55506	A	25276	652	2689	KFSVGYAVQNFNATVSTKQFQ
						VFSEQNTSSYFAEPQLDVNYYQ
						NDVVHFVTTRDDMPEATRVHL
						EPTINLPLSNNWGSINTEAKLLA
						THYQQTNLDWYNSRNTTKLDE
						SVNRVMPQFKVDGRMVFERD
						MEMLAPGYTQTLEPRAQYLYV
						PYRDQSDIYNYDSSLLQSDYSG
						LFRDRTYGGLDRIASANQVTTG
		Ī				VTSRIYDDAAVERFNISVGQIY
						YFTESRTGDDNITWENDDKTGS
						LVWAGDTYWRISERWGLRGGI
						QYDTRLDNVATSNSSIEYRRDE
						DRLVQLNYRYASPEYIQATLPN
						VNHHITMEHLHMKTRTQQIEEL
						QKEWTQPRWEGIT\RPYSAEDV
						VKLRGSVNPECTLAQLGAAKM
						WRLLHGESKKGYINSLGALTG
						GQALQQAKAGIEAVYLSGWQV
						AADANLAASMYPDQSLYPANS
						VPAVVERINNTFRRADQIQWSA
						GIEPGDPRYVDYFLPIVADAEA
						GFGGVLNAFELMKAMIEAGAA
						AVHFEDQLASVKKMRHMGRT
						ASDQPWLAYAPYADLVWCEPP
						PPDLELARRFAQAIHAKYPGKL
						LAYNCSPSFNWQKNLDDKTIAS
						FQQQLSDMGYKFQFIT\LAGIHS
						MWFNMFDLANAYAQGEGMK
						HYVEKVQQPEFAAAKDGYTFV
		ĺ				SHQQEVGTGYFDKVTTIIQGGT
						SSVTALTGSTEESQF

SEQ ID		Met	SEQ ID NO:	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	noa	in USSN 09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25139	55507	A	25277	134	1695	FPDPARLPPVSVNHHITMEHLH MKTRTQQIEELQKEWTQPRWE
						GITRPYSAEDGGKLRGSVNPEC
						TLAQLGAAKMWRLLHGESKK
						GYINSLGALTGGQALQQAKAGI
	1					EAVYLSGWQVAADANLAASM
						YPDQSLYPANSVPAVVERINNT
ŀ						FRRADQI/QWSAGIEPGDPRYV
						DYFLPIVADAEAGFGGVLNAFE
						LMKAMIEAGAAAVHFEDQLAS
						VKKCGHMGGKVLVPTQEAIQK
						LVAARLAADVTGVPTLLVART
						DADAADLITSDCDPYDSEFITGE
						RTSEGFFRTHAGIEQAISRGLAY
	İ					APYADLVWCETSTPDLELARRF AQAIHAKYPGKLLAYNCSPSFN
						WQKNLDDKTIASFQQQLSDMG
						YKFQFITLAGIHSMWFNMFDLA
						KAYAQGEGMKHYVEKVQQPE
						FAAAKDGYTFVSHQQENRSSK
	•		}			QQQPLLTVGRIRRSRRIRQSVPR
						TGIGCASRRFNTAKPWADAVIS
						NRPFAGNTGSVDDNDEIQRNLN
						DTNYNRMWEYNNRGVGSKVV
						AEAKK
25140	55508	Α	25278	230	380	
25141	55509	Α	25279	432	1247	PSQEPSVHGRWMA*KGHSRIV*
						WRAYD*TH\FNPVLKKSVSLGS
						NIRHMLAEEATTEELDGT\GPV
						LV*PNRH*PAYWMRAYLNLKK
						MSCRSFRRKA*RW*CETQTVV
						HRDRVDQGNNHFDVVARHYH
						LYAFLRKERQLIFFKFKYARIQY
05140	155510	 	25200	242	120	DDDCVCVI ODI DCAVII DVV*D
25142	55510	A	25280	243	430	RRPSYSVLQRLPSAVLLPYY*R DWYHRTAGRRRDGNAGRQHQ
						NGCYPDPPDRDGRRSAFRNP
25143	55511	A	25281	10	638	SSVPTAGSRYNHLRAPRYSPLF
23143	33311	^	23201	10	038	ANYSMSDRCCKPFG/LDSSTG*
						WFQ*RSVPLPILLPDTSRHQL*C
			1			SDPTRNGPA\QACQRFFHIVERV
		1				ARVHHARFAATVTVDHVVIDQ
		1	ľ			RFFQICRT/PWCRLHRHHWRSSS
		1				GTR*TF*SPARHFCLLHNDSSYR
		1				STARPTCSGTDVPDRRCSDAHL
		1				CDHWSGSRAHADTDAECWCL
						NPQPAPSLLQCRR
25144	55512	Α	25282	803	1622	
25145	55513	A	25283	498	686	RRPSYSVLQRLPSAVLLPYY*R
			1			DWYHRTAGRRRDGNAGRQHQ
						NGCYPDPPDRDGRRSAFRNP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25146	55514	Α	25284	1	2063	MKNFMENVLRYLSDDKWKPD
						AKASMTVGTNLDTVYFKRHGQ
						VTGNSAAFDFHPDFAGISVEHL
		1				SSYGDLDPQEMPLLILNGFEYV
			,			TQVGNDPYAIPLRADTSKPKLT
						QQDVTDLIAYLNKGGSVLIMEN
						VMSNLKEESASGFVRLLDAAG
				į		LSMALNKSVVNNDPQGYPNRV
						RQQRATGIWVYERYPAVDGAL
						PYTIDSKTGEVKWKYHVENKP
						DDKPKLEVASWLEDVDGNRKR
						NFSNDARANGTAAFTDCETQT
]						VVHRDRVDQGHNHFDLVARH
						YHLYAFRQFDGTSHVSSTEVEL
1						RTVAFEERSMTAAFISWTECTL
						QIRTCPQNPTGKVWTCDELEIM
·		1				ADLCERHGVRVISDEIHMDMV
						WGEQPHIPWSNVARGDWALLT
						SGSKSFNIPALTGAYGIIENSSSR
		İ				DAYLSALKGRDGLSSPSVLALT
						AHIAAYQQGAPWLDALRIYLK
						DNLTYIADKMNAAFPELNWQIP
		1				QSTYLAWLDLRPLNIDDNALQ
		ŀ				KAL\IDQEKVAIMPGYTYGEEG
						RGFVRLNAGCPRSKLEKGVAG
						LINAIRAKKSATMIDTTLPLTDI
						HRHLDGNIRPQTILELGRQYNIS
						LPAQSLETLIPHVQVIANEPDLV
						SFLTKLDWGVKVLASLDACRR
						VAFENIEDAARHGLHYVELRFS
	ļ					PGYMAMAHQLPVAGVVEAVID
						GVREGCRTFGVQAKLIGIM
25147	55515	Α	25285	3	371	
25148	55516	Α	25286	63	180	
25149	55517	Α	25287	2	205	
25150	55518	Α	25288	495	707	REFSSHQKGLRDRPAHKAVLG
						DNQLFSGGTGAPVWPG/HSENV
						VPVDPT\MKRLPDDVNHPALDY
	<u> </u>					YWRLSFA

NO: of peptide sequence nod in USSN 09/540,217 location of first codon for peptide sequence nod feptide sequence nod nod feptide sequence nod	n,
Sequence	
25151 55519 A 25289 1 1713 MTWAYSPSYGKPLSVPQ MTRFGMDVTLAHPEGYL VVEVAKNNAKASGGSFR MEEAFKDADIVYPKSWA MEERTELLRANDHEGVK HCL\AQNAQHK\DWHSIE EP\TREGEAQNKHGRP\AF SCKEGRSDQKAYDEKSR. PIDDNVVLNKGDVLQVS RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLIFAGIMLGFFN PTFGYIPQGALSMVKEFG MAGEIQVDCNTTYPHIWM GVLFAKQYLLRLGIILYG SQIADVGISGIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIG GVDVPNASLMIENPERL\ LHQLRGRVGRGAGLLT KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKU DHEGLKAVLERQCLAQN\ DWHCTEEMMELTRDGE\(TRUST)	rtion)
MTRFGMDVTLAHPEGYT VVEVAKNNAKASGGSFR MEEAFKDADIVYPKSWA MEERTELLRANDHEGVK HCL\AQNAQHK\DWH\SIE EP\TREGEAQNKHGRP\AR SCKEGRSDQKAYDEKSR PIDDNVVLNKGDVLQVS RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWR GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGGWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN DWHCTEEMMELTRDGE	
MTRFGMDVTLAHPEGYT VVEVAKNNAKASGGSFR MEEAFKDADIVYPKSWA MEERTELLRANDHEGVK HCL\AQNAQHK\DWH\SIE EP\TREGEAQNKHGRP\AR SCKEGRSDQKAYDEKSR PIDDNVVLNKGDVLQVS RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWR GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGGWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN DWHCTEEMMELTRDGE	HIGL
VVEVAKNNAKASGSFR MEEAFKDADIVYPKSWA MEERTELLRANDHEGVK HCL\AQNAQHK\DWH\SIE EP\TREGEAQNKHGRP\AB SCKEGRSDQKAYDEKSRI PIDDNVVLNKGDVLQVS RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL- LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/ DWHCTEEMMELTRDGE/	
MEEAFKDADIVYPKSWA MEERTELLRANDHEGVK HCL\AQNAQHK\DWH\SIE EP\TREGEAQNKHGRP\AE SCKEGRBQKAYDEKSR! PIDDNVVLNKGDVLQVSG RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFN PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWE GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGG GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKE YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN DWHCTEEMMELTRDGE	
MEERTELLRANDHEGVK HCL\AQNAQHK\DWH\SIE EP\TREGEAQNKHGRP\AE SCKEGRSDQKAYDEKSR PIDDNVVLNKGDVLQVSG RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGG GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKE YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/ DWHCTEEMMELTRDGE/	•
HCL\aQnaQhk\dwh\sie Ep\tregeaQnkhgrp\ab SCKEGRSQQKAYDEKSRI PIDDNVVLNKGDVLQVSG RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGG GVDVPNASLMIENPERL/LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAL GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI GAPLPLTANSDCNGYWR AAPLPLTANSDCNGYWR ASGRFREVTG/MEEAFKE YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/DWHCTEEMMELTRDGE/	
EP\TREGEAQNKHGRP\AI SCKEGRSDQKAYDEKSRI PIDDNVVLNKGDVLQVSG RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWM GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERLI LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKLD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNI DWHCTEEMMELTRDGEI	
SCKEGRSDQKAYDEKSRI PIDDNVVLNKGDVLQVSG RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWN GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERLI LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKLD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNI DWHCTEEMMELTRDGEI	
PIDDNVLNKGDVLQVSG RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKE YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/ DWHCTEEMMELTRDGE/	
RVKTIADRIGFISIHSQVTI CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKE YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/ DWHCTEEMMELTRDGE/	
CAFFVIGLMIGMITFQFST MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
MGNAAGLLFAGIMLGFM PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
PTFGYIPQGALSMVKEFG MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
MAGEIQVDGNTIYPHIWK GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
GVLFAKQYLLRLGIILYG SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERLE LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKE YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNE DWHCTEEMMELTRDGEE	
SQIADVGISGIIIDVLTLSS ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/ DWHCTEEMMELTRDGE/	
ACFLGQKVFGLDKHTSW GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERL LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
GSSICGAAAVLATEPVVK KVTVAVATVVIFGTVAIF YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERLE LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERLA LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
YPLMSQWFSPETFGIYIGS GVDVPNASLMIIENPERLA LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
GVDVPNASLMIIENPERLA LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	
LHQLRGRVGRGAGLLTA KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/ DWHCTEEMMELTRDGE/	
KRRFLKAAPEVTRTGLAI GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/ DWHCTEEMMELTRDGE/	
GLPLQTGYELASMQGLV LSPQGTDTFAMLDAFRAI AAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/ DWHCTEEMMELTRDGE/	
LSPQGTDTFAMLDAFRAMAAPLPLTANSDCNGYWR 25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKE YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQN/DWHCTEEMMELTRDGE/	
25152 55520 A 25290 629 1054 ASGRFREVTG/MEEAFKD YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNADWHCTEEMMELTRDGEA	
YPQSWAPYKVMEERTVL DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	RLAG
DHEGLKA\LEKQCLAQNA DWHCTEEMMELTRDGEA	ADI/V
DWHCTEEMMELTRDGE	LRAN
	QHK
HOWDADISGVSCKEGEV	LYM
I I I I I I I I I I I I I I I I I I I	EGVF
EKYRIATYKEASWKPYIL	\AMI
CPVNTPNQVHCSSNC	
25153 55521 A 25291 235 780	
25154 55522 A 25292 1 2783 MTYRNNHQTGVAFLFQT	
DGGVKTFDGYRVQTQSR	-
EVTDVEINLFCHPLCIIMQ	IFTV
HISEELATFIVRGFRFRRG	KAAI
GIFLVNNQLQPDIVHRGF	TEH
HDVRGIKHFTLVEHVITG	3GFG
NTRFTFFRAGNNKMPRLO	iVGA
GWAVLQGVPVRFGVWPI	PEYP
AYACGKFNGAIRAGDAA	QLAA
YAQAFIQLHGPIDAGDGV	NRA
DHRAGDFFEIVFQNLFAI	DVD
LAINHAVNAQLRLRNP	

SEV ID	ISEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
SEQ ID NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25155	55523	A	25293	365	722	TSCLSALAIK/QQHLDEKKELG
		1				HLSAGARRLILGIIVTF/CADSG
						VNLRYSAV*PAGAVYLPDAAV
		1				GGSADRTADAGALLGANVDCA
		Ī				VADRFLPLYLVALHLYAELGRS
						GQPGVRAYSALR
25156	55524	Α	25294	798	1094	
25157	55525	Α	25295	1	2780	MGIVASASVQAAEIYNKDGNK
						LDVYGKVKAMHYMSDNASKD
						GDQSYIRFGFKGETQINDQLTG
						YGRWEAEFAAWTDMFPEFGG
						DSSAQTDNFMTKRASGLATYR
						KTTSSAYRWPELNLQYHRCTS
		1				AARAMLLSGRPVMQINERTAV
						RRQMTVYLRVERIHEIDPLVSL
						SHSMSVIPIDVERPIAAAPCTPG
						LWRTKTPLRVPSTYPLRLPGRA
						RVVCHRTFRLHLCKDWVFMFS
25150	55506	ļ	25206		200	GLLIILVPLIVGYLIPLRQQA
25158	55526	Α	25296	66	300	QSTYCDNPPVPVSRGL*P*RRSS
		i				STSSAGYQK*RYCQHRHDPASR
		ļ				IRTVQRTDSQRTVKRKFMLLVP EASVPASEIC
25150	55527	 	25297	240	424	RCSRDEHDFQLIANLRIVVITFA
25159	33321	Α	23297	240	424	TFA*CTA*LPLGNHSVVAAH*A
				1		G*GGAPVTAQVFVQHG
25160	55528	A	25298	1	1425	O GOAL VIAQVI VQIIG
25161	55529	A	25299	1	471	
25162	55530	A	25300	1269	1390	
25163	55531	Α	25301	601	1119	VAAGAV*RGH*NVQLGKLFFV
						ASDLRINAIAGGVVVFS*FIQGL
		1				TNAIGSGFNNARCRKPTGQVA
		1				ADGGRDAGFFTIANNQCTYAA
						GIFFQCSGEFVGIQFQFAIAGIGR
						DTNLRQRFIAGRTDGITQHRFQ
						LRLNRPQRGVAEQCTIARTLAIS
ļ						SRMAVYLVRLLKVSISEL
25164	55532	A	25302	1666	1769	RLKRHPPLRPSWPPY*TGAHVW
1						HFSPLANWKPGI
25165	55533	Α	25303	1	1970	MKDDIFFRTSGGGVTLSGGEVL
						MQAEFATRFLQRLRLWGVSCA
						IETAGDAPASKLLPLAKLCDEV
						LFDLKIMDATQARDVVKMNLP
						RVLENLRLLVSEGVNVIPRLPLI
						PGFTLSRENMQQALDVLIPLNIR
						QIHLLPFHQYGEPKYRLLGKTW
						SMKEVPAPSSADVATMREMAE
						RAGLQVTVGEKWGVSIETQGA
						LGTENRLADEDIRRADVALLIT
						DIELAGAERFEHCRYVQCSIYA
						FLREPQRVMSAVREV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25166	55534	Α	25304	2804	3494	LSLAEWKCLNPSQRALYREVM
		ŀ				LENYRNLEAVGQLQPQSTQRIP
						*GRICNGDRLTSQKGLDL\VLEA
			İ			LPGLL\EQGGQLALLGAGDPVL
		ł				QEGFLAAAAEYPGQVGVQIGY
						HEAFSHRIMGGADVILVPNRFE
						PCGLTQLYGLKYGTLPLVRRTG
						GLADTVSDCSLENLADGVASG
		ſ				FVFEDSNAWSLLRAIRRAFVLW
						SRPSLWRFVQRQAMAMDFSW
						Q\VAAKSYRELYYRLK
25167	55535	Α	25305	1	1306	QTT. III. III.
25168	55536	A	25306	818	1658	
25169	55537	Α	25307	2611	2826	
25170	55538	Α	25308	609	2359	PPPKIAPVWGCRKKSLPARSKSI
			,			FCFALFFPFFLNGEIILPESPCPF
						WTLFRNDGGKKRDPLAPVYLL
						GKLTISPGPICPDMIGVLFDSTV
	2					RREVAHIGNVQHRFCGPLFLKL
						VEFIDFILTIDIAAIIRQYLVVICE
						VDQRINQIAIATRIFRTGYTAAD
						LRQHLMQLLIFLVVFTRFVALT
						TQFFHFFRCVTKNKDIVSTDMI
					:	QHLDIRTVQRTDSQRTVKRKLH
						VTGAGSFRPCQRNLFRQICRRN
						DQLRQANAVVRDEHDFQLIAN
						LRIVVDHFRYVIDQMNNVLRH
						VIGRSRLTAKNIHARYPLRIRVG
						LDAVIAEMASGLDPFWRPDVV
						HAHDWHAGLAPAYLAARGRP
						AKSEFTVHNLAYQGMFYAHH
						MNDIQLPWSFFNIHGLEFNGQIS
						FLKAGLYYADHITAVSPTYARE
						ITEPQFAYGMEGLLQQRHRERR
						LFGVLNGVDEKIWSPETDLLLA
						SRYTRDTLEDKAENKRQLQNA
						MGLKVDDKVPLFAVVSRLTSQ
			-	}		KGLDLVLEALPGLLEQGGQLA
						LLGAGDPVLQEGFLAAAAEYP
						GQVGVQIGYHEAFSHRIMGGA
						DVILVPSRFEPCGLTQLYGLKY
						GTLPLVRRTGGLADTVSDCSLE
						NLADGVASGFVFEDSNAWSLL
						RAIRRAFVL/WSRAGSWRYSAR
						AIRCCRKVSLRRQRNTPVRWAF
						RLAITKHFRIALWAARTSFWCP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	•	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			:	sequence		
25171	55539	A	25309	1028	1632	TSASAGTARNFSSNFAVRTTGH
23171			23303	1020	1002	STSEATSSSRLSLKSALPPILRAA
						SSASALMFFVIGDDFPTSRRISG
		j]		Y*SALSMVNSGSPIKRWPRITRS
		ĺ				D*MPRMVAGMTLSP/MQQGHG
						VHRTHEVHVVAPQRISFGIGSF
						AREVATIFGSSASVFRR*YRNH
						APNLLTLCSVCLQRRTPGQSPG
						RVFRFHDPVAFRQVSYFQRQTP
ļ						IA
25172	55540	Α	25310	1	336	
25173	55541	A	25311	1889	2257	SAMTFPRSRRISGY*SALSMVN
20110						SGSPIKRWPRITRSD*MPRMVA
						GMTLSPSSRVTVCTGRTKCTSL
						APQRISFGIGSFAREVATRRPYR
E						DIKEGFSQREAALLPQSLRVPQ
						TGTWSAAGAQA
25174	55542	В	25312	1	735	
25175	55543	Α	25313	1439	1744	SAMTFPRSRRISGY*SALSMVN
						SGSPIKRWPRITRSD*MPRMVA
						GMTLSPMQQGHVPWQLMVVL
						WNTRQRWKPSSPDRYVNRAMS
	٠.					LPSRKGEMLKPAPCRK
25176	55544	Α	25314	1209	1972	SAMTFPRSRRISGY*SALSMVN
						SGSPIKRWPRITRSD*MPRMVA
		1				GMTLSPSSRVTVCTGRTKCTSL
1						APQRISFGIGSFAREVATIFGSSA
1	:					SV/HFALHMGAIQQPFAFIGSQT
						LSLVNGNTATT\PQPSAALLGLP
1	1					SASNAWAIAGPRFSISRSGCASA
			1			RLATFSARRRGASKPLNGCLLR
1			1			ATLSSPDKFQQGSTGGMLWGV
				-		LRHSPKFSITADGREFTLHWPN
						TGAMTGCATPGEYVWYSTFDN
						TQRKYPHPWEL

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NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	Ì	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25177	55545	Α	25315	1	1521	METQHRLMRTFQPRQQDWTY
25177	33343	l'`	25515	1	1321	ALWGGVKLRWLFFFLWGLFLF
						AGEEELGIRQTRTNDFLVTGDN
						LLRIFRFDVGNEDKVRQQFAVV
						RIHREVFLVTFHGVNQRFSRHR
						EEFLFEFCVTPKLNEGTTQRTN
						NRGIAVLNTGHRHPDLVAAVE
						QQLQQFTHTAYQIVPYESYVTL
						AEKINALAPVSGQAKTA\FFHP
						GSETG\ENGVKMVRAHTGTPG
						V\IAFRGG\FHGRTYMTMALTG
						KVAPYKIGFGPFP\GSVYHVPYP
						SDLHGISTQDSL\DAIERLFKSDI
		l				EAKQVAAIIFEPVQGEGGFNVA
		1				PKELVAAIRRLCDEHGIVMIAD
						EVQSGFARTGKLFAMDHYADK
						PDLMTMAKSLAGGMPLSGVVG
						NANIMDAPAPGGLGGTYAGNP
						LAVAAAHAVLNIIDKESLCERA
						NQLGQRLKNTLIDAKESVPAIA
						AVRGLGSMIAVEFNDPQTGEPS
						AAIAQKIQQRALAQGLLLLTCG
						AYGNVIRFLYPLTIPDAQFDAA
25178	55546	Α	25316	114	187	RSTISSVRYGDDAFKP*RQAWN
						VL
25179	55547	Α	25317	105	317	YLFFLSRFNHWISMEKKLGLSA
						LTALVLSS\SWARVFSVCRKIW
						RQLPARQHCSSAGVLLALAFYC
						WPLPC
25180	55548	A	25318	1	593	
25181	55549	A	25319	1	729	
25182	55550	A	25320	1	1005	
25183	55551	A	25321	1	1361	
25184	55552	В	25322	1	2793	
25185	55553	Α	25323	27	255	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	I .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25186	55554	Α	25324	225	1408	RIIYMHMESQKIWFALSTPMEIR
						NECCLPSHSSPKMYLGACLF\PL
						SSSWGIDDRDDLLRTIHRMIDN
					Ì	GHAARLAGFYHRWFRYSPCEW
					:	RDYLAELNEQGQAYAQFVAST
						AECCGEGGIKAWDYVRMGFLS
						RMGVLNNWLSEEESLWIQSRIH
						LRALRYYSNWRQYFAGYTFGR
ŀ				ĺ		QYWQSPEDDHLPLLREFLAQET
						TDVDIIRRAYLALLPSFHTETDP
						QGFKQLRHAYDDALPIAQSPAK
						SVLQPEEYEWEALLVEMLGLL
						HRIAMVQLSPAALGNDMAAIE
						LRMRELARTIPPTDIQLYYQTLL
		ĺ				IGRKELPYRTCQLHACTSADTP
		ļ				LRKIPRFSGKLHFYAFCPNIYSS
						YHSAAKYGGSCQPGSTAHRLG
						YYWRWHFIAGLCHADPHAHSS
25187	55555	Α	25325	230	380	
25188	55556	Α	25326	432	1247	PSQEPSVHGRWMA*KGHSRIV*
						WRAYD*TH\FNPVLKKSVSLGS
						NIRHMLAEEATTEELDGT\GPV
					İ	LV*PNRH*PAYWMRAYLNLKK
						MSCRSFRRKA*RW*CETQTVV
						HRDRVDQGNNHFDVVARHYH
						LYAFLRKERQLIFFKFKYARIQY
						AG
25189	55557	Α	25327	10	638	SSVPTAGSRYNHLRAPRYSPLF
						ANYSMSDRCCKPFG/LDSSTG*
						WFQ*RSVPLPILLPDTSRHQL*C
						SDPTRNGPA\QACQRFFHIVERV
						ARVHHARFAATVTVDHVVIDQ
		ŀ				RFFQICRT/PWCRLHRHHWRSSS
						GTR*TF*SPARHFCLLHNDSSYR
						STARPTCSGTDVPDRRCSDAHL
•						CDHWSGSRAHADTDAECWCL
25100	66550	_	05220	002	1622	NPQPAPSLLQCRR
25190	55558	⊢	25328	803	1622	PPDOVOVI ON POATE PARTE
25191	55559	Α	25329	498	686	RRPSYSVLQRLPSAVLLPYY*R
						DWYHRTAGRRRDGNAGRQHQ
	<u>L</u>	<u> </u>				NGCYPDPPDRDGRRSAFRNP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
25102	155560	1.	105220	1.	2063	 MKNFMENVLRYLSDDKWKPD
25192	55560	Α	25330	1	2003	t ·
						AKASMTVGTNLDTVYFKRHGQ
						VTGNSAAFDFHPDFAGISVEHL
				ļ		SSYGDLDPQEMPLLILNGFEYV
						TQVGNDPYAIPLRADTSKPKLT
-			}			QQDVTDLIAYLNKGGSVLIMEN
		ł				VMSNLKEESASGFVRLLDAAG
		ŀ				LSMALNKSVVNNDPQGYPNRV
		ĺ				RQQRATGIWVYERYPAVDGAL
1				İ		PYTIDSKTGEVKWKYHVENKP
-						DDKPKLEVASWLEDVDGNRKR
						NFSNDARANGTAAFTDCETQT
						VVHRDRVDQGHNHFDLVARH
						YHLYAFRQFDGTSHVSSTEVEL
						RTVAFEERSMTAAFISWTECTL
		İ				QIRTCPQNPTGKVWTCDELEIM
						ADLCERHGVRVISDEIHMDMV
						WGEQPHIPWSNVARGDWALLT
						SGSKSFNIPALTGAYGIIENSSSR
						DAYLSALKGRDGLSSPSVLALT
						AHIAAYQQGAPWLDALRIYLK
						DNLTYIADKMNAAFPELNWQIP
						QSTYLAWLDLRPLNIDDNALQ
}		ļ				KAL\IDQEKVAIMPGYTYGEEG
						RGFVRLNAGCPRSKLEKGVAG
1		ĺ				LINAIRAKKSATMIDTTLPLTDI
						HRHLDGNIRPQTILELGRQYNIS
		İ				LPAQSLETLIPHVQVIANEPDLV
				:		SFLTKLDWGVKVLASLDACRR
						VAFENIEDAARHGLHYVELRFS
						PGYMAMAHQLPVAGVVEAVID
İ						GVREGCRTFGVOAKLIGIM
25193	55561	A	25331	2	696	FLLLLWEIRKSSQQTTPTEMNA
				<u> </u>		AEMAQLVAGVDEVGRGPLVG
						AVVTAAVILDPARPIAGLNDSK
		1				KLSEK\RRLALYEEIKEKALSWS
		į				LGRAEPPEIDELNILHATMLAM
ŀ			}			QRAVVGLHIAPEYVLIDGNRCP
						KLPMPAMAVVKGDSRVPEISA
						ASILAKVTRDAEMAALDIVFPQ
						YGFAQHKGYPTAFHLEKLAEH
						GATEHHRRSFGPVKRA/LGTCV
						LILVSRLSKPESEDVL
25194	55562	A	25332	2	63	LIL V SINLSINF ESEU V L
25194	55563	В	25333	138	182	
25196	55564	A	25334	356	706	ISDICAPNMVSAIHAIPYTATMA
	1	`			- 30	IIPERKTSFFEIDAGLVLVRIIISA
		1				PVSSINI*ITSTIDSGLPPKDGRRS
						ESAPRRATTAIAPRKIHIASQLL
						VVIIIRSLVGCRMRRWRVLSD
25197	55565	A	25335	1746	1873	T TIMBLY GORWING WRYLSD
23171	122202	1,,		11.10	1.07.5	

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NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25198	55566	A	25336	11998	3626	<u> </u> PKAARMANVPNNTTGTAMVGI
23190	33300		23330	1770	5020	SVA/RHILQEQIHHQEHQHNGFE
	1					QRFYHFVNRKLDEWRGVIRVE
						NLHS/AAGRMAVIPPVLP*WLS
		1				RYREHSRRLPA*SPKGEAASNP
						EVIARTLRKLKNQPELSEDTIKK
						AVESLSLELVLTAHPTEITRRTL
1		ŀ				IHKMVEVNACLKQLDNKDIAD
						YEHNQLMRRLRQLIAQSWHTD
						EIRKLRPSPVDEAKWGLCRNGK
						TACGKAYQITWAELNKQLEEK
	<u> </u>	!				PRLQTCPSKFGSGPFYF
25199	55567	Α	25337	243	604	PRFPFPLPPATSSVQTAMTDG*N
						ECERICVGYLRYSSHSAPDARR
						QRARTHVPVGKHALPALTKAT
						HPSWWWQCAAMAEDSTDARQ
						LKA*WGVNGFLDLRSATMDGR
						LYPVAMCLLPATK
25200	55568	Α	25338	1	3287	MPITERRSVEKEQLIEIANTIMPF
						GKYKGRRLIDLPEEYLLWFARK
						DEFPAEARYTHIDLHVPAPLLV
15		1				MFTLDTRQSACDRNPHLPIHVC
						SSWTSPKCAPRLWTRALLPRTR
		1				TPPYATGTTIGSRASWFVTFPD
		1				ASFYRRKAPRQEFHTSLQGRSL
		ł				YVRQRSTANPTEITRRTLIHKM
		1			,	VEVNACLKQLDNKDIADYEHN
	İ					QLMRRLRQLIAQSWHTDEIRKL
1						RPSPEAIMTEQEKTSAVVEETR
						EAVDTTSQPVAT
25201	55569	A	25339	1	1425	
25202	55570	Α	25340	534	1391	RQKRRLYQTYWYKQQPRYLPP
						EHRQRHRHQSAGVSRPYSGYG
						EVRPLSQYQPEWQCWEPDVEW
		1				VRQPPQDAITDPDFFCFYQPGM
						TFEQFVREFAEWFSQKRPAAM
						MIGIRADESYNRFVAIASLNKQ
						RFADDKPWTGGHSWYIYPIYD
		1				WKVADIWTWYANHQSLCNPL
				•		YNLMYQAGVPLRHMRICEPFG
		1				PEQRQGL\WLYHVIEPDRWAA
		Ì				MCAR\VS\GYTTGGLYPGQARG
						AAV*TEALKPSGLPQVCALNQC
			Ì			LLSVHRYAGHVRQERCDGADG
						RPAVHERRQLL
25203	55571	A	25341	786	1009	HHSHEQQFQWPVGASGVDRW
						AVYLHQICPLTQFQY/WCRARQ
						EGIMSSPGQQVGFIA*VTSSFSP
						R*KGRRVSSA
25204	55572	A	25342	2446	2970	
25205	55573	A	25343	1	2184	
25203	55571	A	25341	786	1009	RPAVHERRQLL HHSHEQQFQWPVGASC AVYLHQICPLTQFQY/W EGIMSSPGQQVGFIA*V
-	55572	A	25342	2446	2970	
25205	55573	A	25343	1	2184	

SEQ ID	SEO ID NO:	Met	SEQ ID NO	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25206	55574	I _A	25344	706	1293	IHRLLIRRIHQIIDLRIWORTVEI
23206	33374	A	23344	700	1293	` ` `
						HGAPVRFIQMAAWTHIAVLLT*
	1					QLRQLRAGFQRNSWAIFYFFHH
						RKQYIFHFDLRRFPVIMHALFC
1						AVQRCADLMAHRRQKRRFCLA
						GFFCFRPCLSVFYHQFLQFSCTR
		1				FDLRRQLFAVAIQCMNIAFAAA
		1				LVDFDLPDIDGITLARQLAQQY
						PSLVLIGFSAHVIDETLQ
25207	55575	Α	25345	1	3291	
25208	55576	Α	25346	882	1019	
25209	55577	Α	25347	1	2265	
25210	55578	Α	25348	284	535	CVAASVTGTRVLIPPLLNNRSR
						RSPVRYVSKGNWWGSVCNCAS
		1				NNSNSVSR*SLPPMRSHAWRKV
		<u>L_</u>				RRIMRQLPLERPRPGFTI
25211	55579	Α	25349	131	208	LVRWLLSPGW*WKISPIISICLFP
						V
25212	55580	Α	25350	1	3108	MDSQDKYFEATQTVYEWCGV
	1					ATQLLAAYILLFDEYNEKKASA
						QKDILIKVLDDGITKLNEAQKS
						LLVSSQSFNNASGKLLALDSQL
						TNDFSEKSSYFQSQVDKIRKEA
						YAGAAAGVVAGPFGLIISYSIA
						AGVVEGKLIPELKNKLKSVQNF
						FTTLSNTVKQANKDIDAAKLKL
						TTEIAAIGEIKTETETTRFYVDY
						DDLMLSLLKEAAKKMINTCNE
						YQKRHGKKTLFETYLTDHPVTF
						RERLOMSIYKIPLPL
25213	55581	A	25351	1	296	
25214	55582	Α	25352	3	164	VGD/NVGTTARWGIFALIIVETL
						AWFTVVASLFAQHKQRAENLI
						QRLHLLWSFNP
25215	55583	В	25353	91	990	
25216	55584	Α	25354	1146	1881	RCGVQ\WTMYIRAVFVNLTNP
						KSIVFLAALFPQFIMPQQPQLM
						QYIVLGVTTIVVDIIVMIGYATL
						AQRIALWIKGPKQMKALNKIFG
						SLFMLHNAFAWFYLGAFLLTVI
		1				AWFLLGNAQKMPQTTLQWGIL
						VFLGVVASGIGYFMWNYGATO
						VDAGTLGIMNNMHVSAGLLVN
						LAIWHQQPHWPTFITGALVILA
						SLWVHPNKRFRNWLTLLAIAH
						GGVQSAPQAFAQGFGHHQTLA
						LKTLYYPMR
25217	55585	A	25355	1943	2287	LK I L I I FIVIK
25217	55586	A	25356	44	274	
23210	72220	17	22330	177	15''	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25219	55587	A	25357	876	1400	YRHVRDSPGNDRLFETWRSAG
						CAARLLRQSGETRLLSRVVRDY
						GGRWPVSLLDGLPDATWCTEK
					-	RGGFCTCATGRAGEKWAQFPE\
						SLLTNLANPKAIIYFGSVFSLFV
						GDNVGTTARWGIFALIIVETLA
						WFTVVASLFALPQMRRGYQRL
						AKWIDGFAGALFAGFGIHLIISR
25220	55588	A	25358	1	1428	
25221	55589	A	25359	421	797	IIFPFLLFHLCNQLSHLLQYAVV
20221		-				NAPVRRILPIQLLWQQLIQPGEK
						LKSIRRAIQHIGQTQIIGMFIQMP
						IMIAYETDRATGDGI/WAAH*T
						HEYPCHVRQSQFHENHDDVQE
						NPPHPWKIQTPGH
25222	55590	A	25360	1	1320	
25223	55591	A	25361	1	1251	MLLSIITVAFRNLEGIVKTHASL
23223	33371	1.	20001	1		AHLAQVEDISFEWIVVDGGSND
						GTREYLENLNGIFNLRFVSEPD
						NGIYDAMNKGIAMAQGKFALF
						LNSGDIFHQNAANFVRKLKMQ
						KDNVMITGDALLDFGDGHKIK
					İ	RSANRAGLFLIGYGAFRIIVEFF
						RQPDAQFTGAWVQYISMGQILS
		-				IPMIVAGTMKQYLELMQKVLD
						EGTQKNDRTGTGTLSIFGHQMR
						FNLQDGFPLVTTKRCHLRSIIHE
ŀ						LLWFLQGDTNIAYLHENNVTI
		İ				WDEWADENGDLGPVY\ITTVL
					•	NQLKNDPDSRRIIVSAWNVGE/
				İ		LDKMALAPCHAFFQFYVPDGK
		1				LSCQLYQRSCDVFLGLPFNIAS
1						YALLVHMMAQQCDLEVGDFV
		1				WTGGDTHLYSNHMDQTHLQLS
						REPRPLPKLIIKRKPESIFDYRFE
25224	55592	A	25362	3	1327	REFREINGE EST DIRE
23224	22392	A	23302		1321	

SEQ ID NO:	SEQ ID NO: of peptide sequence		_	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25225	55593	A	25363		2443	MGLIGFVLTALWIKLIHNPTDH PRMSAEELKFISENGAVVDMD HKKPGSAAASGPKLHYIKQLLS NRMMLGVFFGQYFINTITWFFL TWFPIYLVQEKGMSILKVGLVA SIPALCGFAGGVLGGVFSDYLI KRGLSLTLARKLPIVLGMLLAS TIILCNYTNNTTLVVMLMALAF FGKGFGALGWPVISDTAPKEIV GLCGGVFNVFGNVASIVTPLVI GYLVSELHSFNAALVFVGCSAL MTMSARSATGHECVFWCNGKI RRLAMRLIYWCAAAPTGDVVC KLTGKWALIANSHRAGQPTRN VNEEVGQRLLEEMEWYDNYL NMGKTDRSANPSPGNKKGGLA NVVEKALGSIAKSGKSAIVEVL SPGQRPTKRGLIYAATPASDFV CGTQQVASGITVQVFTTGRGTP YGLMAVP/SH*NGNWKITASVT SIQPNTNELPNCCMNGVSTANT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25226	55594	Α	25364	1	2701	TFFLPAGEILPPRLEPQITLPVGS
						RRIISIAVTDLPEPESPHLRSGLG
		1				WASLCCFMVICKFFPAAEGLIL
						AAVCDSRGSRYWCNGNRRYG
		ł				YASDLLVRCGATVMFSEVTEV
						RDAIHLLTPRAVNEEVGKRLLE
						EMEWYDNYLNMGKTDRSANP
						SPGNKKGGLGKRGSSKALWLP
						LLQIQARKQVGLRVYTVACVL
]						RTGTWYDRNGPDWRVPGQLN
						MGNPAPETGRYRLAHPATPHD
						PRTTPDHPSHIKPHAPTNQQPDT
						LTPTHHHHTDTRDPSPPPPRTRT
						PRQSTHTTPPHPTTTTRHTDIHP
						PTHTNPPPPTRVLTRQLHHTNRI
						IPHRTHTTTCRRNHHNQMNTTT
						PPPPHTPQITHRHHNTTLREQTQ
						КНРОНІНСТОННТТРКРРТРТТ
		1				RQYNTSIVGTIGGG\MVERKVIE
						ESLQALQERKPRLFHGRMARN
						GADAVGSDCGGAMSVFISVHG
		1				MRPRLVLIGAGHVNRAIAQSAA
		1				LLGFDIAVADIYRESLNPELFPP
		Ì				STTLLHAESFGAAVEALDIRPD
		1		1		NFVLIATNNQDREALDKLIEQPI
						AWLGLLASRRKVQLFLRQLRE
						KGVAEEHIARLHAPVGYNIGAE
						TPQEIAIRVLAEILQVKNNAPGG
						LMMKPSHPSGHQMVVIRGAGD
						IASGVALRLYHAGFNVIMLEVE
			-			KPTVIRCTVAFAQAVFDGEMT
						VEGVTARLATSSAEAMKLTER

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25227	55595	Α	25365	1	1262	MGNWHLSPCPAPAPGHSCLFL
						VGTSPRILAVPGHTGSKAINKA
						ALLLESYMSQALKNLLTLLNLE
						KIEEGLFRGQSEDLGLRQVFAG
	,					QVGG\QPLYAAKEPVPEERLVH
						SFHSYFLRPGDSKKPIIYDVETL
						RDVAPVLDVAGATPPTIRHQRV
						TALVAPKNGSRDVRSCAGKMP
						TDGSIRAVLLPFQVSTIGGVTYE
						RVGTKDQGPQCPHVQRSSAVR
						PGPEAAPGDNSYPPYEDRSTCG
						MQAPDASYSANPDLSFTWSPCL
						SEDALHTSPLYCTTPTSGGEAF
						KGLASDLVPHEDKMVLQNGKC
						FTSPRHTEWAVLRAGHALARG
			ŀ			RNLLDLAAGGMAWVSMSQEC
						PGPGTICSRDLQGTECLRMIQIL PPKDPVTRGSTHCNAGTKRELE
						EFSSQVTLTALIQPLMQVSAQF
						RAADGAP
25228	55596	Α	25366	2	176	RAADOAF
25229	55597	A	25367	1	1395	MRESLELPRDLLNCCDQNANS
23229	33371		25507	1	1373	DMDMKSRLRGYQMEIMNLLG
İ						AGVKDFELESDDLVYLVEEISK
						QQSIHDVAWLLLVAFVYICEQR
						NDLKSELIFTREAEHKSLENLEP
						DHVPEELDTSARNAGALTRRRE
				:		IRDAATLLRLGLAYGPGGMSLR
	·			•		EVTAWAQLHDVATLSDVALLK
1						RLRNAADWFGILAAQTLAVRA
		1				AVTGCTSGKRLRLVDGTAISAP
						GGGSAEWRLHMGYDPHTCQFT
1						DFELTDSRDAERLDRFAQTADE
Ì						IRIADRGFGSRPECIRSLAFGEA
1						DYIVRVHWRGLRWLTAEGMRF
						DMMGFLRGLDCGKNGETTVMI
						GNSGNKKAGAPFPARLIAVSLP
						PEKALISKTRLLSENRRKGRVV
						QAETLEAAGHVLLLTSLPEDEY
						SAEQVADCYRLRWQIELAFKR
				ŀ		LKSLLHLDALRAKEPELAKAWI
						FANLLAAFLIDDII\SHRWISPPE
25230	55598	Α	25368	482	765	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25231	55599	Α	25369	1	1575	MGSVTKSRGPTDSSAFFQINRD
						YSFLDYILGGCQLMFTPWARLL
						QSTCCEQCSKKAHDQFLADLA
						SILPSNTTPLIVSDAGFKVPWYK
						SVEKLGWYWLSRVRGKVQYA
						DLGAENWKPISNLHDMSSSHSK
						TLGYKSLTISNPISGQILLYKSRS
						KGRKNQRSTRTHCHHPSPKIYS
						ASAKEPWILATNLPVEIRTPKQL
						VNIYSKRMQIEETFRDLKSPAY
						GLGLRHSRTSSSERFDIMLLIAL
						MLQLTCWLAGVHAQKQAFRF
						MRLVDGTAISAPGGGSAEWRL
						HMGYDPHTCQFTDFELTDSRD
						AERLDRFAQTADEIRIADRGFG
						SRPECIRSLAFGEADYIVRVHW
						RGLRWLTAEGMRFDMMGFLR
						GLDCGKNGETTVMIGNSGNKK
						AGAPFPARLIAVSLPPEKALISK
						TRLLSENRRKGRVVQAETLEA
						AGHVLLLTSLPEDEYSAEQVAD
						CYRLRWQIELAFKRLKSLLHLD
						ALRAKEPELAKAWIFANLLAAF
0.7000	55500	ļ.,	25250		1044	LIDDII\SHRWISPPEVPDPKRRT
25232	55600	Α	25370		1341	MAGGRKFPDGGDRTTLCGLSQ
						PGVLAPRSPEKRRAINQRYPSK
						TGQLPASITDMMRTARHHLSG
						NGISVPKGAELAHPSTVLELFAI
						SAKPIHPEELDTSARNAGALTR
	ļ					RREIRDAATLLRLGLAYGPGG
						MSLREVTAWAQLHDVATLSDV
						ALLKRLRNAADWFGILAAQTL AVRAAVTGCTSGKRLRLVDGT
						AISAPGGGSAEWRLHMGYDPH
		ŀ				TCQFTDFELTDSRDAERLDRFA
						QTADEIRIADRGFGSRPECIRSL
						AFGEADYIVRVHWRGLRWLTA
		ĺ				EGMRFDMMGFLRGLDCGKNG
				•		ETTVMIGNSGNKKAGAPFPARL
1						IAVSLPPEKALISKTRLLSENRR
1						KGRVVQAETLEAAGHVLLLTS
1						LPEDEYSAEQVADCYRLRWQIE
						LAFKRLKSLLHLDALRAKEPEL
]						AKAWIFANLLAAFLIDDII\SHR
						WISPPEVPDPKRRT
25233	55601	В	25371	1	1233	
	122201		200,1	·	1.200	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25234	55602	Α	25372	1	2197	SHSRGSPGKAVDFTLVSHAAW
2323	33002	, `	23372	•	2197	FGLPHFSTPAFNGQAMMLIAPV
						AVILVAENLGHLKAVAGMTGR
						NMDPYMGRAFVGDGLATMLS
						GSVGGSGVTTYAENIGVMAVT
l						KVYSTLVFVAAAVIAMLLGFSP
						KFGALIHTIPAAVIGGASIVVFG
						LIAVAGARIWVQNRVDLSQNG
			,			CNPAYAEHHQHPGYSDKLKTR
						VSFSCLRIISTNLRRECRAQFRF
						HVDASARHGFRLWQIQGVAQP
						VFIITIREVEAAMRATAFGTEVG
						1
						RNSRCIRRFHQVIQFQALNALG
		1	:			VELAGIDSRDPRLKVLEEMKRT
						FHWGRQTISKHIKIWLGLMLGR AMTPLMLDATSGKLTVWDGA
		1				i i
						HAGAAMGILAVTADQNSAELA
						YYKSGSFRIEDVLWPSAVTDDN
						IKRNAFAADGSVNSYSVPFSSV
						PLLQRQGRIKYAVTLAKYRTNS
						NEQQESKFAQATLQWGGPWGT
						TWYGGGQYAEYYRAAMFGLG
						FNLGDFGAISFDATQAKSTLAD
						QSEHKGQSYRFLYAKTLNHLG
						TNFQLMGYRYSTSGFYTLSDT
						MYKHMDGYEFNDGDDEDTPM
						WSRYYNLLYTKRGKLQSLISKT
1						RLLSENRRKGRVVQAETLEAA
						GHVLLLTSLPEDEYSAEQVADC
						YRLRWQIELAFKRLKSLLHLDA
						LRAKEPELAKAWIFANLLAAFL
						IDDII\SHRWISPPERIPSARKWT
25235	55603	Α	25373	1	2754	
25236	55604	Α	25374	1	652	
25237	55605	Α	25375	1	1800	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	!	
25238	55606	Α	25376	1	2187	MAGPRYPVSVQGAALVQIKRL
						QTFAFSVRWSDGSDTFVRRSW
						DEFRQLKKTLKETFPVEAGLLR
		Ì				RSDRVLPKLLGQASLDAPLLGR
						VGRTSRGLARLQLLETYSRRLL
						ATAERVARSPTITGFFAPQPLDL
		ŀ				EPALPPGSRVILPTPEEQPLSRA
						AGRLSIHSLEAQSLRCLQPFCTQ
		Ì				DTRDRPFQAQAQESLDVLLRHP
						SGWWLVENEDRQTAWFPAPYL
						EEAAPGQGREGGPSLGSSGPQF
						CASRAYESSRADELSVPAGARV
						RVLETSDRGWWLCRYAGAGPE
						ELDTSARNAGALTRRREIRDAA
						TLLRLGLAYGPGGMSLREVTA
						WAQLHDVATLSDVALLKRLRN
						AADWFGILAAQTLAVRAAVTG
						CTSGKRLRLVDGTAISAPGGGS
						AEWRLHMGYDPHTCQFTDFEL
						TD\SRDGER\LARFAQPPDEIRIA
				-		DGEFVWRPKCIRSLAFGEADYI
!		1				VGVHWRGLRWLTAEGMRFDM
			•			MGFLRGLDCGKNGETTVMIGN
						SGNKKSP\GFPFRARFIAVSLPPE
						KALISKTRL\LSENRRKGRVVQ
						AETLEAAGHVLLLTSLPEDEYS
		1				AEQVADCYRLRWQIELAFKRL
						KSLLHLDALRAKEPELAKAWIF
		İ	Ì			ANLLAAFLIDDII\SHRWISPPEV
						PDPKRRTNSLWRITKMVIWSLQ
		1				VAIRGTVSLTAPSLCNSACCCC
						VSTNSATTLNDFAFARSVIDLTI
25239	55607	Α	25377	2	333	RLGVWQDILSRRASCYHGMEV
						WDKDSFGHISFDDQSMGYSHL
						GHIVENSVIHYA\ARLVIGADGV
						DSWLRNKADIPLTFWDYQHHA
					ĺ	LVATIRTEEPHDAVARQVFHGE
						AFW
25240	55608	Α	25378	3	235	VAVLEQRVHEPLAANAPPQLR
						VS/ARLGVWQDILSRRASCYHG
						MEVWDKDSFGHISFDDQSMGY
						SHLGHIVENSVIHYA
25241	55609	A	25379	1	774	
25242	55610	Α	25380	1	1076	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25243	55611	A	25381	1138	1737	SVSTEPSVAAFSSIKLRODPP/H
		į				DNLHHQYN*GDIAFC\FTPYFH
!		l				NCLCQS*WARAFQ*RANEF*R
		1				MNCTQLARTSGSHHLIPLTLRF*
						QICISSGQLIQYSVVCRFIHPPEH
						RLTIHPLAGQGVNLGFMDAAE
						LIAELKRLHRQGKDIGQYIYLR
	1	ŀ				RYERSRKHSAALMLAGMQGFR
						DLFSGTNPAKKLLRDIGLKLAD
25244	55612	В	25382	1	735	
25245	55613	В	25383	1	1941	
25246	55614	В	25384	847	849	
25247	55615	Α	25385	1	1227	
25248	55616	Α	25386	324	1533	EGFMEHQRKLFQQRGYSEDLL
						PKTQSQRTWKTFNYFTLWMGS
		l				VHNVPNYVMVGGFFILGLSTFS
		ł				IMLAIILSAFFIAAVMVLNGAAG
						SKYGVPFAMILRASYGVRGAL
						VPGLLRGGIAALMWFGLQRGS
					,	PFYDLIQTALSSPHKVTIEQFYR
						EVGVFLGIALIAVVISVLNNFFV
						SHYVFRWRTAMNEYYMANWQ
		ŀ		-		QLRHIKGRTAFINAIMTLIAFLP
					}	VLVTLSAHVPELPIIGHIPYGLVI
						AAIVWSLMGTGLLAVVGIKLP
						GLEFKNQRVEAAYRKELVYGE
		ŀ				DDATRATPPTVRELFSAVRKNY
					ł	FRLYFHYMYFNIARILYLQVDN
						VFGLFLLFPSIVAGTITLGLMTQ
						ITNVFGQVRGAFQYLINSWTTL
						VEL\MSIYKRLRSFEHELDGDKI
						QEVTHTLS
25249	55617	Α	25387	1526	1683	
25250	55618	Α	25388	2709	2918	CWCFWHRRSCCGSVRYALSAV
	1					PGCQCPET*RRRFPHSAF*RFRS
		l				SETGQTGAYVSGPDLQPERLQR
						LWC
25251	55619	Α	25389	1	1812	
25252	55620	A	25390	134	386	RLKPSAAIRRRVSSSRISTPLNPA
1			1			STTAFVGTDCA\IPRLRATSGLA
1					1	GSPLIQNRFCRARQPRWSAPVA
	<u>L</u> .					RHAAVYARHRWNQII

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25253	55621	A	25391	181	1630	RIRQFCFYHHCVLTLAICAFIVIT
23233	33021	^	23391	101	1030	LTIWVSFRVSVLVFAMADDIKV
						AVVGAMSGPIAQWGDMEFNG
1			•			ARQAIKDINAKGGIKGDKLVGV
						EYDDACDPKQAVAVANKIVND
						GIKYVIGHLCSSSTQPASDIYED
						EGILMISPGATNPELTQRGYQHI
		1				MRTAGLDSSQGPTAAKYILETV
						KPQRIAIIHDKQQYGEGLARSV
		1				QDGLKAANANGVFFDGITAGE
						KDFSALIARLKKENID\FVYYGG
						1
		ŀ				YYPEMGQMLRQARSVGLKTQF
						MGPEGVGNASLSNIAGDAA\EG
						MLAPVLITVDQPFVQAGFQPLR
İ						RLLPAHETGRRTRAYGVGRLT
						RQIRRQIATTFRHNAQAAESKD
						FQWYRCDPCQLFHLMNRQHAR
						QHHASNVKMAMIKVNRLFIGR
				1		RSLHRYVALNMRITLGGVLHH
1						GEVGEDQRVGTQLRRHIHGAL
						PTGVTVRMRKSVNRDVKFAA
		<u> </u>			50.5	MLMDKTHRFLQFFLGKVKAGE
175757	55622	IA	25392	2	1505	
25254	!		<u> </u>			
25255	55623	Α	25393	1	2038	GKOTSTSPAGWENSI RMRYT
	!		<u> </u>			GKQTSTSPAGWENSLRMRYT\ MSFSLIATGLI GVYLTTMPGY
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN FIQTDASINRGNSGGALLNLNG
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN FIQTDASINRGNSGGALLNLNG ENPIDQLKVVGRPHDRIDGPLK
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN FIQTDASINRGNSGGALLNLNG ENPIDQLKVVGRPHDRIDGPLK TTGTARYAYEWHEEAPNAAYG
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN FIQTDASINRGNSGGALLNLNG ENPIDQLKVVGRPHDRIDGPLK TTGTARYAYEWHEEAPNAAYG YIVGSAIAKGRLTALDTDAAQK
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN FIQTDASINRGNSGGALLNLNG ENPIDQLKVVGRPHDRIDGPLK TTGTARYAYEWHEEAPNAAYG YIVGSAIAKGRLTALDTDAAQK APGVLAVITASNAGALDKGDK
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN FIQTDASINRGNSGGALLNLNG ENPIDQLKVVGRPHDRIDGPLK TTGTARYAYEWHEEAPNAAYG YIVGSAIAKGRLTALDTDAAQK APGVLAVITASNAGALDKGDK NTARLLGGPTIEHYHQAIALVV
25255	55623	Α	25393	1	2038	MSFSLIATGLLGVYLTTMPGY WGILFVWALFGVTCDMMNWP VLLKSVSRLGNSEQQGRLFGFF ETGRGIVDTVVAFSALAVFTWF GSGLLGFKAGIWFYSLIVIAVGI IIFFVLNDKEEAPSVEVKKEDG ASKNTSMTSVLKDKTIWLIAFN VFFVYAVYCGLTFFIPFLKNIYL LPVALVGAYGIINQYCLKMIGG PIVLEKVLPPVVSVRVKGTASQ GQKIPEEFKQFFGDDLPDQPAQ PFEGLGSGVIINASKGYVLTNN HVINQAQKISIQLNDGREFDAK LIGSDDQSDIALLQIQNPSKLTQI AIADSDKLRVGRSGLNLEGLEN FIQTDASINRGNSGGALLNLNG ENPIDQLKVVGRPHDRIDGPLK TTGTARYAYEWHEEAPNAAYG YIVGSAIAKGRLTALDTDAAQK APGVLAVITASNAGALDKGDK

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25257	55625	A	25395	356	849	GSACRVREIPRPASQMP/HTLPA GSRPPGSEAEPGPEAAPPPARRE AHQIPRPRRGHLPSSPGPRTHVA
						AHNIRVVTEAHADSHALLSDLG
						AAPFVVMSRILRVDGDEDPPHV
						DESIQPTTENAVVFRPVQLTSAI
		1				ETGGKEEPYGLSAASLGRAESS
		<u>.</u>				AASLAGRR
25258	55626	Α	25396	154	379	LVPRLKLGDLPSEINPLSSCSLV
						REKDPPTTSCTHT\TNPRNISPIS
		l				NPDSTGNRTVQLTW*PLPEPLE
						LWPKAL
25259	55627	Α	25397	4761	5127	LGSGDLPWEINPLSSCSLLREKD
						PPTTSGPQT\TSPRNISPISNPHTR
		1				TSKRLNRSGQAFLQNLLPQELA
			1			TSARNLTTRPRNACSPGFLLSR
		1				VPSVRDPTGNWTVQLTWQPLS
						EPLELWPKAL
25260	55628	Α	25398	1	753	MGSWLQGLRAMVFALNYMVT
		l				RVRNKKDPPTTSGPQT\TSPRNI
		ŀ				SPISNPR/PKETRFICGPKTPAPL
	1					MDWEGSLPLMFNHCRDTSLIIH
1						PCFQGVRPCRDACLSPSPLAASP
						AFLGKGQVPLNPFFTLSGKSRF
ŀ						SGGGASTPTPSFHVSTPSLLFW
						GRGKYPSTPSSPLVASPAFLGK
				1		GQVPLNPFFTLSGKSRFSGEGA
						KAPETITDAELRVTLTVEAAVC
						STIALSLGWEILPRHWGKEEVT
	}					KTIYYPVIP

SEQ ID		1	SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, (=possible nucleotide insertion)
		ļ		Jacque ii e		
25261	55629	Α	25399	174	2238	LRSGDLPWEINPLSSCSLLHEKD
•				1		PPTTSGPQT\TSPRNISPISNPRQR
						RHILSMDPKLRRRSWTWVGSLP
]			LVFNHCRDASLIIHPGFRGVRPR
						RDVCLGPSPLATITDAELYVTL
						TVEGKSIPFLIDTEATHSTLPSFK
						GPVALASIHVQNVQIKRDKEGH
						YIMVKGSIQQEELTILNMYAPN
						TGAPRFIKQVLNDLQRDLDSHT
						IIMGDFNTPLSTLDRSTRQKVN
						KDIQDLNSALHQADLIDIYRTL
						HTKSTECTFFSAPHRTYSKIDHI
						VGSKALLSKCKRTEIIINCLSDH
		l				SAIKLELRIKKLTQNHSTTWKL
						NNLLLNDYWVHKEMKAEIKM
		1				FFEINENKNTTYQNLWDTFKAV
						CRGKFIALNAYKRKQERSKIDT
						LTSQLEELEKQEQTRSKASRRE
						EITKIRAELKEIETQKTLQKINES
						RSWFFEKINKIDILLARLIKKKR
						EKNQIDAIKNDKGDIATDPTEIQ
						TTIREYYKHLCPNKLENLEEMD
						KFLDTYTLPRLNQEEDESLNRPI
						TGSEIVAIINSLPTKKSPGPDGFT
						AKFYQRYKEELVPFLQKYKEEL
						VPFLLKLFQSIEKEGILPNSFSEA
						SIILIPKPGRDTTKKENFRPISLM
						NIDAKILNKILANQIQQHIKKLI
						HHDQVGFIPGMQGWFNIRKSIN
·						VIQHINRTKDKNHMIISIDAEKA
2 2 2 2		<u> </u>	2.5.100		0.6	FDKIQQPSC
25262	55630	Α	25400	3	267	EKDPLTTSGPQT\TSPRNISPISN
						LRLFAFTWTDPDTHQAQQITW
						AVLPQGFTDSPRYFSQAQISSLS
05062	55621	 	25401	167	400	VTYLSIILIKTHVLSLPIMSD
25263	55631	Α	25401	167	408	LGSRTFPWEINPPSSCSLLREKD
						PPTTSGPQT\TRPRNISPISNLVS
						GLFLLSSPTSLTIPQPLSSFNLDD
25264	55(22	 	25402	142	441	TLQSLPSLNF LRLGDLPWEINPLSSCSLLCEKD
25264	55632	Α	25402	142	441	PPTTSGP\PRNISPISNPVSGLFLL
					•	SSPTCLTIPQPLSPFNLGATLQSL
						PSLNFNSFHFLVETKETRFIRGP
25265	55622	<u> </u>	25402	70	201	KTPAP
25265	55633	Α	25403	79	381	LGSGDLPWEINPLSSCSLLREKE
						PPTTSGPQT\TRPRNISPISNPELA TLAGNLATGPRNARSPGFLLSH
						VLSVWDPTENQTVQLTWQPLP
						QPLELWPKAL
	L	<u> </u>	L		L	AI PEP MLKVP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25266	55634	A	25404	1	511	MWKGPKGLDMYGKSSVSPKTS
						DILGRDTLLLALKVQTVVLQTA
						CGEGHVAGNCGRPLETEGSLQ
						LTATKKLRDSVLQPKSPEFCQQ
						FTRAWNRTQVPDETEAPAGTY
						AAQSGDLPWEINPLSSCSLLHE
						KDPPTASGPQT\TSPRNISPILNR
						VSEVSDHAGTPALVLHP
25267	55635	Α	25405	570	1182	LGSGDLPWEINPLSSCSLLHEK
						DPPTTSGPQT\TSPRNTSPISNLH
						ALKGLKPAITRLLQHGLLKPINS
						PYNSPILPVLKPDKPYKLVQDL
						CLINQIVFPIHPVVPNPYTLLSSI
						PPSTIHYSVLDLKLAFFTIPLHAS
				1		SQPLSAFTWADPDTHQVQQIT
						WAVLPOSFTDSPHYFSQAQISS
						LSVTYLSIILIKTHVLSLPIVSD
25268	55636	A	25406	489	615	LRNTWNSPRLMACALHSGSPSC
,						TWGPYS*SGLSENLASQRVCPP
						YQNENVGRVRDTEIKEHCYEES
						SYRAATQIQVRKVGIITEPYPFM
						ASLRTHCIICETCYEMKISFSKS
					i	LNPLEKNKKSQPANCAVKEVS
					•	EQLRRRQAFSVAAGLKGKGSP
		ĺ				AQSIRKNLQKPYQHFQTLQQLL
						PLQWAPCYGPSNFATHGTHQG
						LWLVLSTVAAQAVPGALIAEA
						TALLAWIQGAVS
25269	55637	A	25407	579	715	LGSGDLPWEISPL\SCSLLHEKD
		l				PPMTSGPQT\TSPRNISPISNLR
25270	55638	A	25408	1553	1896	
25271	55639	Α	25409	964	1332	SCRFIRIYQGACCNLHPGEINSH
İ						VAHTKPVWWSLHTDTHENCHL
		1				NTAVFFYHWLALEFFLNPLRR/
						CSC*HSLPGQFPVSLCLRVLSVD
		1				CAHPWGKPEAPGS*HPGPWQFS
						SLPSPLWPLYQHP
25272	55640	В	25410	1	717	
25273	55641	A	25411	590	1142	PNSSWMRGEPKKDPPTTSGPQT
1						\TSPRNISPISNPR/PKETRFICGP
1						KTPAPLMDWEGSLPLMFNHCR
1		1				DTSLIIHPCFQGVRPCRDACLSP
						SPLAASPAFLGKGQVPLNPFFTL
						SGKSRFSGGGASTPTPSFHVSTP
		1				SLLFWGRGKYPSTPSSPLVASP
						AFLGKGQVPLNPFFTLSGKSRF
i	1	1				SGEGA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
į	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1		l		sequence		
25274	55642	A	25412	<u> </u>	790	MGLVHLQRQSYWTVQRSSINH
		-				FLGCNPHTGKDKTLYMRWTKS
	-	l				FRKVEDPPTTSGPQTDQPKKHL
						TKFKSETKETRFIHGPKTPAPV
	ļ					MDWEGSLPLVFNHCRDASLIH
						SHFKGVRPRRDACLGPSPLAAS
1						PAFLGKGQVPQPLISLCPDPLFP
						HPNLISLRPNPLCPHPDLVSLCP
						DPFPAFLEAHKNFQTPEPQQPGI
						PPEPPPPGACYKC/HEI*PPGQG
						MPAAQDSS*AMS/LSVRDPTGN
						QTVQLTWQPLPEPLELWPKAL
25275	55643	Α	25413	1	736	MOAMEKWKREAKVETEKDOK
23213	33043		25415		730	NQYQQTWLSDSASGYRYTKLP
						FYFRHNNLIPALAHLLFLDSLYS
		1				DLLTAAFFMQFWLSAQMSSDQ
				İ		RGLPGYLLWAEEISLLEISELTS
						GKQDSSWPEVKAGLKKEANYL
					<u> </u>	SSDSARLHPGEINSLVAHTKPV
						WWSLHMDTHEIWCRDSNWGD
						LPWEINPLSSCSLLHEKDPPTTS
						I .
İ						GPQT\TSPRNILPISNPPSSKHQE KPPEAISTLPNAAATAAAAVGS
į		ŀ				
25276	55644	A	25414	1644	2010	LLWSL LGSGDLPWEINPSSSCSLLREKD
23276	33044	A	23414	1044	2010	PPTTSGPQT\TSPRNISPISNPHTR
						TSKRLNRSGQAFLQNLLPQELA
					ļ	TSARNLTTRPRNACSPGFLLSR
						VPSVRDPTGNWTVQLTWQPLS
						EPLELWPKAL
25277	55645	A	25415	1	1035	MGKEYSLDVKKSIKVFKDNRS
23211	33043	^	23413	1	1033	QGNRLQKLGLEDTDREDAMGF
İ		1				GSHRAKLTVVAALGACHCPEN
		1				EGQTVLPSSTSGRSDKRERVSA
·					<u> </u>	GYTPPFFVKEGVPSPLFKLHVV
						RCCSIQSHHSRRSQNCAEDVIR
					1	KTKTDQAVSSMSSAPVTVQQL
		i				NIIPALLVALTCGWAFCLMVSQ
						`
						EQYDEASKQAASFSNNAVIPVY
						MSHMSKTLYKSEVFPINTYAQK
						ICFIAHTKPVWWSLHMDAHEI
						WCRGRRSTDLPWE\INPLSSCSL
		1				LREKDPPMTSGPQT\TSPRNISPI
		1				LNQELATRAGNLATRPRNACSL
		1				GFLLSRISSVWDPT*KFGLVQLT
		1		<u> </u>		LGKPLPEPLELWPKAL
25278	55646	Α	25416	174	393	LRSGDLPWEINPLSSCSLLHEKD
		1				PPTTSGPQT\TSPRNISPISNPGET
						KETRFIRGPKTPAPVMDLGRQP
				1		SLGV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	l '	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25279	55647	I .	25417	2	4574	WDVLGAVIGTECGTIESGLSMV
23219	133047	Α	23417	2	4374	
İ	-	ŀ				FLKDGERKLCTPSMDTTGYGN
					<u> </u>	LRFYFVMAKWIYIPENVVKGR
		İ				KEIILVLDFTWCMVHRGICDPG
						NSHENDIILYAKIEGRKEHITLD
						TLSYSS/L/SSLYWPVMSQILFW
						QRTVH*TWL\QL*DGIPDIPNVY
						F*KLWQFQALLLP*LLLYPWC*
						SQLWLWCLGQW*GPGFQQRW
						AASANYIFP*QLTIQNNLRRTTR
						*CKAVWNSVQMVATVSFFPER
						RCMGY**DYHDICA
25280	55648	Α	25418	1	363	
25281	55649	A	25419	1	301	
25282	55650	A	25420	2	309	
25283	55651	A	25421	3	512	YIGPSCLKFCSGRGQCTRHGCN\
						CEMASQTFPMFISESFGSSRLSS
						YHNFYSIRGAEVSFGCGVLASG
						KALVFNKDGRRQLITSFLDSSQ
						SRIISVELPGDAKQFGIQFRWW
						QPYHSSQREDVWAIDEIIMTSV
						LFNSISLDFTNLVEVTQSLGFYL
		ŀ				GNVQPYCGHDWTL
25284	55652	Α	25422	2	878	<u> </u>
25285	55653	A	25423	1	750	
25286	55654	A	25424	1	1404	

SEQ ID	SEQ ID NO:	L	SEQ ID NO:		i -	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	•		,	sequence		
25287	55655	Α	25425	1	2506	GCSRLLVTVDLNLTNAEFIQFY
						FMYGCLITPNNRNQGVLLEYSV
						NGGITWNLLMEIFYDQYSKPGF
						VNILLPPDAKEIATRFRWWQPR
						HDGLDQNDWAIDNVLISGSAD
						QRTVMLDTFSSAPVPQHERSPA
1		ŀ				DAGPVGRIAFDMFMEDKTSVN
1						EHWLFHDDCTVERFCDSPDGV
İ						MLCGSHDGREVYAVTHDLTPT
					1	EGWIMQFKISVGCKVSEKIAQN
			ļ			QIHVQYSTDFGVSWNYLVPQC
			ŧ			LPADPKCSGSVSQPSVFFPTKG
						WKRITYPLPESLVGNPVRFRFY
						QKYSDMQWAIDNFYLGPGCLD
						NCRGHGDCLREQCICDPGYSGP
						NCYLTHTLKTFLKERFDSEEIKP
						DLWMSLEGGSTCTECGILAEDT
						ALYFGGSTVRQAVTQDLDLRG
1						AKHDYILLPEDALTNTTRLRW
						WQPFVISNGIVVSGVERAQWA
						LDNILIGGAEINPSQLVDTFDDE
						GTSHEENWSFYPNAVRTAGFC
						GNPSFHLYWPNKKKDKTHNAL
						SSRELIIQPGYMMQFKPFGFCRS
	-					DSWQLVQTQCLPSSSNSIGCSPF
						QFHEATIYNSVNSSSWKRITIQL
						PDHVSSSATQFRWIQKGEETEK
						QSW\AIDHVYIGEACPKLCSGH
						GYCTTGAICICDESFQGDDCSV
						FSHDLPSYIKDNFESARVTEAN
						WETIQGGVIGSGCGQLARYAH
						GDSLYFNGCQIKRAATKPL\DL
25288	55656	Α	25426	146	10561	GGGGGGGGGMERSGWARQT
İ						FLLALLLGATLRARAAAGYYP
						RFSPFFFLCTHHGELEGDGEOG
		İ				EVLISLHIAGNPTYYVPGQEYH
						VTISTSTFFDGLLVTGLYTSTSV
						QASQSIGGSSAFGFGIMSDHQF
						GNQFMCSVVASHVSHLPTTNLS
						FIWIAPPAGTGCVNFMATATHR
						GQVIFKDALAQQLCEQGAPTD
						VTVHPHLAEIHSDSIILRDDFDS
						YHQLQLNPNIWVECNNCETGE
						QCGAIMHGNAVTFCEP
25289	55657	A	25427	1	296	QCG/HMHOHWA IT CEI
23209	123037		23721	l •	270	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25290	55658	A	25428	1	557	MARSLGVLVALPFPLPVGFNAE
			23120			EAHNIVKEFSPGKSHPRESLSQQ
						RETLVQAGAFHWFGWRGKEK
:						LKPKFNTFGRLPNEMLEQWLSP
						TNQCVDGV/LKGGED\YNHNNI
						NQWTASIVEQSL\THLVKLGKA
						YKYIVTCAVVQKSAYGFHTASS
						CFWDTTSDGTCTVRL/WENRT
						MN\CIVNVFCHCLFVL
25291	55659	Α	25429	178	2270	VRRLFCVQTGGSPVGRGSLHHL
						WLVFSHVLSLLCSPCLLAPGM
						WGFHDRDLVLRKALYTMMRT
						GAEREALKRRWRWQQTQQNK
						ESGLVYTEEEWEREWTELLKL
						ASSEPRTHFSKNGGTGGGHLPP
		ŀ				EGKPLHGCSSLLRSGKGGHVK
						AEPSRLQQSQAKPPLTSQIRALH
						FPIPSQINEKPGAGHWSAKLHFP
						YWQLGEAGEEGSSPPDIMRCL
						LTCLSVPSTAVIPLTDSEHKLLP
						LHFAVDPGKDWEWGKDDNDN
						ARLAHLILSLEAKLNLLHSYMN
		ļ.				VTWIRIPSETRAPLAQPESPTAS
						AGEDVQSLADSLDSDRDSVCS
						NSNSNNGKNGKDKEKEKQRKE
						KDKTRADSVANKLGSFSKTLGI
						KLKKNMGGLGGLVHGKMGRA
						NSANGKNGDSAERGKEKKAKS
						RKGSKEESGASASTSPSEKTTPS
						PTDKAAGASPAEKGGGPRGDA
						WKYSTDVKLSLNILRAAMQGE
						RKFIFAGLLLTSHRHQFHEEMIG
						YYLTSAQERFSAEQEQRRRDA
						ATAAAAAA\PPPPPRP/ERPPRRP
						ETEGVPVPERASPGPPTQLVLK
						LKERPSPGPAAGRAARAAGG
1						TA/CPGGRRAACERQRTSAWPQ
						PPGASAPERHPRAGVGRAGRG
						VRAGRGGAAAVRHVPAAEPLA
			1			VVAELQPGARRRPAHRQHGRV
		<u> </u>				AGARGARGPTGRGGDRGGGRA

SEQ ID			SEQ ID NO:		•	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	1 '	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25292	55660	Α	25430	404	1116	SLGPLMLSGQKLQTSYTMEYY
						AAIKR/DKIVSLVGTWLELEAIIL
						KKLMQEQKTKYHMFLLDSLSH
						GMQQAERVLIADGTMLLSAQY
						QFENNLLVPILRVSFRKSLQRKE
						EPGRKAKKSQTSGEGIKKRRFW
		l				FEWKEPVALSSQGWYEAKGSE
						RPEKGHLGLLRAESFQDLRTAL
						ISKPYFSVPGKVGPAIKCPETLP
		l				ELKTYPQYGVTLGEPVRNEQQ
						QASSFPSLSNTHLSKKRNES
25293	55661	Α	25432	1571	1782	WLLCRLPPRVPDQL*WCGCQPE
		İ				KCAGAEFQDGSAMPLPSRTCPH
						SPRMCTGWSTTCATTDSATTA
		ŀ				CPLAL
25294	55662	В	25433	69	1160	
25295	55663	Α	25434	14	437	LQTSHPYPTTSKC/PPP/CEKPSP
						TSL/C*RRSAPHLQPPE
25296	55664	Α	25435	782	997	MMLCQLQRPV/CGSHSCSRG/C
						PPAQ/CPSPVPVPSPQSAFPVPQS
				ŀ		PSSTCPNPSHPIHPIPMVPSSWSG
						HWDSK
25297	55665	A	25436	1117	1815	GDAHTEQCLQNLYPRGSRPPLP
						LESHPSSSKHSPKACPTGRS/CG
						PWK/CPGPEVRP*PPPSCTR*DP
						HFRGLLEGLLEPRHVTCLALCG
						PQRVLYWPVYHERLGEGWDW
				1		CPSSWPGA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25298	55666	Α	25437	1261	2757	ALGKDEKSQGPPIQTGGLGPRL
						FRLPSSQGQERRFAAAKAPSSL
						VPHNGSPLSCWRGLREEGGLSL
						ATLWTPCGVGSGVPAAPPSAW
						CDLGKLLVCWRGQNRGPRSTQ
						TDVRRHEARSRQRRRKCVAAP
İ						VAPRSRRWRCPAALAAPAVAV
						PVVFALIFLLGTVGNGLVLAVL
	1					LQPGPSAWQEPGSTTDLFILNL
	1					AVADLCFILCCVPFQATIYTLD
						AWLFGALVCKAVHLLIYLTMY
						ASSFTLAAVSVDRCAVPG\HPL
						GRAVGAGVGGGVLNVGLVWL
						LAALFSAPYLSYYGTVRYGALE
						LCVPAWEDARRRALDVATFAA
						GYLLPVAVVSLAYGRTLRFLW
						AAVGPAGAAAAEARRRATGRA
						GRAMLAVAALYALCWGPHHA
						LILCFWYGRFAFSPATYACRLA
						SHCLAYANSCLNPLVYALASR
						HFRARFRRLWPCGRRRRHRAR
						RALRRVRPASSGPPGCPGDARP
						SGRLLAGGGQGPEPREGPVHG
						GEAARGPE
25299	55667	A	25438	1	1624	MKDKSKTLGLEASIFRNNWKC
				-		KSIFEGLKGHQEGYFSQMIISYE
-						KIPSYRKSKSLTPHQRIHNTEKS
						YVCKECGKACSHGSKLVQHER
	İ					THTAEKHFECKECGKNYLSAY
						QLNVHQRFHTGEKPYECKECG
						KTFSWGSSLVKHERIHTGEKPY
						ECKECGKAFSRGYHLTQHQKIH
İ		ŀ				TGVKSYKCKECGKAFFWGSSL
						AKHEIIHTGEKPYKCKECGKAF
			1			SRGYQLTQHQKIHTGKKPYEC
}		1				KICGKAFCWGYQLTRHQIFHTG
		İ				EKPYECKECGKAFNCGSSLIQH
-		l				ERIHTGEKPYECKECGKAFSRG
						YHLSQHQKIHTGEKPFECKECG
						KAFSWGSSLVKHERVHTGEKS
						HECKECGKTFCSGYQLTRHQV
1						FHTGEKPYECKECGKAFNCGSS
						LVQHERIHTGEKPYE\CKECGK
					1	GFS\GGYHLTQHQKIHTGEKPF
					1	KCKE\CGKAFSWGSSLVKHERV
		1				HTNEKSYECKDCGKAFGSGYQ
1						LSVHQRFHTGEKLYQRKEFGK
						TFTHGSKLVHERTHSNDKPYK
						YNECGEAFLWTTYSNEKIDTDE
	ــــــــــــــــــــــــــــــــــــــ		L		<u> </u>	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	ł .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25300	55668	Α	25439	32	447	VLGGSMMFREGQRGNRQKGP
	ŀ			1		KKRRNLALSSALLASTA\PAGG
						QPRHWRPG*CCLRQQL*PLQGN
						WAPVSPLQGHRSQLRAGYSISS
		ł				FLQMFAP*VQGAARAQPAPGA
						AVPRGSGRQGGPRAVDLHGFR
		1				VGWNRLRAASM
25301	55669	Α	25440	1	858	
25302	55670	Α	25441	147	1088	SRTTYKGKSSFQTYSDYLRWES
						FLQQQLQALPEGSVLRRGFQTC
						EHWKQIFMEIVGVQSALCGLVL
						SLLICVAAVAVFTTHILLLLPVL
						LSILGIVCLVVTIMYWSGWEMG
		1				AVEAISLSILVGSSVDYCVHLVE
					:	GYLLAGENLPPHQAEDARTQR
:						QWRTLEAVRHVGVAIVSSALT
		1				TVIATVPLFFCIIAPFAKFGKIVA
		İ				LNTGVSILYTLTVSTALLGIMAP
						SSFTRTRTS/CPQGPGCRAAGRG
		1				PGAGCLPRAPAERL*DSPARRG
						LPIARDGLWTLAPLVPWVGDR
						SCFPARLQLAVSPGLGPGRPAG
25303	55671	Α	25442	1	1596	MGVSVRVDCGCARASEFLGRP
		1				RGAVRGADPGSGLTETCAQSR
j		1				TWARARSKGGFRLTLNFYGPR
		l				YPSEGTSRGQRSEALPFLDIQHP
		1				TPLGRPRMLQSRGEMVRSWGP
		1				VVEGKLGFCPPLTVFPGGLRGP
		1				HPGLAGERENFARGAKQEACL
		1				LQGPGDAGLTHPCPATGYFPEA
		l				SCTSRSIRMFINSQERQLADMSL
						FIADSWLCYSGIICWKSLEHQR
						GASLSCVYMEGKGGNIWMKAS
						NVLPLCQMLPTSGHSKSDLFGG
		ļ				LAVEKQMRQDHHILLHDRSGF
						QLAVTSPLLTRLGKGHIIQVPV
						YVLDAPSRWLGGLRLFRDSSCG
						LVLSLLICVAAVAVFTTHILLLL
	1					PVLLSILGIVCLVVTIMYWSGW
]						EMGAVEAISLSILVGSSVDYCV
						HLVEGYLLAGENLPPHQAEDA
						RTQRQWRTLEAVRHVGVAIVS
						SALTTVIATVPLFFCIIAPFAKFG
						KIVALNTGVSILYTLTVSTALLG
						IMAPSSFTRTRTS/CPQGPGCRA
						AGRGPGAGCLPRAPAERL*DSP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25304	55672	A	25443		2355	MDHPGFREFCWKPHEVLKDLP LGSYSYCSPPSSLMTYFFPTERG GKIYYDGMGQDLADIRGSLEL AMTHPEFYWYVDEGLSADNLK SSLLRSEILFGAPLPNYYSVDDR WEEQRAKFQSFVVTYVAMLAK QSTSKVQVLYGGTDLFDYEVR RTFNNDMLLAFISSSCIAALVYI LTSCSVFLSFFGIASIGLSCLVAL FLYHVVFGIQYLGILNGVAAFV IVGIGVDDVFVFINTYRQATHL EDPQLRMIHTVQTAGKATFFTS LTTAAAYAANVFSQIPAVHDFG LFMSLIVSCCWLAVLVTMPAA LGLWSLYLAPLESSCQTSCHQN CSRKTSLHFPGDVFAAPEQVGG SPAQGPIPYLDDDIPLLEVEEEP VSLELGDVSLVSVSPEGLQPAS NTGSRGHLIVQLQELLHHWVL WSAVKSRWVIVGLFVSILILSLV FASRLR\SASRAPLLFRPDTNIQ VLLDLKYNLSAEGISCITCSGLF QEKPHSLQNNIRTSLEKKRRGS GVPWASRPEATLQDFPGTVYIS KVKSQGHPAVYRLSLNASLPAP WQAVSPGDGEVPSFQVYRAPF
						GNFTKKLTACMSTVGLLQAAS PSRKWMLTTLACDAKRGWKF DFSFYVATKEQQHTRKLYFAQS HKPPFHGRVCMAPPGCLLSSSP DGPTKGFFFVPSEKVPKARLSA TFGFNPCVNTGCGKPAVRPLVD

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25305	55673	A	25444		1737	MLYAAECLRNVMKLQVIPSAL NEALQAQSTWSDLGLASHALS STWCLHGESAAWSQPAVVECG QPRDQLQTHSEAWLCALVATF SQELEQFAVTGAQISDRQGHAV CTAPPRGRPSTLMTNLVCASSA DECGGGKTETQTAGGRLQGAE TRSRGQLTRLITRTQAAEPRWF LQLLKRSANRSRALTRPFSGLSS DGARRLRLSFVSAVSSADTKPT VPVSSDSSGRDGCGETRAEAGP GGPHVAQPQRVAPPAAAARDF RKPRGLNRQNVSP/PGPGEQGP G/PRPQKPAGRAP\PEPQGEPGL GLFPR\GRPPRSFPGSPADPAAS VSHTQGPSPDTGLPGTCQNRLP NPAAVDEQTCTRGSLNCRLSRS PRVSERRGPEGTPGRRPAAPPQ CAGTRGLSPRADLGAAIRTPRA PYRPHGQGRPSRHNCDSVSSQG WPPHSCWWKTTSNGMPWKAS FCSRTAQPANQNTGNHERGLRS VAMFGDRASREATPALSLCESQ GCFEDEKEVFSPEPHVETSDEPL
						PICSGPGDGWGDPIARPGRGNN LSPGTSAWEVPRWIRVTGEDW LSTGPAECVFINDLTT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25306	55674	Α	25445	2	1642	LLSSISAWFGPPASTPAFTMSIR
		1				VTQKSYKVS\TSCPRAFSTRSYT
		Į	į			SRPGSRISSSSFSRVGSSNFRGDL
						GGGYGGASG\MGGITAVTVNQ
		1				SLLSPLVPEVDPNIQAVRTQEKE
						QIKTLNNKFASFI\DEVGFLEQQ
						NKMLGTKWSLLDQQKTA\RSN
						MDNMFESYINNLRRQLETLGQ
		1				EKLKLEAELGNMQPLVEDFKN
						KYEDEINKRTEMENEFVLIKKD
						ADEASMNKVELGSRLEGLTDEI
						NFLMQLYEEEIRELQSQISDTSV
						VLSMDKSRSLDMDSIIAEFKAQ
						YEDIANRSRAEAESMFQIMYEE
						LQSLAGKHGDDLRRTKTEISEM
						NRNISR\LQAEIEGLKGQR\ASL
		1				GGRPLQDAE\QRGK\$WPIK\DA
						NAK\LSEAGSPPLQAGPKQDMG
						R\QLREY\QKLMNVKAGPWTIE\
						IATYQESCLEGEEEPGWSLGCQ
						NMSI\HT\KTTQRGYAGRPEPPP
	-	l				MGGFTSP\GFSYKPGAPGFGSG
						AGS\SSFNRHQLSPGAVVVKKIE
						TRDGKLVSES\SNVLPKVKQLR
		Ì				QPLPSLPLLRCPRGLGKEAPYP
25307	55675	Α	25446	1	1280	MAYLCNAICMTHMVTLDPVDQ
		l				ALPGATTATSVPGPQCDASCM
		ŀ				MLFAVVPFNGIALAATQGAQS
	İ	l				MLPPRVQGSLSSKPSTRRGRDA
		ļ		İ		PGLQVSQAPPPRRGFAVGRRYS
		l				PPALAPGRCAAPHGGGRKELPT
				i.		RRPGHGMAPKFPDSVEELRAA
						GSESFRNGQYAEASALYGRAL
						RVLQAQGSSDPEEESVLYSNRA
						ACHLKDGNCRDCITDCTSALAL
	1	l				GPFSIKPLLRRASAYEALEKYP
	1	l				MAYVDYKTVLQIDDNVTSAVE
	İ					GINRGPGLKEDTTQKRWNSLPS
						ENHKEMAKSKSKETTATKNRV
			ł			PSAGDVEKARVLKEEGNELVK
						KGNHKKAIEKYSESLLCSNLES
						ATYSNRALCYLVLKQYTEAVK
						DCTEALKLDGKNVKAFYRRAQ
						AHKALKDYKSSFADISNLLQIEP
						RNGPAQKLRQEVKQNLH
			L	1	L	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25308	55676	A	25447	1	1297	MHLLSAYFVPGSMLVGSGYM MVNITDVSPPSWSFLCSMLITTT
						QGAQSMLPPRVQGSLSSKPSTR
	ļ					RGRDAPGLQVSQAPPPRRGFAV
						GRRYSPPALAPGRCAAPHGGG
						RKELPTRRPGHGMAPKFPDSVE
		İ				ELRAAGNESFRNGQYAEASAL
						YGCALRVLQAQGSSDPEEESVL
						YSNRAACHLKDGNCRDCIKDC
						TSALALVPFSIKPLLRRASAYEA
						LEKYPMAYVDYKTVLQIDDNV
						TSAVEGINRMTRALMDSL\GPE
						W/RALKLPSFPLVPVSAQKRWN
	}					FLPSENHKEMAKSKSKETTATK
						NRVPSAGDVEKARVLKEEGNE
		1				LVKKGNHKIAIEKYSESLLCSN
		1				LESATYSNRALCYLVLKQYTEA
		1				VKDCTEALKLDGKNVKAFYRR
						AQAHKALKDYKSSFADI\SNLL
		<u> </u>				QIEPR\NGPAQEVAGREVKQNL
25309	55677	Α	25448	3	491	GITFTHSPAATGGGAQRVRRRD
						PPPGVQLRNMAQETNHSQVPM
						LCSTGCGFYGNPRTNGMCSVC
8						YKEHLQRQNSSNGRISPPATSV
						SSLSESLPVQCTDGSVPEAQSAL
						DSTSSSMQPSPVSNQSLLSESV\ ASSQLGQYICGTKAVPETEDVQ
		1				ASVSDTAHV
25310	55678	A	25449	1	860	HLLLAIDYNLPIAGVLMESQY
23310	33076		2377)	1	1000	LGASPKRLVIPNLYAHRKSLAT
						LEPYAPRRPMPIARRYAIPYMS
						HHNGYIGDVYYRLTVEEKKSSF
						IARRSILTTEFTIRRTKKVPVPSI
						NMSSASPLEDESRPSAGVQLRK
ļ						GRYRLLRDRYRPGCNSVGESPR
						KSSFSDDIMATESRESIFAEEPR
:						TGEHSVRGPVSNQSLLSESVAS
						SQLDSTSVDKAVPETEDVQDSL
						NASPTKQQCG/DVQTVDLYSNN
		İ				KELFAQKCYRHRYISRLKKCCL
						CHELVPRDTIKSPESLSVGS
25311	55679	Α	25450	880	1196	SPTTRRGTPGTCLKPTACAGAA
						*PGCSARRTCASAAPLSTCPPSS
		1				CAAPPPAPAAVPSTPRPTSPSPW
						AAPASPSRRRTQTASTPASTNR
						APSSCWAPTTRPLAP
25312	55680	Α	25451	254	579	IEKISLEPKNRPSPQIPNLVGP/R
						LFLVPGDFQSQVPNFLPFKPSSG
						PHPAAGKGQPFSFLPAWRSTGP
						ERATPGPGRPAACSALEAPSLR
	<u> </u>		<u> </u>			GPSGYSAQEPPRRPISARI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
ļ	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
25313	55681	A	25452	6	1442	RSELIRHSWPRHAQLRGARART
						AVSIRECISVHVGQAGVQIGNA
		İ				CWELFCLEHGIQADGTFDAQAS
				}		KINDDDSFTTFFSETGNGKHVP
						RAAMIDLEPTVVDEVRAGTYR
		İ				QLFHPEQLITGKEDAANNYAPG
		1				PPTPGGKESIDLV\LDRIRKLTD
		1				ACSGLQGFLIFHSFGGGTGSGFT
						SLLMERLSLDYGKKSKLEFAIY
						PAPQVSTAVVEPYNSILTTHTTL
						EHSDCAFMVDNEAIYDICRRNL
						DIERPTYTNLNRLISQIVSSITAS
						LRFDGALNVDLTEFQTNLVPYP
		1				RIHFPLVTYAPIISAEKAYHEQL
						SVAEITSSCFEPNSQMVKCDPR
		1				HGKYMA\CCMLYRGDVVPKD
						VNVAIAAIKTKRTIQFVDWCPT
		ŀ				GF\KVGINYQPPTVVPGGDLAP
1		:				VQRAVCMLSNTTAIAEAWARL\
						DHKFDLMYAKRAF\VHWYVGR
						GDWKKGEFSEAREDLAALEKD
İ		l			ļ	<u>}</u>
25214	55692	 	25452		618	YEEVGVDSVEAEAEEGEEY SSAGREPDPSDLPRRLCFTHRLP
25314	55682	A	25453	3	018	AARRWVQLCVHASPEPGGQGV
						CPGRSERMVIRVFIASSSGFVAI
						1
						KKKQQDVVRFLEANKIEFEEVD ITMSEEQRQWMYKNVPPDKKP
1						TQGNPLPPQIF\NGDRYCGLLVS
1						FSVICIKNPNWHNLFLLIPWSGI
1						NPYCEQDSSFSENVGDEILKNS
						GVPRDFTSILIQKERKSEKVKG
25015	55600	١.	05454	2	404	VDQGHR
25315	55683	A	25454	3	424	SWTMAATIQAMERKIESQAAH
						LLSLEGQTGMA*S*GTPPCCPG
						AAAGSRSSCCAAGSPRSPAASA
						AARTPAAGSPARPTCPPAGSRT
						PRLSSRNQPASSRPSRFDLLGKA
						GEQPAIQSSSPWPESWLPSSTK
25316	55684	A	25456	268	445	
25317	55685	A	25457	3	205	
25318	55686	A	25458	27	272	AKCSGQGPGRVRAQGERADHE
23310		[*	23 .50	 -'	[-,-	CPGAGAGGGGCNSAASAREES
						SRLISG\SLQMQNVSLASRRKEE
						EVRAAAAGGAAAGRPRV
25319	55687	A	25459	1	253	2.70mmioommioom
25320	55688	A	25460	2145	2399	
23320	133000	1'1	123700	14177	1-3//	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25321	55689	A	25461	174	1309	HLLCCRAORRPOTPPAARGLEA
						CSEGALKMPEAPP\LLLAAVLL
						GLVLLVVLLLLLRHWGWGLCL
						IGWNEFILQPIHNLLMGDTKEQ
						RI\LNHVLAACGSPGNAQSVLG
						GHLTPNCEQKEW/APLNVGDK
						KGQDSWDALISREQPALPCLLG
						NLGAYFGLLQLLRMAR\LLVNQ
						GARLIHHSRFNPDLCPPSPKRM\
ŀ		ŀ				VDFAGVKDKALFQVTL\VCGAS
						PETFHPPSLKKKYDVGHNWTW
						VFLDHWKDRYL\PDTLLLE\EC
			ŀ			G\LLPEGGQLLLAEQRLSSPGAP
						\DFL\AHVSREPACFG\CT\HYQI
1						VPWKYRE\VVDGLGRRPI\YKG
						P\GSEAGALTAPPRPPSRALSPK
						PGTEGARPWLLLTLVRLRACVL
						NAKSHARAESLRA
25322	55690	A	25462	2470	3460	SGPCPRCCAECRPYKTRPRSRV
						PGTHGPGPADHGQPPCCMAGA
ŀ						HPPRPQAWMLLQTHSQDCEGK
}						VGCGGIFCPCYHHCKHTHHHH
		1				ННРИНННҮНҮНННИННОННН
						ннниннуннунзнуннуннн
						НСННН\НННННРҮРННҮННН
						RGQDHНРНРНННН/НННҮННН
						НҮНННҮНРНННННОРОН
		1				НННОНУНННУНННРННРНН
1]		РНННННҮНҮННННННҮ\НРҮ
						РННҮНННННННРНРНННН/
	8					НННҮННРННПНҮННННРН
						НННКРНННКНОНРННҮННН
						НРНРСНННКІНННКНННҮНН
						TSSVQGPGSQPAGASLPGQACR
25323	55691	Α	25463	1	407	DAERQEALGIVRRIGTDTEAAT
						EPAGATVPAAAAAARIGTVGP
						QPPAMPRRKRNAGSSSDGTEDS
						DFSTDLEHTDSSESDGTSRRSA
						RVTRSSARLSQSSSRISRSCSKS
		<u> </u>			<u> </u>	GSLLALRSLLTLPEE*PVVSSSL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25324	55692	Α	25464	3	2539	RILYIPDGHRAPGASQSGNWEH
ļ.						PLLLLEPGNLASSPSMSLAYPHP
						CGLTIHQEHRRAHEELAYTPND
		l				RASSTGHPAFIEDGNPSPVLAFA
ŀ	ł	İ				ASPRPNDSYILKREPPESCEKER
						VFEEATTRGKYGEGAKQETFTF
						ALTLVFIQCVINAVFAKILIQFF
						DTARVDRTRSWLYAACSISYLG
						AMVSSNSALQFVNYPTQVLGK
						SCKPIPVMLLGVTLLKKKYPLA
						KYLCVLLIVAGVALFMYKPKK
						VVGIEEHTVGYGELLLLLSLTL
						DGLTGVSQDHMRAHYQTGSN
						HMMLNINLWSTLLLGMAVSCP
						DQGPELVPRCPFVQALEKPSWK
						NLHQQDLFATCYWHNEGESCV
						SCHGKTLSSKTQGGILFTGELW
						EFLSFAERYPAIIYNILLFGLTSA
						LGQSFIFMTVVYFGPLTCSIITTT
						RKFFTILASVILFANPISPMQWV
						GTVLVFLGSTQIILDNLKILNTS
						AKTLLYKTPLSWQELEGERASS
						CAHKRSASWGSTDHRKEISKLK
						QQLQRTKLSRSGKEKERGSPLL
						GDH/VSAGSTEGVPS/RASPQGP
]	ŀ				LSCDSAPACT/VSLEGLNQELEE
		İ				VFVKEQGEEELLRILDIPDGHR
						APAPPQSGSCDHPLLLLEPGNL
						ASSPSMSLASPQPCGLASHEEH
						RGAAEELASTPNDKASSPGHPA
						FLEDGSPSPVLAFAASPRPNHSY
]						IFKREPPEGCEKVRVFEEATHQ
25325	55693	Α	25465	845	1316	LSLGDSAQCLLPHASWCQVAG
						HPAFLEDGSPSPVLAFAASPRPN
						HSYIFKREPPEGCEKVRVFEEAT
						S/RRVLTGPFLTSCPDK\NKVHF
						QP\TGSAFCPVNLMKPLFPGMG
		}				FIFRNCPSNPGISSSPGQPQATTS
ĺ						EGSGSLQGLPTAIRAMAAHPYH
		•				Q

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25326	55694	A	25466	1077	1506	CDACGRRCRTCRTFCLGLQPAG LDGHHHRHPDCWFPWSPRHR* GMIIDVFSRYSGSEGSTQTLTKG ELKVLMEKELPGFLQILTNEDE PLVTIPFLSHSCSLAYLLTTSGN RVNALLKWLLKLGERWQMTE EGIKGQRSGHGPEQAENPLGDS VPQDTTKDVPLTQHRLHQGLE AGVPKTSVPARPGLPVPALQHA QIPGPCERALLHCHNGPQRLQH SLQGEEQRETHLRGQDWPCTL QMRTLKREVHALPGGRAGGAA REGLGASICETGEHQMTNFQVP RWPPCFPGQAGPVLGTGTRHG LDLLSGRPGTVRKGSSVARIMK EEVTVTKQSAADLRHTGQGPT CCVLSGGRCGSQACSRRPFSLL LGDESEPHGRGPFAAALHHRR NPLNDVMLVGDDAGPAGHFAS VYNPLAWTVTTIVTLTVGFPGV RVTDEAGHPVPSQVSGIQRCLQ GMKAPPVTVTVSGEKGSCLCA SCVLCLEHPYFPLVPWLPPVFR DSVIPSSTSPQEAVLADVGFRN NVPQRAQLKPQKQILTPF
25327	55695 55696	A	25467 25468	846	783 1392	PDPAAHRFGHPTLHPGSLRTSS GAGTWYQNPQHHNDHDYYHH ННННОДННҮНҮННННННННН ННҮННННННННННННННН
25329	55697	A	25469	181	412	LRSDQQTRKFVSRSSGACSPPTT TELSWPPSLLPSL*FHSPSSQP* MNHSASTTSPLPSFITERESILAT EWDTARN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25330	55698	A	25470	1	848	MPSLNTIVSPLGSPHTSLIPPML
						LSANLPFDTTIMIKLQTACSAPI
						HNLQRPCGENLRTSTFVRRLDR
1						NLVKSPQPGGGGQPSRQWEAR
						GAEPQGRRDPSEVQ/RPAGRGF
						GRISRAPRKPSRAPTPTQGLGPP
						LGAGGQGSLASCRPARKNARPP
						TRAAAHSAHPHSHWHSHARPQ
						PQSPSAAGQSGDPWPPARVPPP
						PLLRLPQRRTAGRTPVDAPARG
						IFTLSLSSSHSKSSGKHRGARKT
						PEMWPLFRGSLSKLSRRRKVSP
		1.				SAALHWRLRRTQKRLCC
25331	55699	Α	25471	92	1083	TMRTHGHRKGNITPWGLSGVG
						GL/ETGRALGEIPNVDEGLMGVI
						AAVAIVLVSLLFVMLRYMYRH
						KGTYHTNEAKGTEFAESADAA LQQRERALDSSRDSHLETLGAC
						PGRNGGGLALQEATPRDPGRR
						WPPQRPPFAPRRWEKIWAHGPL
						GSAGQHQLTGRKVLVEGLGCI
						CMAHTDLQNTSVAKMAINRPN
						EYAQVSLENDVSCKVKAVQAP
						QRLHWPSVDADTGGRGAVHIA
						FPKHVEPETPFAHTIPARNSWT
						KWSSEHILETLSPQKPALPWAP
					1	RQQGRPLGLTAPISKRLGPGDG
						PEGEAGERLAQAHFINTRPPST
						GPPGTPAAD
25332	55700	Α	25472	73	424	RPGMWSTRSPNSTAWPLSLEPD
						PGMASACTTMHTTTIAEPDPG
						MSGWPDGRMETSSPTIMDIVVI
						*CAIAAEAIVLVSLLFVMLRYM
		İ				YRHMGTYHTNEAKGTGVADS
		 	2.1-2	100		ADACPAGDPA
25333	55701	Α	25473	139	546	RPGMWSTRSPNSTAWPLSLEPD
						PGMASASTTMHNYHHCRSLIPG
1						M\SGWPDGRMETSTPTIMDIVVI
						AGVIAAV\AIV\LVSLLFVMVAL
						TCNRA/HRGTYHTNEAKG\TEF
						AESADAALQG\DPAL\QDAGDS SRK\EYFI
25334	55702	C	25474	142	408	SMX/E I F1
43334	20/02	л~_	1234/4	144	1700	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
2	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25335	55703	A	25475	44	727	ARAGSRSRGLPFCGTAGPPPKA
						TLWGGLLRLGSLLSLSCLALSV
						LLLAQLSDAANNFEDVRCKCIC
		l				PPYKENSGHIYNKNISQKDCDC
ļ	}			İ		LHVV\DPMPVPGA\NVEAYCLR
						CECKYEE\RSS\STIKVTIIIYLSIL
				İ		GLLL\LYMVYLTLVEPILKRRLF
		ŀ				GHAQLIQSDDDIGDHQPFGKCT
						RCASPLPQFEPTCWNKVEYAQ
						QALESFQVQEQRKSV\FDRACC
				İ		PQLNLGN
25336	55704	A	25476	11	1323	VVLLVSVNTEAEESEKAATEQR
		ĺ				/PLEGTDQTLDVEEEQEESKAA
						ACGSKKRVVPGIVYLGHIPPHF
						QPLHVRNLLSAYG/RSPSHYDL
						WNLKYLHHFTWSHHSEHLAFE
						RQVC\HRQHLRVEVTQAKCETI
						FYLQSVEWGQCFLAVDGDLAH
<u> </u>						PDGSWTFAQRPTEQELRARKA
						AQPVGKVLNYYPTQLSLECEVP
						SQPMGTGHSHRGLCQDVKVIN
						VPVSFVWCALVAGLLVVVPPPP
						PQAPEAEVSDISLKRGLQREIEQ
						CRRDIQNFPFPCASEELASQLFP
						LMEVPQGRGTTGFMNAPLTTS
						EVRGLKKELKPLLDDPERVAEQ
		1				IDQFLGSKLYTWTELMSILGILF
						SKEERNMICRAAMGAWERDYP
						AGQNIPAADVTFPARDPQWNN
	ļ					NNAAHQKNMRDLQELIIKGIKE
	}			1		SAPRPQNLTKAFDEQQEKDEGP
25337	55705	Α	25477	1	490	GTSGTRPLVSVNMEAEESEKA\
	}					ATEQEPLEGTEQTLYAEEEQEE
						SEEAACGSKKRVVPGIVYLGHI
						PPRFRPLHVRNLLSAYGEVGRV
						FFQAEDRFVRRKKKAAAAAGG
						KKRSYTKDYTEGWVEV\RDTR\
						IAKRVA\AALLK*PMGARRRSP
						FRYDLWNLKYLHR
25338	55706	A	25478	2	574	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	l • · · ·
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25339	55707	A	25479	160	1548	KTSSQTLSLALTMFQRLNKMFV
23337	33707		23477	100	1540	GEVSSSSNQEPEFNEKEDDEWI
		1				LVDFIDTCTGFSAEEEEEEEDIS
ŀ		l				EESPTEHPSVFSCLPASLECLAD
}		1				TSDSCFLQFESCPMEESWFITPP
ŀ		1				PCFTAGGLTTIKVETSPMENLLI
]				EHPSMSVYAVHNSCPGLSEATR
l						GTDELHSPSSPSILPNKMLSVHV
						GTAIHNQAALCQSVESYWQCGI
						QLLTQFQSQSKLGQLLAATCKE
						LPGPKESRRTAKDLWEVVVQIC
						SVSSQHKRGNDGRVSLIKQRES
						TLGIMYRYVLEPLVLTIILSLFV
						KLHNVREDIVNDITAEHISIWPS
						SIPKKQMSSRTFMSQEETVCRA
						AHTPSLPEEKWVEQLIYALVVA
						AARIMAMWGPNAAWLVFLAA
İ		1				AGPPPLTPPHSPP/PPPPPPALGR
						WMGPPLRDSASGLPRPPPGRISE
						DSGAWACGPALCPRPAIPSPAP
						ALRVPEALRLWGTCSV
25340	55708	A	25480	1	380	FTSPKTARNWGWLMQVRNQR
23340	33708	^	23400	['	360	LVLGKAGGKKGSPLEQRGGNG
						HHGGTRLICALV\LVS\MRPLAT
					ļ	FAEPQTETCTVAPRERQNCGFP/
						GVSRPPQCANKGCCFDDT\VRG
						VPWCFYPNTIDVPPEEECEF
25341	55709	A	25481	3	2367	VI WEI II NIID VII EELEEL
25341	55710	A	25482	2	1230	WRRSRRRRPPAPQAGGGDFRA
23342	33710	^	23402	2	1230	GISPPTGKKSLGLMEPQGNHYR
1						CRCLQVAGSQAWARCVSMPEL
						VVQKVVGHP/LVLLSVVDHFNR
						IGKVGIQKCVIGLFWGSWQKK
						VLDVLNSFAVPFDEDDKDNSM
						WFLDHDYLENMYGMFKKVNA
						RERIVGWYHTGLKIHKNGITIN
						ELMKRYYPNSVLIIIDVNPKDL
						GLPTEAYISVEEIQDDGTPTLKT
						FEHVTSEIGAESYLEKVATGKL
		1				RINHQIIYELQDVFNLLPDVSLQ
					1	EPIKAFYLRTNDQMVVVYLASL
						IHSVGLTDPFC\VALHNLINNKI
						ANQDGDKKEGQEKKES/KKDR
		1		1		KADKGKDKDKEKSDVKKEQK
						NHCLKEKYRFRQDSLPDDPRVL
				1		GLELTPPVARQYSPQDLSEIPRH
L	<u> </u>	L	i	<u> </u>	1	ADFRCDPAHFQLWWSQGETPS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25343	55711	A	25483	3	1042	DRYCCRCLRVAGSQAWRAGC
						VAMPELAVQKVVVHPLVLLSV
						VDHFNRIGKVGNQKRVVGVLL
						GSWQKKVLDVSNSFAVPFDED
		İ				DKDDSVWFLDHDYLENMYGM
						FKKVNARERIVGWYHTGPKLH
						KNDIAINELMKRYCPNSVLVIID
						VKPKDLGLPTEAYISVEEVHDD
8				1		GTPTSKTFEHVTSEIGAEEAEEV
						GVEHLLPDIKDTTVGTLSQRITN
		į]		HVHGLKGLNSKLLDIRSYLEKV
}						VTG\KLPINHQIIYQLQDVFNLL
						PDVSLQEFVKGFYLKTNDQMV
						VVYLASLIRSVVALHNLINNKI
						ANRDAEKKEGQEKEESKKDRK
						EDKEKDKDKEKSDVKKEEKKE
25344	55712	Α	25484	257	1566	GLEHLCNPRWPLLFLRAMDST
						VPSALELPQRLALNPRESPRSPE
						EEEPHLLS/SLAAVQTLANVIRP
						CYGPHGRQKFLVTMKGETVCT
						GCATAILRALELEHPAAWLLRE
						AAQTQAENSGDGTAFVVLLTE
		1				ALLEQAEQLLKFGLPRPQLR/EA
						YATATA/EEKQVGQL/AAAGIN
						VAVVLGEVDEETLTLADKYGI
						VVIQARSRMEIIYLSEVLDTPLL
		İ				PRLLPPQRPGKCQRVYRQELGD
						GLAVVFEWECTGTPALTVVLR
						GATTQGLRSAEQAVYHSIDAYF
				′		QPCQDPRLIPGAGATEMALAK
						MLSDKGSRLEGPNGPAFLAFAR
		ŀ				ALKYLPKTLAENAGLAVSDVV
						AEMSGVHQGGNLLMGVGAEGI
						INVAQEGVWDTLIVKAQGFRA
						VAEVVLQLVTVDEIVVAKKSPT
						HQQIWNPDSKKTKKRPPPVEK

SEQ ID	1 -	l .	SEQ ID NO:	l .		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	of peptide sequence	detetion, (=possible nucleotide insertion)
	<u></u>					
25345	55713	Α	25485	145	1918	PLEYFQRSVSGVPQLLFLEHLC
						NPRWPLLSLRAMDSTVPSALEL
						PQRLALNPRESPRSPEEEEPHLL
 					1	SSLAAVQTLASVIRPCYGPHGR
1						QKFLVTMKGETVCTGCATAILR
						ALELEHPAAWLLREAGQTQAE
			ŀ			NSGDGTAFVVLLTEALLEQAEQ
			:			LLKAGLPRPQLREAYATATAEV
						LATLPSLAIQSLGPLEDPSWALH
ŀ						SVMNTHTLSPMDHLTKLVAHA
					1	CWAIKELDGSFKPERVGVCALP
		İ	:			GGTLEDSCLLPGLAISGKLCGQ
			:			MATVLSGARVALFACPFGPAH
			:			PNAPATARLSSPADLAQFSKGS
						DQLLEKQVGQLAAAGINVAVV
						LGEVDEETLTLADKYGIVVIQA
			:			RSWMEIIYLSEVLDTPLLPRLLP
						PQRPGKCQRVYRQELGDGLAV
						VFEWECTGTPALTVVLRGATT
						QGLRSAEQAVYHGIDAYFQLC
						QDPRLIPGAGATEMALAKMLS
						DKGSRLEGPSGPAFLAFAWAL
				-		KYLPKTLAENAGLAVSDVMAE
						MSGVHQGGNLLMGVGTEGIIN
				•		VAQEGVWDTLIVKAQGFRAVA
				:		EVVLQLVTVDEIVVAKKSPTHQ
				•		EIWNPDSKKAK\KHPPPVETKKI
25346	55714	В	25486	1	642	DIWIN DOMARKATI II V DIKKI
25347	55715	A	25487	3	395	FLPVNLTHDWQGSSALATLERP
23317	33713	l' `	25 107	ľ		LSQVRLKRFVGTLIAFMVSAIVI
						LATASMAVASITESVQTAAFID
						NMARNVSNKLLLQQGIDQKIL
						ALLQSLEAALEYVGEQQDALA
						FQQQ*NCNWGHKHICIISLPWN
25348	55716	A	25488	3	358	HEPMCGETHQALQGAMEKLW
23310	33710	` `	25100	ľ		SRFMELMQE/KKVDLKERVEEL
						EHCCI*LSGERQTPSGSGKPGHG
		İ	1			KESCTLVRGAPASESCPPAGEYI
				1		ALYQSQRAVRKEEECISRLAQD
}]		KGEVKVKLLE
25349	55717	Α	25489	1	250	VQCGGIPPGQNNKEEMEVLPEP
22347	33111	l'^	23407	l'	250	PPPINRKKDKSYATAMGPFLRQ
						EALSGELLACLVIQD*QGNWV
						YKPISFNIYKKLRKSIRG
25350	55718	A	25490	1	702	I INTISTINI I KALANSIKU
25350	55719	A	25490	1	252	
25351	55720	A	25491	1	122	LAPLVTYFSSLSLGFFNLKGKL
عدوده	33720	^	23792	1	144	APSSWRC*GLNEIIRGKH
25353	55721	A	25493	3	505	711 SUNICO GENERIKOKII
23333	133,21	1.7	25795	l-'	505	

SEQ ID			SEQ ID NO:	L	1	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		02/340,217	sequence	or peptiae sequence	deterion, i possible adelectide insertion,
25354	55722	Α	25494	1	3345	MRVGFRDIVGSLSEYSFGCPVN
						YEVFHSVWITILCCLMANDRKP
						QFLYFFQFFSFHGGRNLMSSFH
		1				PGNGHNDSRRSVFYANEKWEF
		1				LDPTPKDLEESIVQEEKKEPTPE
		1				GNKVSQRLKNLPHTSLKAKQL
						LQTSSTNRGTVITATRLAFDLRT
		1				QSTKCSHPASGSSGHSTDFQLE
	1					GEWGLWDLGTKGFKLPYSLSI
		1				DIDNVKSPHFPHELKTLTVSLGS
						NRRMGLEKKECHQKQGALREQ
		<u> </u>				LQVHIQNVEILVSE
25355	55723	Α	25495	296	1350	TLWLQGEQPSTQEIHEKV/LNE
						AMGAMMYHTIILTREDLEKFK
						APRVIVQIGSGYDNVDIKAASE
						LGIAVCNIPSAAVEETPDSTICHI
						LNLYQRNTWLYQALRGQAVA
						VRAKAFGFSVIFYDPYLQDGIE
		l				RSLGVQRDLLYQSDCVSLHCN
						LNEHNHHLINDFTIKQMRQGAF
]	LVNAPHGGLVDKKALAQALKE
]						GRIRGAALYVRESEPFSFAQGP
					[LKDAPNLICTPHTAWYSKQASL
					}	EMREAAATEIRRAITGHIPESLR
						NCVNKEFSVTSAPWSVIDQQAI
						HPELNGATYRYPPGIVGVAPGG
		ŀ				LPAAVEGIIPGGIPVTHNLPTVA HPSQAPSPNQPTKHGDNREHSN
25356	55724	A	25496	694	1185	PKPFKEGTIRGAALDMHESEPF
23330	33724	^	23490	1054	1105	SFAQGPLKNAPNLICTPHTAWY
İ		l		ļ		SEQASLEMREAAATEIRRAITG
						CIPESLRNCVNKEFFVTSAPWS
		l				VIDQQAIHPELNGATYRYPPGV
						VGVAPGGLSAAMEGIIPGGIPV
						THNLPTVAHPSQAPSPNQPTK*
						MK*KQMGEVA*GAARIRGETL
						GLNGFGCTGQA/VAVRAKAFG
						FSVIFYDPYLQDVVERSLGVQR
						VYTLQDLLYQSDCVPLHCNVN
						EHNNHLINDFTIKQMRQGAFLP
				1		PKPFKEGTIRGAALDMHESEPF
						SFAQGPLKNAPNLICTPHTAWY
]		SEQASLEMREAAATEIRRAITG
						CIPESLRNCVNKEFFVTSAPWS
						VIDQQAIHPELNGATYRYPPGV
						VGVAPGGLSAAMEGIIPGGIPV
						THNLPTVAHPSQAPSPNQPTKH
L	<u> </u>		L	L	1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25357	55725	I _A	25497	290	1251	 PFMLYVSISTLYIAFCHILNLYR
23337	33723	ļ'`	25177	2,0	1231	RNTWLYQALWEGTRVQSVEQ
						MGEVA*GAARIRGETLGLNGF
						GCTGQA/VAVRAKAFGFSVIFY
						DPYLQDVVERSLGVQRVYTLQ
						DLLYQSDCVPLHCNVNEHNNH
	1					LINDFTIKQMRQGAFLVNAARG
						GLVDEKALAQALKEGTIRGAA
	}					LDMHESEPFSFAQGPLKNAPNL
						ICTPHTAWYSEQASLEMREAA
	1					ATEIRRAITGCIPESLRNCVNKE
		1				FFVTSAPWSVIDQQAIHPELNG ATYRYPPGVVGVAPGGLSAAM
						EGIIPGGIPVTHNLPTVAHPSQA
25358	55726	-	25498	1	1520	PSPNQPTKHVDNREHPNEQ
23338	55726	A	23498		1538	MLLQKTQFEYAFKKKRKLEES
						KKRGAGPASSDPRWRGSSQTA
						PHASEVSGAPLGRSCETTRDTG
						VGPSPRQWLGAGAGTWQHRA
						RAASTPSSRGLRALQTWGGGE
						VMNGPLH\PPPPRVALLD/SRNC
						TVEMPIPKDLATMAFCDTHSTQ
						EIHEKILHEALGAMRYHTITLA
		1				RADLEKFKALGVIVRIGSGYDN
			ľ			VNIKAACELEIAVCNIPSAAVEE
						TANSTICHILSLYRRNTWLCQA
						WARKHVCYSMGQIREVALGG
·						AHIGGETQG\LIGFGSTGQAVPV
						RAEAFGFSVIFYDPYLQDGIERS
	İ	1	·			LGVQRMSQGAFLVNAARGALV
						DEKALAQALNNGKIR/GAALDV
	1					PQSELFSFAQG\SLEMREAAATE
						IRRTITGCIPESLRNCVNKEFFVT
						SAPWSVIDQQAIHPELNGATYR
	İ					YLPGFVCVAPGGLPAATEGIIPG
						GIPVTHNLPTVAHPSQAPSPNQP
		1				TKHGDNPEHPNEQSRECRKVII
						QIHLRPRDSEKLMNSEKTNLTV
	1	1.	0.5555		2505	FLADSGHMHY
25359	55727	A	25500	1	2595	CCHD A V DEGIGE V D VICE LA SUB-
25360	55728	Α	25501	561	1023	SGHDAYREQIQEYRVISLLLNP
						N\DHVNKCQSTNDAYPTGFRIA
						VYSSLIKLVDAINQLREGFERK
]			AVEFQDILKMGRTQLQDAVPM
1						TLGQEFRAFSILLKEEVKNIQRT
1		1			:	AELLLEVNLGATAIGTGLNTPK
						EYSPLAVKKLALKSLAFVGNLF
25361	55729	A	25502	2	227	
25362	55730	Α	25503	262	428	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25363	55731	A	25504	389	2310	ATSGPPGRSLGSACTIWVLVWT
		1				GSIPIYSFHGKVEKYMCFHNMS
	·					DDTWSAKVFFPLEVFGFLLPMG
			¥			IMGFCCSRSIHILLGRRDHTQD
						WVQQKACIYSIAASLAVFVVSF
						LPVHLGFFLQFLVRNSFIVECRA
	Ì		i			KQSISFFLQLSMCFSNVNCCLD
						VFCYYFVIKEFRMNIRAHRPSR
						ATEEVSKNLVAMKEILYGTNE
						KEPQTEAVAQLAQELYNSGLLS
		1				TLVADLQLIDFEASLGLHGLEQ
	•					AVDLALPIAQAQGEVLNNGKC
						MDQFPVDVYQGGAGT\YVNMS
			•			TNEVLANIGLGLMGHQKGEYQ
		l				YLNPNDHVNKCQSTNDAYPTG
						FRIAVYSSLIKLVDAINQLREGF
						ERKAVEFQDILKMGRTQLQDA
						VPMTLG\QEFRAFSILLKEEVKN
						IQRTAELLLEVNLGATAIGTGL
						NTPKEYSPLAVKKLAEVTGFPC
						VPAEDLIEATSDCGAYVMVQG
						ALK\RLAVKMSQI\CNDLRLLSS
						GPPG\SSIMPAKVNPVVPEVVN
1						QVCFKVIGNDTTVTMAAEAGQ
		1				LQLNVMEPVIGQAMFESVHILT
ŀ	1	-				NACYNLLEKCINGITANKEVCE
						GYVYNSIGIVTYLNPFIGHHNG
į		1				DIVGKICAETGKSVREVVLERG
				1		LLTEAELDDIFSVQNLMHPAYK
25364	55732	Α	25505	133	375	
25365	55733	Α	25506	3	505	ARGREGVSRRERPLLSARRLGA
		1				EWDSAGAETASGLQVPRLGGS
						WPQTSVFSAAVKARGCRIATLP
						MDLIGFGYAALVTFGSIFGYKR
						RGGVPSLIAGLFVGCLAGYGAY
ļ						RV\SNDKRECKKCHWFTAFLPG
		1				LPSMGVRFKRSKKIM\PAGLVA
		L				GL\SLM\MILRLVLLLL
25366	55734	Α	25507	244	696	

SEQ ID NO:	SEQ ID NO: of peptide sequence	•	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25367	55735	A	25508		1442	MGQLHQAQASADIATSRLQQT SLTDVTRHQQFFSTYNTDDFIQ FTATYREQTRTRRQRQYAVNH VTFFFGKCTFRDRHRHRVIGIVL NIGLTFPAHQTQDGIGSTRSQR QSRLVANKVATRNLVKHFDDD REANRGIQEAQTEHHHRGVLV NESRQRFGCQQHNRHRNHYRR HHHRQMVNHPYCSNYRIQRED GVKDDNLCDDHPETGIQLYASL LLQVFFFAANIYGWYAWSRQT SQNEAELKIRWLPLPKALSWLA VCVVSIGLMTVFINPVFAFLTR VAVMIMQALGYLQGVMPELQA DAFPVWDSCMMVLSIVAMILM TRKYVENWLLWVIINVISVVIF ALQGVYAMSLEYIILTFIALNGS RMWINSALIHQVVLDLIQQGIVI VWRDHLHMQRLHRLLAYHPC MYLVHIADFRDFPAHTRLQVQ RFPAIPVHLQVIHSRYLSTVATR YAESEATPVSGALGLLCPTLPIV
25368	55736	A	25509	133	375	TAESLATI VSGALGLECT TETTV
25369	55737	A	25510	2	471	AFAQRETAGRRVGQRWCGDCF RTPGTALGGSWPQTSVFSAAV KARGCRIATLPMDLIGFGYAAL VTFGSIFGYKRRGGVPSLIAGLF VGCLAGYGAYRV\SNDKRECK KCHWFTAFLPGLPSMGVRFKRS KKIM\PAGLVAGL\SLM\MILRL VLLLL
25370	55738	A	25511	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
25371	55739	A	25512	59	882	SRLKNASIFVASPSGKKAKGKK VAP/APAVVKKQEVKKVVNPLF EKRPKNFDIGQDIQPKRDLTSFV KWPPLYQRQRAILCKWLKVPP EINQFTQALDHQTAALLLQLAH KYRSETKQEKKQRLLALAKKK AAGKGGIPTKRPPVLRAGVNTI TTLLENKKAQPVVIAHDVDPIE LVVFLPALCHKMRVPYCIIKGE ARLGRLVHRKTCTTVAFIQVNS EDKGALAKLVGAIRTDYNDRY NEIRRHWGGNVLGPKSVACIG KLEKAKAQELATKLG

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25372	55740	A	25513		833	GTRPKMPKGKKAKGKKVAPAP AVVKKQEAKKVVNPLFEKRPK NFGIGQDIQPKRDLTRFVKWPR YIRLQRQRAILYKRLKVPPAINQ FTQALDRQTATQLLKLAHKYR PETKHEKKQRLLARAEKKAAG KG\DVP\TKRPPV\LRAGVNTFT PL\VENKKAQLVVIAH\DVDPM RGWLSFLPAL\CRKMGVPYCIIK GK\ARLGRLV\HRKTCTTV\AFT QVNSESQRRLWAKLVEAIRTN YND\RYDEIRRHWGGNDLRPK\
25373	55741	A	25514		1176	SVARI\AKLEKAKAK\ELATKLG MEKELVDHTGLFLSAHASEAL ALKLMIYSEVAHKLRAVRSQH PDMGVSLPLTPANSCPKTIERM RRSRELEREKDQSIETDHLPWA FGSTFLKTPLSCKTLMKYICYA FIINLSFVKGVSAVTLMMSEES NMQMQFSVSITSGFGPFKSHIIA AIPNAERKESQGEKMAPAPAVI KKQEAKEVVNPLFEKRLKNFGI GQDIQPQRDLTRFVKWPHYIRL QRQRAILS\AHKYRPETKQEKK QRLLAQAKKKATSK/EDIPTKR PPVLRAGVNMVTTLVENKKAQ LVMTAHDVDPIELAVFCLPAPC CKKGVPYCIIKGKARLGHLVHR KTCTTVVFTKVNSEDKGALAK LVEAIRTNYDRYDEIHCHWGG NVLGLKSVAHIIKLEKAKVKEL
25374	55742	A	25515	2	524	
25375	55743	A	25516	144	412	AGSCPFAAGPGPLGSGRCFVLIR FILIQNRAGKTRLAKW\YMQFD DDEKQKLI\EEVHAVVTVRDAK HTNFVGVSGTFKIILPPLWLASN
25376	55744	Α	25517	38	476	
25377	55745	A	25518	235	892	RSRVGTNRLFGETYPRASPGPQ STALLTAYKKMTDLVAVWDV ALSDGVHKIEFEHGTTSGK/REV VYVDGKEEIRKEWMFKLVGKE TFYVGAAKTKS/ATINIDAISGF AYEYT\LEINGKSLKK\YMEDRF KNPPILWVLHM\DG\ENFRIVLE KDAMDVWCNGKKLETARDFC KMSDTISDDTKVDEQERALSRT PEDKWNFRPAVPMRGERGSPS HCGQAH

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	sequence	ł	,	sequence	,	
		<u> </u>				
25378	55746	Α	25519	1	1233	MQLKFPGRQKIHISKKWGFTKF
		Ì				NADEFEDMVAEKRLIPDGCGV
					į	KYIPNRGPLDKCHHGKCVATG
						TSYMCKCAEGYGGDLCDNKN
						DSANACSAFKCHHGQCHISDQ
		1				GEPYCLCQPGFSGEHCQQGLLG
						GVREMLRCKVRSNIVTMKAKL
			ŀ			SFRICMTLTILANMWPRPILGG
1						VDQIPIKPKSKVLYLGAASGTT
						VSHVSDIIGPDGLVYAVEFSHR
						AGRDLVNVAKKRTNIIPVLEDA
		1				RHP/HQPDQ\ARSVALNAHTFLR
		1				NGGHFLISIKANCIDSTASAEAV
		1				FASEVRKLQQENLKPQEQLTLE
		1				PYERDHAVVDYSSSATEQRRT
į						ENDSDKLTEVGFRKLVINFSKL
						KEDVRTHHKEVKNLEKRLDEW
	ľ					LTRINSVEKTLNDLMEAENHGT
1						KKYVTQAQASVAYLIKWKKG
25379	55747	A	25520	78	978	AAGHSAKKSCLSLLPAWSFPLG
						STRAQWHVRRLQARISGGGRH
						RCGRRGQ\GKTRRRMGPMVVS
						VEPHRHEGVFIYRGAEDALVTL
	İ					NMVPGQSVYGERRVTVTEGGV
1						KQEYRTWNPFRSKLAAAILGG
						VDQIHIKPKSKVLYLGAASGTT
						VSHVSDIIGPDGLVYAVEFSHR
						AGRDLVNVAKKRTNIIPVLEDA
						RHPLKYRMLIGMVDVIFADVA
						QPDQSRIVALNAHTFLRNGGHF
		1				LISIKANCIDSTASA\EAVFASEG
						EKLQQENLKPQEQLTLEPYERD
						HACV\VGVYRPLPKSSSK
25380	55748	$\frac{1}{A}$	25521	230	314	QMPGNNPAFSA*CDAGASYQA
23380	33748	A	23321	230	314	YVNSAIY
25291	55740	A	25522	1360	1848	RFRALV/TEGFSLRELFPVATVL
25381	55749	A	23322	1300	1040	VASST\VTKRFIFLLAAD\VRLA
						LRRSI\THPFVRKQELTVYTLNN
					,	ELENLLTNVVNQAQQGGKVML
						DSVPVDPNMLNQFQSTMPQVK
				1		1
						EQMKAAGKDPVLLVPPQLRPL
				1		LARYARLFAPGLHVLSYNEVPD
		<u>L</u>		<u></u>		ELELKIMGALM

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25382	55750	A	25523	91	1184	AAACSPPPPARLTYGSETLRGG DCSKMAAGCCGVKKQKLSSSP PSGSGGGGGASSSSHCSGESQC RAGELGLGGAGTRLNGLGGLT GGGSGSGCTLSPPQGCGGGGG GIALSPPPSCGVGTL\LSTPAAA TSSSPSSSS/APASSSSPGSRK\M VVSTE\MC\CFCFDVLYCHLYGI \QQP\RPPRFTNEPYPLFVTWKIG RDKRLRGCIGTFSAMNLHSGLR EYTLTSALKDSRFPPMTRDELP RLFCSVSLLTNFEDVCDYLDWE VGVH\GIRIEIHQCKKASKR\TA TYLPEV\AKEQGWDHIQTIDSLL RKGGYKAPITNEFRKTIKLTRY RSEKMTLSYAEYLAHRQHHHF QNGIGDPLPAYNHYS
25383	55751	Α	25524	3	154	Q.verez. 2
25384	55752	A	25525	575	1707	TALLLTQSLFGGLFTQTHMKFG AVTRI*NRKTGNSKKQSTSPPPK ERSSSPATEKSWMENDFDELRE EGFRRSNYSELREDIQTKGKEV ENFERNLEECITRITNTEKCLKE LMELKTKARELCEECRSLRSRC DQLEDCLLKKLHSHQANPEFDL ITEHLTLCIRISIQIKAYLSLSKA QSSLSHRPPTYLAYLFNGFRLF KNLKAYLHPGEINSFIAHTKPV WWSLHTDAHEIWCRDSDLKLV PTLPLIPLEAALRNITHSLSIPPP KNFRRPNTSTLFCVIFLINIRRQE YQASEPKPSHRIPCDLQRIKYLG IQLTRDVKDLFKENYKPLRNEI KEDTNKWKNIPCSWVGRINIVK MAILPKPLLVIPRQTGSGMDPQ QTSGDLQKCLTVLRKTNKQKAI ASTSRKRMTMQKLHLKEKLINS KDQRTNDKNHMIISIDAEKAFN KTEHRFMLKTLNKLEINSRWIK DLNVKPKTIKTLEENLGNTIQDI VMDKDFMTKTPKAMATKAKI DKWDLIKLKSFCTAKETIIRVY RQPTERESIFVIYPSDKGLISRIY KELAIPGKGNSSNVSKDSKMSK HQKMQGENKHD

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25385	55753	A	25526	110	569	TALLLTQSLFGGLFTRTRMKFG AMTRIG\DLPWEINPLSSCSLLC EKHPPTTSGPQTDQPKKHLTNF KSETKETCFIHEPKTLAPVTDW EGSLPLVFNHCRDGLSDHSATF QGCQTMQGCLPWSFTLSGKSR FSGEGANHHGHRASGNSHSGS
25386	55754	A	25527	2	,	LFGGLFTRRRMKFGAVTRIR\DF PWEINPLSSCSLL/CEKDPRTTS GPQTDQPSKHLTNLKSASTPPP YNPFITSPPHTRSGLQFRSTSSPP APAQQFTLKKVAEAKGIVKVN APFSLSDLSQISVRLGSFIKYEKS SPVHGSFGSNPETLYSPRP
25387	55755	Α	25528	162	206	
25388	55756	A	25529	74	446	TAMLLTQSLFGGLFTWTRMKF GAVTRIG\DLPWEINPLYSCSLL SRFKKIKACYHSPATSWPFKTY KLSLQLPHFTCPKTRQALQVSS GAVPYQPNCFAYPPCGAQPVPS FVLNTFLHNSLCRA
25389	55757	Α	25530	66	311	FGAVTRIG\DLPWEINPLSSCSLL REKEPPTTSGPQTNQAKKHLTN FKSGACYTCRKSGHWAKECPQ PGIPPKPRPICVGPH
25390	55758	A	25531	728	825	MKFGAVTRIG\DLPWEINPRSSC SLLHEKDPPM
25391	55759	A	25532	291	311	TALLLTQSLFGGLFTQTHMKFG AVTRI*NKKNNTK
25392	55760	Α	25533	1	1056	
25393	55761	A	25534	245	487	TALLLTQSLFGGLFTQTRMKFG AVTRIG\DHPWEINPLSSCSLFQ EKDPPTT/SGPQTDQPKKHLTNF KSTSFVFSSCIPPP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	I .	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25394	55762	Α	25535	818	2391	TALLLTQSLFGGLFTQTRMKFG AVTRIG\DIPWEINPPSSCSLFLP/ RLPLLHFPGAGPSTPQPLL/HSPS AASPAFLGQGQDLINLVFKVYN NRKKLQFLASTVTQTPATSPAH KNFQTPEPQQPGVPPEPPSPGAC YKCQKSGHQAKECPQLRIPHLS YAWTFNDNPLYVQEDNRRFVS QETGNLYIAKVEPSDVGNYTCF ITNKEAQRSVQGPPTPLVQRTD GVMGEYEPKIEVRFPETIQAAK DSSVKLECFALGKIDDSIREKG AIRIKPSSILMRCNCLVQSPILVG EGWTGARCQGKSSTANPKLSL KSRTSNKKMKAFMSALQATFE EETLQRVNSFFMHNVLDNCLLP NSGTCLFETAPPEWEQKIQNTH LSIYDNLLWECKASGKPNPWY TWLKNGERLNPEERIQIENGTLI ITMLNVSDSGVYQCAAENKYQI IYANAELRVLGSQLVHFRENGT CLSDEVIRDSDFMSGMTVVHAF TSGSQGTTTENQDELQIKFISAR
25395	55763	Α	25536	425	749	HSQATEGINSTSAKFD IASLLTQSLFGGLFTWTHMKFG AVTRT/RGDLPWEINPLSSCSLL HEKDPPTTSGPQTDQPKKHLTN FKSAQLKASGK/DLQKPYQHFQ TLQQLLPLQWAPCYGPSSVSI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first		*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25396	55764	A	25537	2	2204	I IDMIFTPGPPSTPKHKKSQKGSA
23390	33704	Δ.	23337	2	2204	FTFPSQQSPRNEPYVARPSTSEI
	}					EDQSMMGKFVKVERQVQDMG
						KKLDFLVDMHMQHMERLQVQ
						VTEYYPTKGTSSPAEAEKKEDN
						RYSDLKTIICNYSETGPPEPPYSF
	1					HQVTIDKVSPYGFFAHDPVNLP
						RGGPSSGKVQATPPSSATTYVE
						RPTVLPILTLLDSRVSCHSQADL
						QGPYSDRISPRQRRSITRDSDTP
,						LSLMSVNHEELERSPSGFSISQD
	1					RDDYVFGPNGGSSWMREKRYL
						AEGETDTDTDPFTPSGSMPLSST
						GDGISDSTVPLFLSSEILQKQVG
						QSITSMLGFLSRGPSMKLCMGL
						ACVLSLWNTVSGIKGEAKKEK
						GMTFLPTTDSKKFFSLLSVTSYS
						SFAFHKFSVAVYNISNLKTVDP
						AKFPTRYCYCLNNRTNDLSDFT
						ALLVDIIGNSTSYLTEIFKSTSIL
						SVNQSNESDCIFICVMTGKSGR
						NLSDFWEIEEKYPIINYTFTSGL
						SGVLALLLTQSLFGGLFTRTRM
					İ	KFGAVTRIG\DLPWEINP/LSSCS
						LLHEKDPPTTSGPQTDQPKKHL
						TNFKSAARPTFLGQGQVPLNPF
						SFTLSGKSCFPRRQEPPNRLFPH
						PNLLSLCPNPLFLCPNPFSTFLE
				1		GKNHHPHPFSVSQVFSLGLPPS
						LWEHSPMAHRLRVQPRQQPPDI
						HKQVISLQSGHSLLVKSQSWSQ
						DPIKFQLPHHHKNTASVCINPSV
25397	55765	A	25538	110	542	TALLLTQSLFGGLFTRTRMKFG
2337	ده ۱ دور	^ <u></u>	0502	110	J-12	AMTRIG\DLPWEINPLSSCSLLC
				[EKHPPTTSGPQTDQPKKHLTNF
			!			KSETKETCFIHEPKTLAPVTDW
						EGSLPLVFNHCRDGLSDHSATF
						QGCQTMQGCLPWSFTLSGKSR
						• •
25200	55766	 	25520	1	781	FSGEGASCSLPG MPLQPLATPFTSPGSPSVAQVT
25398	55766	Α	25539	1	/01	
				1		TNTGEPGFAQQEYAETPQTTAR
						PPHPHPALRALQASVHQTPRLG
				1		DCLGSSESATALHGSGEPNKLA
						PPGRPTERGGLFKCSVPLRTVR
						GCRAGLRGTETVPSSLQRQPAG
						DVGWINNKSTTALDRTPTDTQ
						RTRRPRPPKQKQRGRALKERPR
						DSDSAREGPLKAVAGLFGGLFT
						RTCMKFGAVTRIG\DLPWEINPL
						SSCSLLHEKDPPTTSGPQTDQPK
L	<u> </u>	L		<u> </u>		KHLTNFKSDLLSLATED

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
25399	55767	Α	25540	1571	1781	TALLLTQSLFGGLFTRTRMKFG
				·		AVTRIG\DLPWEINPSSSCSLLRE
]				KDPPTTSGPQTDQPKKHLTNFK
						SA
25400	55768	Α	25541	2150	3195	TVLLLTQSLFGGLFIWTRMKFG
		1				AVTRIG\DLPWEINPLSSCSLLH
		1	i i			EKDPPTTSGPQTDQPKEHLTNF
						KSDED
25401	55769	Α	25542	4688	5149	TAMLLTQSLFGGLFTRTRMKFG
		l				AVTR/IRGTDLPWE\INPLSSCSL
						LREKDPPMTSGPQTDQPKKH\L
						TNFKSGACYTCWKSGHWAKER
						PQPGIPPKPRPICVGPHLKIRTCS
		1				THLGQATPRAPGTLAQGSLTDS
		1				FPDLLGLAAEDSHCLIASEAP
25402	55770	Α	25543	1	433	MAAFPAALNRPTRARARRRIS
		1				AHSAASAAAAVVVAGTARGM
						VPGSEGP\CRA\GDEVADWEIVI
						EGTANLGPYFEGLRKHYLLPAI
						EYFNGGPPAETDFGGDYGGTQ
						YSLVVFNTVDCAPESYVQCHA
		<u> </u>				PTSSAYEFVTWLDGIK
25403	55771	Α	25544	1	235	
25404	55772	A	25545	1	301	
25405	55773	Α	25546	2	438	
25406	55774	Α	25547	1058	1494	KSVRLVVN/YLRTQKAVVRVSP
						EVPLQNILPVICAKCEVSPEHVV
						LLRDNIAGEELELSKSLNELGIK
					ļ	ELYAWDNRRVPSAVPMQGPWP
						AEHFLQVNEQPPAGSPSPCPSSS
						SSSSGLRGGMQTANGPACALTP
						TCAQTDCPCPTSH
25407	55775	Α	25548	[1	3965	RRFQPLPSAALRRCPPPARVGG
						RWVSAEKVNEGGSGGGGSQRL
		1				TRRARSTARVPAPGTMDAPRAS
		l				AAKPPTGRKMKARAPPPPGKA
		1				ATLHVHSDQKPPHDGALGSQQ
		1				NLVRMKEALRASTMDVTVVLP
		1				SGLEKRSVLNGSHAMMDLLVE
						LCLQNHLNPSHHALEIRSSETQ
					1	QPLSFKPNTLIGTLNVHTVFLKE
					:	KVPEEKVKPGPPKVPEKSVRLV
1			İ			VNYLRTQKAVVRVSPEVPLQNI
	<u></u>	<u>L</u> .				LPVICAKCEVSPEHVVL
25408	55776	Α	25549	1	388	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25409	55777	A	25550	1	1748	MVLARVARRPAGSAEAQASLA
23409	33111	A	23330	1	11740	GKAALPERARKMSSPGIDGDPK
						PPCLPRNGLVKLPGQPNGLGAA
						SITKGTPATKNRPCQPPPPPTLP
						PPSLAAPLSRAALAGGPCTPAG
İ						GPASALAPGHPAERPPLATDEK
						ILNGLFWYFSACEK\CVLAQVC
			•			KAWRRVLYQPKFWAGLTPVLH
						AKELYNVLPGGEKEFVNLQGF
1						TARGFEGFCL\VGVSDLDICEFI
1						DNYALSKKGVKAMSLKRSTIT
						DAGLEVMLE\QMQGVVRLELS
						GCNDF\TEAGLWSSLSARITSLS
						VSDCINVADDAIAAISQLLPNLA
1						ELSLQAYHVTDTALAYFTARQ
				İ		GHSTHTLRLLSCWEITNHGVVN
						VVHSLPNLTALSLSGCSKVTDD
		1				GVELVAENLRKLRSLDLSWCP
		l				RITDMALEYVACDLHRLEELVL
		1				DRCVRITDTGLSYLSTMSSLRSL
İ						YLRWCCQVQDFGLKHLLALGS
						LRLLSLAGETPVSALTLAVTTH
		l				PHLVHPPNLPGPCANSHPARTH
	:					SPGSEAEEEGGAARPSPPEPWA
		l				ARTEPPSDPAAGCPLLTTTGLS
		l				GLVQLQELEELELTNCPGATPE
	{	ŀ				LFKYFSQHLPRCLVIE
25410	55778	A	25551	1	377	MRRLTRRLVLPVFGVLWI/DGA
25410	33770	ľ` `	25551	[*		AVLLGNQEEVGGAD/WDLKCR
				}		PL/EVNVSKSDDTLKINGVEDH
				-		KTIFDGDGKTYQNVQQFIDEGN
						YTSGDNHTL/SRPSLR*RQRP*IP
		1				CIRSQHGNRKRIPRRRIFI
25411	55779	A	25552	222	287	Chesqueria indui i
25412	55780	A	25553	2	918	GHCEVNRDWLQPLLHRVKEDY
23412	33780		25555	2	710	TRVVCPVIDIINLDTFTYIESASE
	1					LRGGFDWSLHFQWEQLSPEQK
İ						ARRLDPTEPIRTPIIAGGLFVIDK
						AWFDYLGKYDMDMDIWGGEN
						FEISFRVWMCGGSLEIVPCSRV
						į l
						GHVFRKKHPYVFPDGNANT\YI
						KNTKRTAEVWMDEYKQYYYA
						ARPFALERPFGNVESRLDLRKN
						LRCQSFKWYLENIYPELSIPKES
						SIQKGNIRQRQKCLGISKGRTTK
						KPQT*S*A\LCQGQRRRCQSPRV
						WGLSHYTQADSFQGELVALFSS
		<u> </u>		1		FTFVSLGAPVVSCSFARMGD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25413	55781	Α	25554	84	2804	PRGSWRCRRDLKCRPLSHSDA
						DWDDLWDQFDERRYLNAKKW
						RVGDDPYKPVCFSTSGRVSGSP
		Ì				AIRAIPDTRHLRKKATSNSLSRQ
		ŀ				QLASPLPRSSYCGVTPGPIAIGP
						LWTSGSLRTPNHIDTVFAPGLP
Į						QPWFHLNYLRAMPSLSSAPKCT
		ļ		}		LLVYCTDLPPTSIIITFHNEARST
						LLRTIRRPPAVSTSQMAMTAAA
						LTPAPLRTYSVHLSCRAHQLVP
						MPQRKKYDETWVREHTKHSKI
						SLFPSCRLHFSCLSRRRMAVGS
						GKFQVMGDLGEPFLRVRWLRI
						WTLGPDFHGSALNSVLNR\TPT
		ļ				HLIREIILVDDFSNDPDDCKQLI
						KLPKVKCLRNNERQGLVRSRIR
		i				GADIAQGTTLTFLDSHCEVNRD
						WLQPLLHRVKEDYTRVVCPVI
1						DIINLDTFTYIESASELRGGFDW
						SLHFQWEQLSPEQKARRLDPTE
						PIRTPIIAGGLFVIDKAWFDYLG
						KYDMDMDIWGGENFEMMTVQ
						VLQPRRSEALICTWKVHHLTRE
						STALLIALVQAPFTGPQAKKLQ
						QSPCPAMLAPEYAPEASVLVCT
						VSLLTYTTLQSEISFRVWMCGG
		1				SLEIVPCSRVGHVFRKKHPYVF
						PDGNANTYIKNTKRTAEVWMD
						EYKQYYYAARPFALERPFGNV
						ESRLDLRKNLRCQSFKWYLENI
				-		YPELRYPSYLLELWLAESRGPQ
		1				LAWSGEETDNDQLDEGFYVYQ

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
25414	55782	A	25555	1	2439	MPLKKKGDEPQMEKYIQERSM
25414	33762		23333	1	2437	LAPPSCSDHRDTHSRCIPHIQRL
						FQCPLGPWFQGEQRNQARGEG
						GALHPLPVTAGTVALPGAAQPT
						PARGNVTESLQGATVKLVCKK
						TSFIFIYCQHPAQCLALACDHEC
						IDLCTHVASTSLCLRGYQGMKR
						TIERALTATLAQGTAVPPFPSDV
						PSQKDAAVRGKGDGSEWERTL
						TMKRSNLNSEKILPAILLLTEFP
						RHQSPCSFDKPHHPNTLGCWLP
		İ	1		<u> </u>	TVLETRGGTNGQSSGKREATLC
						PCPLLGLPISEEDCVPPALLLPPR
						G\LPPGLQLSWAPVPQFPPLGPS
		1				SLGIPA/LPLVLNLGCLPSLVCPP
						TSAHTSEVAPSLKSPAEPSPPAR
						LPRSHQPALSREMRHSDYSVSV
						HAICWDHDFYTLVTHYMNNTS
						PISSKRSSDKLNPHVLVVQDSM
						TILSLHNHLALAGQDMMVWEP
					1	RKTLQRRQQPDSSSHSPPPALV
		1				ECHPLEPEPLVAGIMYSFSGLQ
						GVGLRDRAVDETNKRNEKRTL
						EMSRVEALSSFENSEFGCPPSIN
						TREITGNSLEGNVKKGVSVPNC
						TAPGKRTEKKYSKIHEMVKHS
						GNCKRTDGIWEEYGWSWRLH
						MKKVFPGFMLVKGGEDAAPGT
						KEIKSVSGIFQRGKKKPRGRKE
						KNRKKRGFAFSKETNFVYLLIL
						VCLIGKVVVWLTSACAEKPKP
						HGEATCRHSGPSAPLNFOPTRV
25415	55783	A	25556	2	1178	AKCVEVCGKREPPSMSPLNQSA
23413	33783		25550		1170	EGLPQEASNRSLNATETSEAWD
		Į				PRTLOALKISLAVVLSVITLATV
		ł				LSNAFVLTTILLTRKLHTPANYL
						IGSLATTDLLVSILVMPISIAYTI
						THTWNFGQILCDIWLSSDITCCT
						ASILHLCVIALDRYWAITDALE
			İ			YSKRRTAGHAATMIAIVWAISI
]	CISIPPLFWRQAKAQEEMSDCL
						VNTSQISYTIYSTCGAFYIPSVLL
						IILYGRIYRAARNRILNPPSLYG
						KRFTTAHLITGSAGSSLCSLNSS
						LHEGHSHSAGSPLFFNH\VKIKL
						VTVALKRKEDSAARERKATKIL
		1				GIILGAFIICWLPFFVVSLVLPIC
						RDSWWIHPALFDFFTWVGYLN
						SLINPITYTVFNEEFRQAFQKIVP
						FRKAS
25416	55791	1	25557	3	146	I ARAS
25416	55784	A	23337	J ²	1140	<u> </u>

SEQ ID	SEQ ID NO:		1		1	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25417	55785	A	25558	45	592	PSPPPPARAPSARTRRAPIPAAG QGRARPPRTVSRCGSAAMATKI
						DKEACRAAYNLVRDDGSAVIW
						VTIKYDGSTIVPGEQGAEYQHFI
						QQCTDDVRLFAFVRFTTGDAM
	İ					SKRSKFALITWIGENVSELQRA
						KTGTDETLVKEVVQNFANEYVI
						SDRKELEEEFIKS\ELKKAVGAN
						YDAQTE
25418	55786	Α	25559	249	1808	INGGTLTVTLSVTNQGAETLPF
						GTGWHPYFPLSPQTRIQAQASG
						YWLEREQWLAGEFCEQLPQEL
						DFNQPAPLPRQWVNNGFAGWN
						GQARIEQPQEGYAIIMETTPPAP
						CYFIFVSDPAFDKGYAFDFFCLE
						PMSHAPDDHHRPEGGDLIALAP
						GESTTSEMSLRAYNDTNRRSDK
		1				AFTPHPTCFPSNQNNSASPPTIT
						PDTATIAPVSHKAFAGNALRSII
						SDGKLTAGSVINNASAGAVPIP
						ASIIVCTIGISAAVGMTNKHPAT
						AIDTTHIMLLSTAPSAWGNNQT
						RAAPNTSLLAAYRFLIDSRDTE
						TDSRLDGLSDAFSVFRCHSIMN CVSVCPKGLNPTRAIGHIKSML
						LQLPPNVEKFAGAYLIQFALFQ
					ļ	PLTHNRLMFFGAFADFLHADQ
						TFPGQITAAVKGQFVRRRLRFF
						AIISPSRTLS/YHTP*PRR*PR*SN
						FVTGRDAGRGLYNRQ*KTS/PS
		1				SICSA*GANPVVHHAMTVKFA*
						WQPIMKISSTSFPSMRPLSHMK
						TINGLTTFVAW
25419	55787	В	25560	1	567	
25420	55788	A	25561	1	741	MLILISPAKTLDYQSPLTTTRYT
		1				LPELLDNSQQLIHEARKLTPPQI
						STLMRISDKLAGINAARFHDWQ
		ŀ				PDFTPANARQAILAFKGDVYTG
						LQAETFSEDDFDFAQQHLRMLS
				ŀ		/GLPYRLEMGIRLENA\RGKDLY
		1				QFWGDIITNKLNEALAAQGDN
		Ī				VVINLASDEYFKSVKPKKLNAE
						IIKPVFLDEKNGKFKIISFYAKK
						ARGLMSRFIIENRLTKPEQLTGF
						NSEGYFFDEDSSSNGELVFKRY
			<u></u>	<u> </u>		EQR
25421	55789	A	25562	3	320	IGLVLPISVRKRHAASARCLVN
1						RRPMPRLHGLPGIPMRPPSLPRV
						RHAGTVFRRHRKRGSPMAY*Y
						GHSDVVKHREALVADLCHKAA
			<u> </u>			FQLCRGQRHCRPALWRHR

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25422	55790	A	25563	1600	1908	
25423	55791	A	25564	142	326	TRRAPSAISSRCCCNSHQTSKSS LVRTSSSLRSSSHLRTIA*CSSV HLPISCMQIRPSQAR
25424	55792	A	25565	1	1599	
25425	55793	A	25566	393	611	HSRAVCRFYPAKTSPFPVRRCR YRQFVPR*HQNE*AGRE*QPCSI ATVLPYRALPSLAHPRLSADQL PAAHL
25426	55794	Α	25567	971	1628	
25427	55795	Α	25568	3	1895	
25428	55796	С	25569	1	2505	
25429	55797	Α	25570	1	3345	
25430	55798	A	25571	457	790	PSFRRRYRQVVVISVRKRHAAS ARCLVNRRPMPRLHGLPGIPMR PPSLPRVRHAGTVFRRHRKRGS PMAY*YGHSDVVKHREALVAD LCHKAAFQLCRGQRHCRPALW RHR
25431	55799	Α	25572	1662	1767	
25432	55800	A	25573	3	603	RLRSLFFLPDKMKLKDCVMIKK IFALPVIEQISPVLSRRKLDELDL IVVDHPQPPSGDYTLHPLPPIIR ANRPNRFRINAGCTRTFTLSTPI NVFRHKILRTQEFPSLTHHAYSP LLVVINKAKFDGLSPEFQQALV SSAQEAGNYQRKLVAED/LAK NHRRHERSGRGS/LSPISTAKPL ATHWGIRFATCLLKMCRRELIC
25433	55801	A	25574	2271	2519	HRQLVIVFQQPLVSGFHEAELS LDDAKWVLHP\ARMLAFMYSM LMAVLFLRGCCFKVLTLPGRSA ISQSTSTSASSSRCGAPW
25434	55802	Α	25575	931	1213	
25435	55803	A	25576		2767	MIAILSGLRCSIVANYIYAENNL FWLRLNNPKAIWCLRICTFATV IGGTLLSLPLMWQLADIIMACM AITNLTAILLLSPVVHTIASDYL RQRKLGVRPVFDPLRYPDIGRQ LSPDAPLTTTRYTLPELLDNSQ QLIHEARKLTPPQISTLMRISDK LAGINAARFHDWQPDFTPANA RQAILAFKGDVYTGLQAETFSE DDFDFAQQHLRMLSGLYGVLR PLDLMQPYRLEMGIRLENARG KDLY\QF\WGDII
25436	55804	Α	25577	395	467	
25437	55805	Α	25578	1	675	
25438	55806	Α	25579	1	4014	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
ĺ	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			1	sequence		
25439	55807	ĪA	25580	1802	2385	I IRKISAPALIKSRTG*EMASLPTS/
23439	33007		23300	1002	2505	HDKQIEQALADVDVPIVGVGGS
						YHLAESYPPVHYIATDNYALVE
						SAFLHLKEKGVNRFAFYGLPES
						SGKRWATEREYAFRQLVAEEK
						YRGVVYQGLETAPENWQHAQ
						NRLADWLQTLPPQTGIIAVTDA
						RARHILQVCEHLHIPVPEKLCVI
1						GVMNRRTVRSPFRESLKISP
25440	55808	A	25581	1	1568	MVKQLKLVSFLLRPGDSKQGY
23440	33808	I ^A	23361		1300	DKHSSLQVGLMIPVCSCIRFRKP
						SEQSFKFEEGTDAAFHGFWLW
		1				PCTMLNVTPIKGMMTVIYEFPV
						DSETTLQNYDIYFTNEELTDEQ
						KSLIEWYRDVFRPEDLRLVESV
						QKGLKSRGYRGQGRIMADSSG
	İ					SGISEHAWCMSRGAQGRQFCK
						GAKMSQVLITGATGLVGGHLL
						RMLINEPKVNAIAAPTRRPLGD
]					MPGVFNPHDPQLSDALAQVTD
1						PIDIVFCCLGTTRREAGSKEAFI
						HADYTLVVDTALTGRRLGAQH
						MLVVSAMGANAHSPFFYNRVK
						GEMEEALIAQNWPKLTIARPSM
						LLGDRSKQRMNETLFAP\LFRL
						LPGIILLEELNWKTWAERWNS
						MLGPRAVKVFFSLAFLPGTLEP
	ļ.					AQILFPTQRQGKKAALLLGLW
						KLEIYSDNRRSPEVSTAWNSPP
						TGKLDNKQYMIMIPRKRETNTT
						TRGASNARLDPPSRKGYKGHY
		1				ETIGHALEHDKQSQGSYNVEHT
	i					IKROTPRVRRCTSIIAGIYQELG
25441	55809	В	25582	1	1560	
25442	55810	A	25583	1	2115	
25443	55811	A	25584	3036	3957	RIYDAVSEPAEPVDCPRNPVCR
						FY*QYRDHRGKTVYDVASGDA
		į				LFISELG/PLPENVTWLSPEGEFQ
						KWN/GTAWVKDTEAEKLFRIRE
						AEETKNNLMQVASEHIAPLQD
						AADLEIATEEEISLLEAWKKYR
						VLNSRAMALILTPDLIRSNTACF
	}					CSSFVLAGQTAKAAADDGLFPP
						IFARVNKAGSPVAGLIIVGILMT
						IFQLSSISPNATKEFGLVSSVSVI
	-					FTLVPYLYTCAALLLLGHGHFG
	1					KARPAYLAVTTIAFLYCIWAVV
						GSGAKEVMWSFVTLMVITAMY
						ALNYNRLHKNPYPLDAPISKD
25444	55812	A	25585	1	2490	
	100012	1.,	,		1	l

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25445	55813	A	25586	368	761	LYCEACIMAFRMSEQPRTIKIY
25 (15	33013	` `	25500		, , ,	NLLAGTNEFIGEGDAYIPPHTGL
						PANSTDIAPPDIPAGFVAVFNSD
		l				ESSWHLVEDHRGKTVYDVASG
		l				DALFISELGPLPENVTWLSPEGE
		ŀ				FQKCSGTTRVKNAKA*TLF
25446	55814	A	25587	1	809	MPVSSYERGHAEKRVVQECCG
23440	33014		23307		1007	INLTSSANTILSDCERVNGYCVL
						CHTTRALVTGNHHRNAVYAET
						PSNSRINYIVSSHNAFRMSEQPR
						TIKVYNLLAGTNEFIGEGDAYIP
						1
						PHTGLPANSTDIAPPDIPAGFVA
						VFNSDESSWHLVEDHRGKTVY
						DVASGNALFISELGSLPENVTW
						LSPEGEFQKWNGTAWVKDTEA
		ŀ				EKLFRIREAEETKNNLMQVASE
		ŀ				HIAPL\QDAADLEIATEEEISLLE
						AWKKYRVLLNRVDTSTAQDIE
		ļ				WPALP
25447	55815	Α	25588	1	2301	
25448	55816	Α	25589	718	1131	
25449	55817	Α	25590	279	513	CRRIDTWQPIYQTCGRLMAVEL
						LTVVTHPLNPSQRLPPDRYFTEI
						TV/SHRMEVVKEQIDLLAQKAF
		ļ				SLAYLSPCESGL
25450	55818	Α	25591	1	407	PQDNAKKLRPHQLSSDEGHTG
						MGGTAKDVGFVSMRTYSWISS
						ALPKRLGGGVMPIGATIATEEV
						FSVLLGNPFLHTTTFGGNPLAC
						AAALATINVLL\GRTYRLRLSK
1						KAICCWTVSVNWRGNIPIWYR
		<u> </u>				KRVVKGC
25451	55819	Α	25592	1	2079	
25452	55820	В	25593	1	700	
25453	55821	Α	25594	1427	1845	ACISGFSTETSASGRVSVITDAS
1						LFRVLPRVCGMAVAATKRSGRI
						TTSEALCCANQLRRRPCVSPTR
l						STPSWLSCAV*ICTSGTT*MKR
						VPNARHCWICSSLIPHSGLHPQP
						ITAKFAPIALSSSVTSPFSSVTFG *IN
25454	55822	A	25595	2	295	
25455	55823	A	25596	1	900	
25456	55824	A	25597	ti —	1422	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25457	55825	I	25500	10	535	VCNDEOD AVCCUTATIVIA ID AL
23437	33823	Α	25598	2	333	YGNREQRAVSSHTNTWVNRAL ARGWSSLGYRWWVSAWTPSR
						RFISQLMSRPVDASAAKVKRSA
						SVPCGSIPFGNCFSVRLRILSASC
						GCIILPVRFSSSSGSEIPSTISSGSI
						TLPLDLDIFWPSSSRIRPVM*TV
						WNGTCGLPFSSLMKCMVIMIM
						RAIQKKMMSKPDTITLVGWN
25458	55826	Α	25599	442	1368	RRTMAAFACGVVRDASEVIRPS
						STLVPLVGEKHAKGLFGTIVDN
						FYLVALIFAMGTSLGLATPLVT
						ECMQWLFGIPHTLLGFI/LYNAI
						CVACGLQKGVRIASDVRSYLSF
						LMLGWVF\IVSGASFIMNYFTD
						SVGMLLMYLPRMLFYTDPIAK
						GGFPQGWTVFYWAWWVIYAI
						QMSIFLARISRGRTVRELCWIL
						WTVLGSNTLLLIDKNIINIPNLIE
						QYGVARAIIETWAALALNNGN
						MWGFFILWFIGPGTLVNAWQNI
						RAQFVHHILRRNGIADGFRHLA
						ALTIHGKAVGQYLTIRRFTLHR
25459	55827	Α	25600	2468	3907	
25460	55828	Α	25601	3	3738	YKTNYTDNSEYYANVGFNVKP
						VKRDGKMSVMSDPDTAIYPFPP
						KPTPLSIDEKAYYREKIKRLLTE
						RNAVMVAHYYTDPEIQQLAEE
				•		TGGCISDSLAMARFGAKDPASN
						LLVAGGGTCRSVVINAVFSYVT
						NVWGWAFEWYMVVMLFGWF
						WLVFGPYAKKRLGNEPPEFSTA
						SWIFMMFASCTSAAVLFWGSIE
						IYYYISTPPFGLEPNSTGAKELG
						LAYSLFHWGPLPWATYSFLSV
						AFAYFFFVRKMEVIRPS
25461	55829	A	25602	1331	1456	
25462	55830	A	25603	549	588	
25463	55831	Α	25604	19	1629	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
25464	55832	Α	25605	1	1995	MVGVRFALGLMWLTLIVAETIS
						ANSGIGYLAMNAREFLQTDVV
						VVAIILYALLGKLADVSAQLLE
						RLWLRWNPAYHLKEATLSAEQ
		ŀ				AARIREMTVITSSLMMSLTVDE
						SDLSVHLVGRKINKREWAGNA
		ĺ			i	SAWHDTPAVARDLSHGLSFAE
		ŀ				QVVSEAHSAIVILDSRGNIQRFN
						RLCEDYTGLKEHDVIGQSVFKL
						FMSRREAAASRRNNRVFFRSGN
		ļ				AYEVENVPDPGVEQADDIILRIT
						ATAICGSDLHLYRGKIPQVKHG
						DIFGHEFMGEVVETGKDVKNL
						QKGDRVVIPFVIACGDCFFCRL
						QQYAACENTNAGKGAALNKK
						QIPAPAALFGYSHLYGGVPGGQ
						AEYVRVLKGMWGRLNDAQPG
						FRSSRPLRYGAGIMTLLNISGLS
		l				HHYAHGGFNGKHQHQAVLNN
						VSLTLKSGETVALLGRSGCGKS
	1					TLARLLVGLESPAQGNISWRGE
						PLAKLNRAQRKAFRRDIQMVF
						QDSIST\VNPQPNRLHIV/RFPLT
						RLNQYQPSFSTDLYHGTLKPAS
						LTMSGVVLLGRM/PRKTSQQV
						QWA\CIARTDKASMPTVYSESL
						FVEPLERVLYVAVILTQIIRGLR
				:		DTEIETINPDIAVHFALCFHGLG
						SIPTKGAEKSPFLTIHKVRVKPD
						IPSPVSIMAPCRAHPTCEALFNN
						STALHSPWFCDSL
25465	55833	A	25606	179	371	CVLQYTHWPACSTVA\HSRRW*
						NRRRLRLAVTKTGSLFSHRCAG
						ARLAFSKKLRCRDALPASRS
25466	55834	A	25607	544	983	SVQNPRVNWIHAALQRTGRGR
						RRHEQHGEDHFVNGAAGVHQ
						AANGLVNPPRHQVFGAHQAKG
						DGENHRQRGAPDGDLQRDGHF
						GEVILPLAEIGREEVGGERRHV
· ·						AAVFDQ/S*AGPFPRPATRRPTR
						RVQRPSSEARTSCAWVGRW
25467	55835	В	25608	1	1746	(
25468	55836	A	25609	1	858	-
25469	55837	A	25610	98	288	LCRNNGEPLARSGAAMGALLD
]						REHSRHP\PDLEG\GSQQQVCDS
						GGSVTAANTSGGQQVKAQLEL
L	<u> </u>	L		L	L	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25470	55838	IA	25611	11934	2812	RPQTYSDAQPGFRSSRPLRYGA
						GIMTLLNISGLSHHYAHGGFNG
						KHQHQAGLNNVSLTLKSGETV
						ALLGRSGCGKSTLSRVLVGLES
1						PAQGNISWRGEPLAKLNRAQR
						KAFRRDIQMVFQDSISAVNPRK
						TVREILREPMRHLLSLKKSEQL
	Ì					ARASEMLKAVDLDDSVLDKRP
						PQLSGGQLQRVCLARALAVEP
<u> </u>						KLLILDEAVSNLDLVLQAGVIR
						LLKKLQQQFGT\ASLFITHDLRL
						VERFCQRVMVMDNGQIVETQV
						VGEKLTFSSDAGRVLQNAVLP
						AFPVRRRTTEKV
25471	55839	A	25612	1	515	MLAVECRSLPFPPLVQPVRYTD
23471	33637	' '	23012	1		VTVKDDYNPETEQYTLTISQRT
	1			İ		PATPDQAEKQPLHIPFAIELYDN
						EGKVIPLQKGGHPVNSVLNVTQ
						AEQTFVFDNVYFQPVPALLCEF
						SAPVKLEYKWSDQQLTFLMRH
						ARNDFSRWDAAQSLLA/ILHQA
						ERRASSARSAAVSAGACG
25472	55840	A	25613	1	1053	
25473	55841	A	25614	1	1521	
25474	55842	Α	25615	430	1120	QTASTFLKRGKCASRQSKLCGN
						RRRKRRQRISSYCLLRGTACSP
						AHQPDAFHQKRGNAGRHYAEC
		1				VLQYSSCSTRYS\PGR\TQLINLF
	1					EVADGKRLVDLPGYGYAEVPE
						EMKRKWQRALGEYLEKRQSLQ
						GLVVLMDIRHPLKDLDQQMIE
						WAVDSNIAVLVLLTKADKLAS
						GARKAQLNMVREAVLAFNGD
						VQVETFSSLKKQGVDKLRQKL
						DTWFSEMQPVEETQDGE
25475	55843	Α	25616	407	1176	AYSTSLRVKICRKTSTLLLRSRV
						TQIRSNTKSTKRAAHCSLTASC
						PPRCSIHATTVTSTTPCLWRRIA
						TMLRALARLLLRICFSGRTLKIA
						CLLLLVAGATILIADR/AALYHA
						GKVKWLLVSGDNGRKNYDEA
						SGMQQALIAKGVPAKVIFCDY
						AGFSTLDSVVRAKKVFGENHIT
				1		IISQEFHNQRAIWLAKQYGIDAI
	1					GFNAPDLNMKHGFYTQLREKL
						VIAKGHGSLLTDLPVAKAGTM
	<u> </u>	<u> </u>				WAIEIDDVARHSRSHL
25476	55844	A	25617	3	168	NPFYSAMR\KSAGIRHILARHVE
						GASHMAEGYTRATAGNIGVCL
						GTSGRCCFRLCW
25477	55845	В	25618	169	1227	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	1	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	Sequence	:	07/340,217	sequence	peptide sequence	detection, 1 possible nucleonide insertion)
25478	55846	Α	25619	489	740	AIARSCADYHPANFRHHRAAA
1			}			RAGDDYLSRRAERQPGAKAGG
ĺ						SRLRAGKRPCSAFRYW*CAAG
						E*SVGEKIMAGDVISPKRRL
25479	55847	A	25620	146	475	
25480	55848	В	25621	38	191	
25481	55849	A	25622	662	4568	
25482	55850	Α	25623	20	2661	AGHIHRPRYQHGVGTESTSIMS
						VASRSAERVFLTKFESWKNFPI
		1				NRGRNKMAKMRAVDAAMYV
		İ				LKKEGI\TPAFG\VPGAA\INPFY
						SPMRKHG\GIRHILARHVEGAS
						HMAEGYTRATAGNIGVCLGTS
						GPAGTDMITALYSASADSIPILC
1						ITGQAPRARLHKEDFQAVDIEAI
		ļ			1	AKPVSKMAVTVREAALVPRVL
						QQAFHLMRSGRPGPVLVDLPF
						DVQVAEIEFDPDMYEPLPVYKP
						AASRMQIEKAVEMLIQAERPVI
						VAGGGVINADAAALLQQFAEL
						TSVPVIPTLMGWGCIPDDHELM
		ł				AGMVGLQTGHRYEKYTEGRKI
						VHIDIEPTQIGRVLCPDLGIVSD
						AKAALTLLVEVAQEMQKAGRL
						PCRKEWVADCQQRKRTLLRKT
	Ī					HFDNVPVKPQRVYEEMNKAFG
						RDVCYVTTIGLSQIAAAQMLHV
						FKDRHWINCGQAGPLGWTIPA ALGVCAADPKRNVVAISGDFD
						FQFLIEELAVGAQFNIPYIHVLV
1						NRPAANGAQGSCHPDAPAVFR
						SSIFIRKSEEKLVVTMNELSASR
						ALPEETMPGRFELKPTLEKVLH
1		1				APDNFLFMDPLPPMHRRGIIIAA
						IVLAVGFLLPSDDTPNAPVVTR
		1				EAQLDIQSQSQPPTEEQLRAQL
		1				VTPQNDPDQNLYRKASQKSSR
						KLPKRDLPHILTPFRAPMASVC
						AKRKGQVLHQQYSLKKYRYK
25483	55851		25624	1	570	ARICKOVENOVISERKINIK
25484	55852	A A	25625	312	873	APRSRVQAKIAASNTGELNALQ
23404	22022		23023	312	073	QLGFS\LVEGEVDLAL\PVNNA\
						SDSGAVVA\QETDIPA*RQLASA
						AFAQSRFRAPWYAPDASSRFYA
						QWIENAVRGTFDHQCLILRAAS
						GDIRGYVSLRELNATDARIGLL
						AGRGAGAELMQTALNWAYAR
						GKTTLRVATQMGNTAALKRYI
						QSGANVESTAYWLYR
<u> </u>		<u> </u>		<u> </u>	<u> </u>	QOUANVESTATWLIK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25485	55853	Α	25626	2	922	FSPPGLHDAGEAVFWRVNKSA
ļ						NYGVLDKLARGYADLSKAESQ
						WDEMMRTAGSLKLGTIHASINS
						LFENITAAPADPILGLADLFRAD
1				İ		ERPGKINLGIGENPSCCRTSSSP
1						VFDAAIWPAPVNNASDSGAVV
						AQETDIPALRQLASAAFAQSRF
						RAPWYAPDASSRFYAQWIENA
						VRGTFDHQCLILRAASGDIRGY
			1			VSLRELNATDARIGLLAGRGAG
						AELMQTALNWAYARGDHMI/R
						I*RTAGGGNRTRLYAVGNG*RQ
						TVWRWRFYPSLPAVAGATFWQ
						RQSVTDAVLHRFAGDGGAAAR
						YPAWR
25486	55854	A	25627	911	1441	AIPSISCFLLAIKALILSAIWLNA
23400	35054	`	23027			TPSRSKLEPSSKWIRSLRCPSPN
		1				RCAAASSFNISCQWFLSEYGPP
		1				NQVASGKTSPFVIVFKQPRYRA
						VTKPNCRLMMRNGCSTLARML
						PVMYAMLMPVLFLRGCCFKVL
		1				TLPGRSAISQSTSTSASSSRCGA
						PW*PASAETNCSSPCSRLPS
25487	55855	A	25628	1	1247	MERVLDNLLNNALRYCHSTVE
23407	33633		25020	1	12-17	TSLLLSGNRATLIVEDDGPGIAP
						ENREHIFEPFVRLDPSRDRSTGG
				ŀ		CGLGLAIVHSIALAMGVNAQA
]			DFMKLTGADEQIAAYCFKMPF
				ļ		VFHLIEEVSRNFGYALCLINIDH
						KAALNITQRTAANILLDGQMQ
						HAVDQAFTQRTARQGSTFVQY
						ARLARKLATANICWSYFVPVR
						ASIEPLTWENAFFGVNSAIVRIT
						SEAPLLTPDALAPWSRVQAKIA
						ASNTGELDALQQLGFSLVEGEV
İ			ļ			DLALPVNNASDSG\AVVAQETD
						IPALRQLASAAFAQSRFRAPWY
						APDASSRFYAQWIENAVRGTFD
			}	ŀ	ļ.	HQCLILRAASGDIRGYVSLREL
			1	1		NATDARIGLLAGRGAGAELMQ
			[TALNWAYARGKTTLRVATQM
				1		GYTAALKRYIQSGANVESTAY
						WLYR
25488	55856	A	25629	1	1925	WLIK
25489	55857	A	25630	402	664	TARRLLFFRD/RTARVAVPNAA
23409	33031	^	23030	1702	1004	VVLPFPLPVKTMIIPRSLGRRRS
				1		GGICRPLGYLVAMDAIDGLQN
						ADNSNGESRIATSSFRSRSARR
L	L	Щ.	1		<u> </u>	ADIOTOLORIA 1001 ROROARK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25490	55858	A	25631	920	1237	IARPGCHLSHCHSEPSGRLSK*P
						FSCNSLKTGDF*PI*GLIQTQIFS
		1				PFAFRRIIPSGSGKVSGSHSKS
		1				HHWKAFIQKQSKWKTCSGRLR
		1				SAIPSIKLFTVASS
25491	55859	Α	25632	1	1341	MVHRFGIRVRFVALGFYQDVIL
		ļ			·	PVRAHRHEWGHYVHLCASIQR
	:					QIDVSFARDATSHSSCPVTGVR
						FWGYPFAANKVVIAGFELEGET
1			}			MTRPGLICAEGGLLVMIVSLRS
			ļ			ELYDSYHEFTRQRVTEIVEKAA
						NHLPAVVEMMTLHRCAINRHN
		1				FVRRVGPAGISTFFASSPDGVN
	1					AGFSTFRVVFTCQRSRPLQRHS
						HADVQTATLLLNTVNLEQKQA
						NAILSGLSDMIPNSSPESAPEIQL
						LQSRMILGKTIAELNLRDIVEQK
						YFPIVGRGWARLTKEKPGELAI
						SWMHIP*TLSKNRPTPFS/DGLS
						DMIPNSSPESAPEIQLLQSRMIL
	1					GKTIAELNLRDIVEQKYFPIVGR
1						GWARLTKEKPGELAISWMHIP
		ļ				QLNGQDQQLTLTVGENGHYTL
						EGEEFTVNGMVGQRLEKDGVA
						LTIADIKAKPGTQFVLSQRTELE
						AINALQETFTVSERSKESGMLE
ļ						LTMTGDDPQLITRILNSIANNYL
						QQNIARQAAQDSQSLEFLQRQL
		İ				PEVRSELDQRKKNSTFIASSAIR
25492	55860	Α	25633	170	935	LTQEDTRINLIPMAVESLHLPTQ
		İ				MLINGGETYAWRNWKRGGQY
						KSATLNTGQPHVRARELVDSD
						TLASDAARLTCRHGLALPALFT
						LIAVVTSLLSPQFIRQILWSRLT
						KTR*AGDQLDAYSTTEWSGSA
						TDTHGWGKRPLYTGR*RVHRQ
						WYGRPASGKRWRCADYRGH*
						GQTRNTVCPEPAYRTGSD
25493	55861	В	25634	42	755	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ĺ		sequence		
25494	55862	A	25635	793	2127	RYCKGTVMDQIRLTHLRQLEA
23494	33802	ΙΑ .	23033	193	2127	ESIHIIREVAAEYSNPVMLYSIG
		1				
						KDSSVMLHLARKAYYPGTLPFP
				•		LLHVDTGWKFREMYEFRDRTA
İ	į.					KAYGCELLVHKNPEGVAMGIN
						PFVHGSAKHTDIMKTEGLKQA
						LNK/YTTSRAKERIYSFRDRFHR
						WDPKNQRPELWHNYNGQIN\K
						GESIRVFPLSNWTEQDIWQYIW
						LENIDIVPLYLAAERPVLERDG
						MLMMIDDNRIDLQPGEVIKKR
		1				MVRFRTLGCWPLTGAVESNAQ
		Ì				TLPEIIEEMLVSTTSERQGRVID
						RDQAGSMELKKRQLIELIINVH
						NLLKNGFGFQVKVNRIALLAIN
				-		VEFFFRLVQLAAHFSSGTLAQD
						KLCSWFGLNVRDSQRNAIFFQT
						LADHTIDGELFTFQCIVAVFPNL
		İ				PIYSYATIYVSSSSIPISSEESPSIR
						FACSQTSRQPPVSDSRFCVSQV
25495	55863	A	25636	360	566	GAETMGDLLWVVGILLMCSLS
						TLVLVWLDPRLKS*RT*A*CGA
						LTSHQAINNGRNEKRKPIRESDP
						LKA
25496	55864	A	25637	1	312	LLRKSVSVIIKGTIKTIIGFMLLQ
						AGSGILTSTFKPVVAKMSEVYG
ĺ						INGAISDTYVMQDG*APELGLS
						PGRFLRHDTDFVLQLGIVMVRL
					:	AGDGSLNINAQANN
25497	55865	A	25638	517	796	PTARFGWVKGVDLPAD/CNRQ
23471	33603	``	25050	317	1,70	DRFAIDVRVQGS*\WGCVLPLF
	İ					RVLLFVSCALLLVSVSCVLRLL
						FCCSS\LSLFLSGLGGGRSPKAG
	1					DVFRDRR
25498	55866	A	25639	47	411	AIKVRELSIKLKMC/YSLIKTLH
23490	33800	^	23039	147		G*KYRNFMVIGSMVFGKKAITH
1						VAGVKRRTAVVVGFKVFDIQR
						SQFRIVVTGDLAQLLYRVIKVIT
1						CGHFVRQHGIVLCAGVLHVGD
						RYQAHVKTLGGLI
25400	55067	ļ.—	05640		1400	RYQAHVKILOGLI
25499	55867	A	25640	1	1488	CCICL/VEVADIDVIV/VIC/WATEA
25500	55868	Α	25641	$ ^2$	298	CCICL/YSYAPIDVW/WG/WNTA
						GQVQAA*TLKAASSSIVTIPLRN
						TFIFNYSLSGLRRRRLIIRSRRHS
						THASNITLIAASTASRIGWFASA
0.555	55060		25645	ļ,	2064	YHTRSNHGR
25501	55869	C	25642	1	2064	
25502	55870	В	25643	1	1116	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25503	55871	A	25644	312	620	SACRCCLVVVPLFVCL/GSSLSL
23303	338/1	^	23044	312	020	APTFPLLASFSSSRASRVVAFGL
		ŀ				GSLRAGSALCLPCAAVVLALRS
						AGTCLEWWWWHSVVLPPETK
						RLPSTSLIPYPASVSI
05504	55070	!	25645		2227	RLPS15LIP 1PASVSI
25504	55872	Α	25645	2	2237	DA CONCOUNT OVER CONTACT IN DATE
25505	55873	Α	25646	692	6383	RMSRSSDYDQYRSRNALIRRHI
		ŀ				EKMDASLHVGTKEFDISKVSEV
	1					DSVDDLLIDNAARYLLKDWKG
						VGELVNGVEVALEYTAERGIAL
1	-					LKQNPELYWQILAEAASIAQVG
		l				GEVWIAPKFERNGLRLLANSEI
		ł				GAASQLQTYHRVDPGRPCKLD
						LSGGMSQRVMIAMAIACRPKL
						LIADEPTTALDVTIQAQIIELLLE
						LQQKENMALVLITHDLALVAE
				1		AAHKIIVMYAGQVVETGDAHA
						IFHAPRHPYTQALLRA
25506	55874	Α	25647	856	1467	
25507	55875	Α	25648	1823	2014	SQEIALMQFRPRLTGASGSP*RP
						PHRTLLRSDQNAATIPQKRASA
		ŀ				LIPLMRILPVRYGHLLLC
25508	55876	Α	25649	1	218	
25509	55877	Α	25650	2740	3293	IFAVNLILQCHVGGTHHQRFLL
						FAGNGDAGNQIRERFPNAGG/E
						LQSPDVALLLRPAFWRRPQSSA
						AAAHGE*SRGSVPEAPYTRRQF
						ALPAPPIKCAPLPERQRPSVPSR
						HLRLPACPGYKNRASSAKPSYS
						FLAQRQHLQRLSPLPQNQNLPQ
						RRRDQRQRAGAMSARVPDLISS
						SRSMRRTS
25510	55878	В	25651	1	1875	
25511	55879	В	25652	1	2981	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25512	55880	Α	25653	11	1649	MTFRNCVAVDLGASSGRVMLA
		1				RYERECRSLTLREIHRFNNGLH
						SQNGYVTWDVDSLESAIRLGL
1						NKVCEEGIRIDSIGIDTWGVDFV
						LLDQQGQRVGLPVAYRDSRTN
1						GLMAQAQQLGKRDIYQRSGI
						QFLPFNTLYQLRALTEQQPELIP
						HIAHALLMPDYFSYRLTGKMN
		į				WEYTNATTTQLVNINSDDWDE
						SLLAWSGGQQSLVWVAEASGE
-						WGVLACTLFAWNRNYFVLLFV
						GVFLSSFGSTANPQMFALAREH
						ADKTGREAVMFSSFLRAQVSL
						AWVIGPPLAYALAMGFSFTVM
						YLSAAVAFIVCGVMVWLFLPS
						MRKELPLATGTIEAPRRNRRDT
						LLLFVICTLMWGSNSLYIINMPL
						FIINELHLPEKLAGVMMGTAAG
						LEIPTMLIAGYFRQTSGPTAYGR
						SVGRIRRSRRIRQSCYYQRIFSL
						LACELANALERPENFCGMHFFN
						PVHRMPLVEIIRGEKSSDETIAK
1						VVAWASKMGKTPIVVNDCPGF
						FVNRVLFPYFAGFSQLLR/ERRG
						FPQDRQSDGKTVWLADGPGIS
						AGRCGH
25513	55881	Α	25654	1590	2855	RNLLGEAADPVSGPHSAIYRPD
						WPKSGDCACQGPIKGSANRPA
						VVPHVHGP\SEDLEVFLNVFGE
						LPQPLIDTQILAAFCGRPMSWG
						FASMVEEYSGVTLDKSESRTD
			!			WLARP\LPERQWEYASPNVWY
						LLPITAKLMVETEASGWLPAAL
						DECRLMQMRRQEVVAPEDAW
						RDITNAWQLRTRQLACLQLLA
						DWRLRKARERDLAVNFVVREE
						HLWSVARYMPGSLGELDSLGL
						SGSEIRFHGKTLLALVEKAQTL
						PEDALPQPMLNLMDMPGYRKA
1						FKAIKSLITDVSETHKISAELLAS
						RRQINQLLNWHWKLKPQNNLP
						ELISGWRGISAVKSSEAGLGAL
						SATSGFGKLQIQHQAFTLRTRT
						TDQHTLLAGTLFIAKILIPMVSF
						TFQYCCFAVPQATYCHRIAPIL
	<u> </u>	l	l		<u> </u>	GNGAMKPGRKIS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25514	55882	A	25655	1	3315	MDELRLVLMTIIHIKLPPIRRAD
						GSFGNDLTTGAGFNDRKTVPR
]		YARVHVYRCRKVICIFTKRIPFC
		İ				LDVPAHRALVVMKGTLYGMP
						VVAAAFEFAFMGGSMGSVVGA
						RFVRAVEQALEDNCPLICFSAS
						GGARMQEALMSLMQMAKTSA
						ALAKMQERGLPYISVLTDPTM
						GGVSASFAMLGDLNIAEPKALI
						GFAGPRVIEQTVREKLPPGFQR
		ŀ				SEFLIEKGAIDMIVRRPEMRLKL
		ŀ				ASILAKLMNLPAPNPEA
25515	55883	Α	25656	246	422	RHADTDLRR*ISDRFSPAPPADP
						ANGGR*TPRHAAKRRDPGTPV
						QPARKPSKPTRLLR
25516	55884	Α	25657	884	1276	LVTRQLSPGNRCNVFAFSSAVE
		1				TSLTCQGWLSPVCAVCQAISSS
		l				HNASIQVRSPAASCGSPFCSKRP
		i i				SALWWTSVSPFLSPRRRTSGAN
		l				AESVSAT*SKRRSSARRSASARS
						TLSGAALRSRTASNEWRS
25517	55885	Α	25658	649	1427	LPLLGWSMSPRMTAQLACDAL
		1				QMALWRRKRPRNVIVHTDRGG
						QSVQQFRALKRHITASRETERF
						YLDVQKQFPKVTAQKVIVSEA
						GASVYSASELAAQEFPDLDVSL
		1				RGAVSIARRLQDPLAELVKIDP
		ļ				KSIGVGQYQHDVSQTQLARKL
						DAVVEDCVNAVGVDLNTASVP
						LLTRVAGLTRMMAQNIVAWR
						DENGQFQNRQQLLKVSRLGPK
						AFEQCAGFLRINHGDNPLDAST
						VHPEAYPVVERILAATQQALKD
						LMGNSSELRNLKASFLDNEEN
						WPLLLDALIPVANTCEMILMPA
						CFGLADDKLWRWLNEKLPCSL
		l				MLLPTLPPSVLGIRLQNQLQRQ
						FVRQGGVWIECGDGGDTTTITI
						TQR**PAGRVYRSPGSLSGGGT
		<u> </u>				HSGSNTAGTERSDG
	55886	Α	25659	1	1878	
25519	55887	Α	25660	1	4329	

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25520	55888	A	25661	2514	4173	PTSCLPDDYVGHCRGVSAAHF AGSVSCVRLLSACARPLWRHL GLALLRVWCRTFLLLSALASVF CPCSVVWGRLLFSASLSVVVW GGVFLSPLGSLSPRGTARLGAA CRSRED/RRR*WRGIFNRDTFAS AVPASVNPDKPCAPAACIRFTS TSAY*VGCSDRNA/DAEASGEG WRRFGDATLSTGQFGGEAREE VILGLIGSQA\KTGGNTPKASAV RKITLVAWPALETGLTMLSM** IG*ETRVFSVFEPSSKSIVPSSRT VTFSSNASRRIAL*ISGSASFDSL IVFA*QPPSKLNTPSSSQPCSSSP IRRRFGSVERVVLPVPERPKNT ATSPFSPTLAEQCIEAIPSAVFA APVRVAASMIISGFCALASIRPS ASTRRPSASVFITSTFLPLR*VMI SPSLNALPLIRLSAQQRNSFTRL FSPRVMANASAPVTVAAPPMS DFIESINAVCLMQARVHWRFFI ASWVVIQPPAIPENVLNRVRLC AAPGTLCLTTFVSSSGDR*NAL CNRCNRPAPCFRSSAIRFATVLA ARRHDWVWPISPLIPRPSS

NO: of peptide sequence load in USSN. voice first conduction of first conduction of peptide sequence addon for last amino acid decision, "possible nucleotide insertion) acid methods in section." 23521 55889 A 25662 2221 4400 RGCVVSGKSSCSKTNLPSDDKF TGASCPLRDLE FRYRAHALY. 23521 55889 A 25662 2221 4400 RGCVVSGKSSCSKTNLPSDDKF TGASCPLRDLE FRYRAHALY. 23521 23521 4400 RGCVVSGKSSCSKTNLPSDDKF TGASCPLRDLE FRYRAHALY. RELEARCH TGASCPL TGA	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
Sequence Sequence	NO:				1	1	
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TGASCPLRDLELRYLRAHAL VI AEQLAHEFSLIGIATIVEQLOQUIL EQCLVMNLQQDIWYSDEVFRR LRLRSLQAAREATRPVAATTY/ RLLLERQGVLPATDGSPALFAS TSRGYYEGVDGVMRVIEQLAA SAINASLWESQEFVYGKPYYAN GENYSGGYYLASFANKUS QGVVDLHGFATNGLYYKSAUPFI RDDMSPAAREADSRWIGEL KLEVSTHYRTGTYKSAVEFFI RDDMSPAAREADSRWIGEL RUTVANARQIPAEQVFPGA QGLLEGLTKTGGDTAKYALEN KLVDALASSAEIEKALTKEFGW SKTDKNYRAISYYDYJALKTEA DTGDSIGVYFANGAIMDEG GNVGGDTTAAQIRDARLDPKV KAIVLRVNSPGGSYTASEVIRA ELAAARAAGKPYVVSMGMA ASGGYWISTPANYIVANPSTLT GSIGIFGVITTVENSLDSIGVHTI GVSTSPLADVSITRALPPFAQI. MMQLSIENGYKRFITLVADARI STPEQIDELAGAGHVAVTGGD DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDARQAMLPAPLASYQVRS PCLTYILLLERYHSVQYHAKEN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSGODARF AIHEYIPRNGSSRFNPGKLAPH/ 25522 55890 A 25663 I 1665 25522 55891 A 25666 1761 1970 25523 55893 A 25666 1761 1970 25524 55894 A 25667 455 1137 GTKPRIDHILGTFTTGMPKG KLDVYAAPELPLKLLGRTTEG YRESFISLLPVVNYLKDKLISNP V/RLDGYDVAGGELV/VLENVR FINGGKKDDEHRAQASTHGIC K/FADVACAGPLLA/AUDSLS //ADQLIVGGGIANTFI/AQGHL YGKSLYEADL/OFAKRLLTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKYKYLPAVAMLEERG 25527 55895 A 25669 1496 1631 25528 55896 A 25669 1496 1631 25528 55896 A 25669 1496 1631 25528 55897 A 25667 462 1152					sequence		
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NYLNTVAANRQIPAEQVFPGA QGLEGLTKTGGDTAKYALEN KLVDALASSAEIEKALTKEFGW SKTDKNYRAISYYDYALKTPA DTGDSIGVVFANGAIMDGEFTG GNVGGDTTAAQIRDARLDPKV KAIVLRVNSPGGSVTASEVIRA ELAAARAAGKPVVVSMGGMA ASGGVWISTPANYIVANPSTLT GSIGIFGVITTVENSLDSIGVHTI GVSTSPLADVSITRALPPEAQL MMQLSIENGYKRFITLVADAR STPEQIDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQYHAKEII LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDAFF AIHEYIPRNGSSRFNPGKLAPH/ AIFE SS892 A 25663 1			1				1
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KLVDALASSAEIEKALTKEFGW SKTDKNYRAISYYVPJALKTPA DTGDSIGVVFANGAIMDGEETC GNVGGDTTAAQIRDARLDPKV KAIVLRVNSPGGSVTASEVIRA ELAAARAAGKPVVVSMGGMA ASGGYWISTPANYIVANPSTLT GSIGIFGVITTVENSLDSIGVHTI GVSTSPLADVSITRALPPEAQL MMQLSIENGYKRFITLVADARR STPEQJIBKILGGHWTYGLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSVQYHAKEII LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AlHEYIPRNGSSRFNPGKLAPHA 25522 55890 A 25663 1 1665 25523 55891 A 25664 475 1182 25524 55892 A 25665 242 3039 25525 55893 A 25666 1761 1970 25526 55894 A 25667 455 1137 GTKPRDIDHILGTFITPGMPKGG KLDVYAAPELPLKLLGRPTEGE YNEEF/SLLPVNYLKDKLSNP VRLDGVDVAEGGIANTFI/AAQGHT VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRYATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25668 1108 1932 25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152 STERN OF THE STANDARD SKTDKNYRAISYSTGGGAFLEL WKVKYLPAVAMLEERG SKTDKNYRAITERSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG SKTDKNYRAITERSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG STERN OF THE STERN OF T				1			1
SKTDKNYRAISYYDYALKTPA DTGDSIGVVFANGAIMOGETT GNVGGDTTAAQIRDARLDPKV KAIVLRVNSPGSVTASEVIRA ELAAARAAGKPVVVSMGGMA ASGGYWISTPANYIVANPSTLT GSIGIFGVITTVENSLDSIGVHTI GVSTSPLADVSITRALPPEAQL MMQLSIENGYYRRFITLVADARI STPEQ/IDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQYHAKEIN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA							1 7
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GNVGGDTTAAQIRDARLOPKV KAIVLRVNSPGGSVTASEVIRA ELAAARAAGKPVVVSMGGMA ASGGY WISTPANYIVANPSTLT GSIGIFGVITTVENSLDSIGVHTI GVSTSPLADVSITRALPPEAQL MMQLSIENGYKRFITLVADARR STPEQ/IDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQYHAKEIN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPH/ AIHEYIPRNGSSRFNPGKLAPH/ A 25664 475 1182							
KAIVLRVNSPGGSVTASEVIRA							-
ELAAARAAGKPVVVSMGGMA ASGGYWISTPANYIVANPSTLT GSIGIFGVITTVENSLDSIGVHTI GVSTSPLADVSITRALPPEAQL MMQLSIENGYKRFITLVADARR STPEQ/IDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQYHAKEIB LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDAFF AIHEYIPRNGSSRFNPGKLAPHA 25522 55890 A 25663 I 1665 25523 55891 A 25666 475 1182 25524 55892 A 25665 242 3059 25525 55893 A 25666 1761 1970 25526 55894 A 25667 455 1137 GTKPRIDHILGTFITPGMPKGC KLDVYAAPELPLKLLGRPTEGE YNEEF/SLLPVNYLKDKLSNP V/RLDGVDVAEGEL/VVLENVR FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK //IADQLIVGGGIANTFI/AAQGHI VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25669 1496 1631 25529 55897 A 25670 462 1152			į				GNVGGDTTAAQIRDARLDPKV
ASGGYWISTPANYIVANPSTLT GSIGIFGVITTVENSLDSIGVHTI GVSTSPLADVSITRALPPEAQL MMQLSIENGYKRFITLVADARI STPEQ/IDKIAQGHVWT/GLGDP DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQYHAKEIN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA 25522 55890 A 25663 I 16665 25523 55891 A 25664 475 1182 25524 55892 A 25665 242 3059 25525 55893 A 25666 1761 1970 25526 55894 A 25667 455 1137 GTKPRDIDHILGTFITPGMPKGG KLDVYAAPELPLKLLGRPTEGE YNEEF/SLLPVVNYLKDKLSNP V/RLDGVDVAEGEL/VVLENVR FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK //ADQLIVGGGIANTE//AAQGHI VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25669 1496 1631 25529 55897 A 25670 462 1152							KAIVLRVNSPGGSVTASEVIRA
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GVSTSPLADVSITRALPPEAQL MMQLSIENGYKRFITLVADARI STPEQ/IDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQVHAKEN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA Z5522 55890 A 25663 1 1665							ASGGYWISTPANYIVANPSTLT
MMQLSIENGYKRFITLVADARH STPEQ/IDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQYHAKEIP LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA							GSIGIFGVITTVENSLDSIGVHTD
STPEQ/IDKIAQGHVWT/GLGDF DDAVAKAAELAKVKQWHLEY YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLLFRYHSYQYHAKEN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA							GVSTSPLADVSITRALPPEAQL
DDAVAKAAELAKVKQWHLEY							MMQLSIENGYKRFITLVADARH
YVDEPTFFDKVMDNMSGSVRA MLPDAFQAMLPAPLASYQVRS PCLTYILLIFRYHSYQYHAKEIN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA							STPEQ/IDKIAQGHVWT/GLGDF
MLPDAFQAMLPAPLASYQVRS PCLTYILLFRYHSYQYHAKEN LRCLHGRDHRDAAFRAGLYTG VRSSTTPTGADAGIPSPGDARF AIHEYIPRNGSSRFNPGKLAPHA							DDAVAKAAELAKVKQWHLEY
PCLTYILLERYHSYQYHAKEIN						,	YVDEPTFFDKVMDNMSGSVRA
LRCLHGRDHRDAAFRAGLYTG							MLPDAFQAMLPAPLASYQVRS
LRCLHGRDHRDAAFRAGLYTG							PCLTYILLLFRYHSYQYHAKEIN
VRSSTTPTGADAGIPSPGDARF							LRCLHGRDHRDAAFRAGLYTG
25522 55890							
25523 55891							AIHEYIPRNGSSRFNPGKLAPHA
25524 55892 A 25665 242 3059	25522	55890	A	25663	1	1665	
25525 55893	25523	55891	Α	25664	475	1182	
25526 55894 A 25667 455 1137 GTKPRDIDHILGTFITPGMPKGC KLDVYAAPELPLKLLGRPTEGE YNEEF/SLLPVVNYLKDKLSNP V/RLDGVDVAEGEL/VVLENVR FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK /IADQLIVGGGIANTFI/AAQGHE VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25668 1108 1932 25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152	25524	55892	Α	25665	242	3059	
KLDVYAAPELPLKLLGRPTEGE YNEEF/SLLPVVNYLKDKLSNP V/RLDGVDVAEGEL/VVLENVR FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK /IADQLIVGGGIANTFI/AAQGHE VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25668 1108 1932 25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152	25525	55893	Α	25666	1761	1970	
YNEEF/SLLPVVNYLKDKLSNP V/RLDGVDVAEGEL/VVLENVR FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK /IADQLIVGGGIANTFI/AAQGHE VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25668 1108 1932 25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152	25526	55894	Α	25667	455	1137	GTKPRDIDHILGTFITPGMPKGG
V/RLDGVDVAEGEL/VVLENVR FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK /IADQLIVGGGIANTFI/AAQGHE VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25668 1108 1932 25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152							KLDVYAAPELPLKLLGRPTEGE
FNKGEKKDDE/HRAQASTHGIG K/FADVACAGPLLA/AVLDSLSK /IADQLIVGGGIANTFI/AAQGHE VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25668 1108 1932 25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152							YNEEF/SLLPVVNYLKDKLSNP
K/FADVACAGPLLA/AVLDSLSK							V/RLDGVDVAEGEL/VVLENVR
							FNKGEKKDDE/HRAQASTHGIG
							K/FADVACAGPLLA/AVLDSLSK
VGKSLYEADLV/DEAKRLLTTC NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG 25527 55895 A 25668 1108 1932 25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152							
NIPVPSD/VRVATEFSETAPATL KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG							1 -
KSVRHSDKISYISTGGGAFLEL WKVKYLPAVAMLEERG							
WKVKYLPAVAMLEERG WKVKYLPAVAMLEERG			1				
25527 55895 A 25668 1108 1932 25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152							
25528 55896 A 25669 1496 1631 25529 55897 A 25670 462 1152	25527	55895	A	25668	1108	1932	
25529 55897 A 25670 462 1152			_			<u></u>	
		-	-				
L.,	25530	55898	Α	25671	545	598	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	l control of the cont	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
	<u> </u>			<u> </u>		
25531	55899	Α	25672	1	1761	MRGHNWIDMDQARQQSTPHT
						DRKICHKNDRPRTTPLRKIDAH
						PHTLIILPAESTLSTTKYKLRAL
						LVENTNKDKSAVSVVFRGSVL
ĺ						HQQAANFPNLMLCFQLKNGVN
ĺ						ACNDFIMLFVDDNAAGSIERAA
ĺ						SPCINEKQHAFSESVPAIAAVRG
ĺ			•			LGSMIAVEFNDPQTGEPSAAIA
ĺ						QKIQQRALAQGLLLLTCGAYG
						NACKRRIDYVCRIKHSRRIRQV
						VLLNFAKSGAFSTTRGTDDKLT
						PVIQPRASGEYNEEFSLLPVVN
						YLKDKLSNPVRLVKDYLDGVD
1						VAEGELVVLENVRFNKGEKKD
						DETLSKKYAALCDVFVMDAFG
[TAHLRAGFLLTGI\GKLRCSLRC
ĺ		1				AGPLLAAELDALGKALKEPARP
İ					i	MVAIVGGSKVSTKLTVLDSLSK
1						IADQLIVGGGIANTFIAAQGHD
						VGKSLYEADLVDEAKRLLTTC
		İ				NIPVPSDVRVATEFSETAPANL
						KSVNDVKADEQILDIVRDLDAA
-						NVVINAVFSYVTNVWGWAFE
						WYMVVMLFGWFWLVFGPYAK
						KRLGNEPPEFSTASWIFMMFAL
		1				LYVCCRTVRLGREIHRRAQIVH
		l				IDIEPTQIGRVLCRISVLSLMLKR
25532	55900	A	25673	1	984	
25533	55901	A	25674	1	1181	MMAVSAPYVGDNIDDGGIYTQ
						SETHTISSDCVLDTAAMWTPLS
			}	•		AVIGCTTNPAQYPANAAEVYN
		1		:		KDGNKLDLYGKVDGLHYFSDN
						KDVDGDQTYMRLGFKGETQVT
		l				DQLTGYGQWEYQIQGNSAENE
<u> </u>						NNSWTRVAFAGLKFQDVGSFD
						YGRNYGVVYDVTSWTDVLPEF
						GGDTYGSDNFMQQRGNGFATY
						RNTDFFGLVDGLNFAVQYQGK
						NGNPSGESFTSGVTNNGRDALR
						QNGDGVGGSITYDYEGFGIG\Y
						TQTYNATRVGSLGWANKAQNF
]		EAVAQYQFDFGLRPSLAYLQSK
						GKNLGRGYDDEDILQICCMSDP
]		TQNRQASAKLALPCQVALLSSA
				1		SPHHAFTPSTSIIQPAHIIIHSSPP
]						PWASSHSISTHQQHTQCSSSSNT
1						
<u> </u>				<u> </u>		LAVH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	1 '	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25535	55903	A	25676	683	947	 QVRDSLQQGRERRIALSIGWLV
	00000	-				WREGCQDQCELEAGGASALTR
						RGSCRELDPAPFATMLLFCPGC
						GNGLIVEDG\QRCHASTDAVPP
25536	55904	A	25677	12	393	RGSCRELEPAEFETMLLFCPGC
						GNGLIVEEGQRCH/RAVACNT\
	-					CPYVHNITPQGNTIWKYPKLKE
						CGSDVLGGAAAW\ENVDSTAE
						SC\PKCEHPRAYFMQLQTRSAD
						EPMTTFYKCC\NAQCGHRWRD
25537	55905	Ā	25678	234	567	YVDETDDCFENNRCGQPVNGA
						YSPAGLSRVAADASLTTPHAK*
						TLRSLTLHQHDKTRTELLNDVA
						GALALDDKLGRSTNQLSGGEW
İ						TPSLARPFLLLGPRKMRLLPLH
						LPP
25538	55906	Α	25679	1	794	HCDGKHFTGVGKIMSIGMQLQ
						DVAESTRLGPLSGEVRAGEILH
						LVGPNGAGKESLTGREWPEMP
						TVKGTIQFPGHPLEAWSAKK\L
						ALLRAYL\SQQQTPPFPPPVWH
						YLTLHQPDKTRPELLNDVAGA
1						LALDDKLGRSTNQLSGGEWQR
						VRLAAVVLQITPQANPAGQLLL
						LDEPMNSLDVAQQSALDKILSA
						LCQQGLAIVMSSHDLNHTLRH
				ŀ		AHRAWLLKGGKMLASGRREE
						VLTPPNLAQAYGMNFRRLDIEG
						HRMLISTI
25539	55907	Α	25680	12	414	RAAPSRNLPPRMPIPIAAPIAAR
						PIITAAAMYSRSIFRFSMTVSSLF
						QLKRSSVGKLMFFRRHRQIDDR
						QNHEDEGLQRNDQDVENGPRH
						IQDPL*PPRQETSNQNEDQLSGV
						HVTEQSQTEGSWFGQHAYPF
25540	55908	Α	25681	568	724	RFSLGTVLDGIYPHQYDGYSR
1						WSAKRYL*WRNL*SGTHRSC*
						VNNFTRSNKK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25541	55909	ĪA	25682	1	974	MNGKLQSSDVKNETPYNIPLLI
23341	33,707	1	23002	1	,,,	NENVISSGISLISLWHTYADEHY
				1		RVIWPRDKKKPLIANSWVAVY
		1		<u> </u>		TVTGCGNSDRLNNIRTLRA\MA
		1				REFSIDVLDEMLQQFRVVTPDR
1				İ		PEHKQLPQHELAERQEKISTWL
						ELMKADGINPEELLGN\SSAAA
				1		
				1		PR\AGKKRQPGSAKYLFT\DVN
						GETKTWTGQGRTPKPIAQALAE
						DCHGKPEYGSAVHGCRCDDGS
						AGNLCFDLNRHCGLGVRLRPR
						KINGDYRSRFCHAGETGVCAG
						AETTQMAESGVSGAGLAVRGE
						RDGKRSPLQIAIMMNGSSGQAI
		1	2.500		1050	SSNVIILQLFLVEVIKSLRMLYM
25542	55910	A	25683	1	1359	
25543	55911	A	25684	72	918	PAPVAGAHCPLGLHRSSEHQEP
25544	55912	Α	25685	12	1090	1
						QLRHVARWPSS*SWLCHGTFR KLLPGKKRRGGNKKF*GRRAR
•						
						GVGCVVSRVWCGPACACSLRR
						WLAHTVHWVFTEAQSIKSHSS
						DMWPDGLALSPGCAMGPSGSC
1						SRGKNVGGATKNFRGVHNIYC
İ						HKPIPTTQHESKYARQTTTEEC
						TQTSSHDFRTTFSAVMQQRLQI
		-		Ī		ARNLVTHPKLVFMDEPTGGLD
						VSVQARLLDLLRGLVVELNLA
	1					VVIVTHDLGVARLLADRLLVM
						KQGQVVESGLTDRVLDDPHHP
<u> </u>						YTQLLVSSVLQN
25545	55913	Α	25686	1334	1545	RSQSRLERSCSVTGSM*RVSPA
1						RSFRRITKRVLAAARLAT*LPAS
	}					GRRTGVGVSVDSEFPSELLSSSF
		<u> </u>	2.50=	1.704	0101	TD
25546	55914	Α	25687	1784	2125	WLQHIHPQLLRCPVLRAQNVW
ļ						IRTLYDRH/RFVTRGTLGWIETG
						DF/DKVPPDLRFFAGGDRSI/RG
						YKYKSIAPKYANGLDIGKSPAA
						GAISPCLTFVMSARRGGHRGQS
	<u> </u>	 				ASGCRA
25547	55915	Α	25688	931	1213	NLHPAPAKRRAPARPQSRLAHR
						QRGRMRGAPRPFRQRQIKLCY
						ARCTPTICPTKVKSRSNTVTSG*
						TWSPRQRAKWWKSAKPPSAGL
						TSSARHP
25548	55916	Α	25689	999	1243	VDPVPWLPMALDITSTAPARQF
	,					RKRIIASLMPT/WGTSLRRYSVP
						PRRSGWKRWRFPPTGSTTCRPP
				<u></u>		FPAVCSSVCRLPATW

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25549	55917	A	25690	1225	2341	ARTFRLSNFGGSTRARGVYWD PNSDLCPTLDFSYKMPLLKNPL EQYYLVQGGFKRTDLNDTESD STTLVASRYWDLSSGWQRAIN LRWSLDHFTQGEITNTTMLFYP GVMISRTRSRGGLMPTWGDSQ RYSIDYSNTAWGSDVDFSVFQA QNVWIRTLYDRHRFVTRGTLG WIETGDFDKVPPDLRFFAGGDR SIRGYQY\KSIGPKLPNGD\LKG ASKLITGSLEYQYNVTGKCTK WQFGEWLAPGEVRLAPGATLA TPELVASCSTEGLNGLAANFHA ELRARLPWHGGAMKPRPVHLN TWEGFYFDLQPDKVKALATAA AALGVERFVLDDGWFNARHH
0.5.5.50	55010		25.601	45	222	DRAGLGDWWPDATKFPQGLG ELVAHVNPFYA
25550	55918	A	25691	45	233	SSYPRWWAAWWASTTARPSTR WRSSPR*SATTWASSPSPTSP*I HDRPGIGATHSSRFIPLK
25551	55919	В	25692	1	558	
25552	55920	A	25693	324	657	
25553	55921	A	25694	831	1244	WQPGGR*WSRQRSADGTGPDD LAAAYFPGDRFYRN*PSERC*H RRG
25554	55922	Α	25695	1	1215	
25555	55923	A	25696	1	840	
25556	55924	A	25697		1365	MPQNRGGFLDKKNPGAPLEGA VYVNCFTRFPGIGYEGRTAVFC GAAKVPPGLNYRGIGAFPGGNF ASKRSRGRNLAGARCLRFCPK\ WQ\NYSETASVQQQN*SVLARA IERGINAPLA\SSCGRFFDAVPA ALGCAPATLSYKGEAACALEA LAASCHGVTHPVTMPRVDNQL DLATFWQQWLNWQAPVNQRA WAFHDALAQGFAALMREQAT MRGITTLHPEGLERMSAGHES WLERRNGELGEGKGSKAYPTG DHKGADLYDDSNFLIQNIFVED TRGLLRQGREDLIERYKDPLNE NPKRCVEQLANWHKELEEYKK ASRIDIKPSREYASTIMNAIWTG EPSVIYGNVRNDGLIDNLPQGC CVEVACLVDANGIQPTKVGTLP SHLAAMMQTNINVQTLLTEAIL TENRDRVYHAAMMDPHTAAV LGIDEIYALVDDLIAAHGDWLP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25557	55925	A	25698	1	950	MPDEENRFNALKAVFSQLMTD ATLTPLFNYHYRISAPPGVNGL
	İ					SMKRAVVVFSGGQDSTTCLVQ
				1		ALQQYDEVHCVTFDYGQRHRA
						EIDVARELALKLGARAHKVLD
						VTLLNELAVSSLTRDSIPVPDYE
						PEADGIPNTFVPGRNILFLTLAA
						IYAYQVKAEAVITGVCETDFSG
						YPDCRDEFVKALNHAHKEKLD
						EDCKRRMYTNPLRVLDSKNPE
						VQALLNDAPALGDYLDEESRE
						HFAGLCKLLESAGIAYTVNQRL
]					AVNPEFKADPVVDIYLVASGA
						DTQSAAMALAERLRDELPGVK
						LMTNHGGGNFKKQFARADKW
						GARVAVVLGESEVANGTAVVK
						DLRSGEQTAVAQDSVAAHLRT
						KEKDSVEIYENENDQVEAVKRF
		1				FAENGKALAVGVILGVGALIG
		1				WRYWNSHQVDSARSASLAYQ
1						NAVTAVSEGKPDSIPAAEKFAA
						ENKNTYGALASLELAQQFVDK
						NELEKAAAQLQQGLADTSDEN
						LKAVINLRLARVQVQLKQADA
						ALKTL*IPD*RPDAGLRCKRSPR
				İ		SPAVCTDRQNAHEIPRPDSHLM PERR*EAPALPDFLNPARAAG
25558	55926	A	25699	1	3314	MKISRLGEAPDYRFSLANERTF
23338	33920	^	23033	•	3314	LAWIRTALGFLAAGVGLDQLA
		1				PDFATPVIRELLALLLCLFSGGL
						AMYGYLRWLRNEKAMRLKED
						LPYTNSLLIISLILMVVAVIVMG
						LRAMLMAMEPIWESDFHTLSY
						GFRPERSVHHAIRTVKLQLTDC
						GETRGRWVIEGDLSSYFDTVHH
						RLLMKAVRRRISDARFMTLLW
						KTIKAGHIDVEDKRAASEGVPQ
						NKIISPLLSNIMLNEFDQYLHER
						YLSGKARKDRWYWNN
25559	55927	Α	25700	997	1716	PYLTASSSAFQQLHLSGENHRD
						DGCAGYSRRTLAAQLQCHCEC
						DHNLPPDTPRLPRSGVVLPARF
		1				PRPLHTLISALHRRVLTRHARH
						ESSTLNPQRLPPAHRFFACQSRY
						VPGPAEYSYAVRSTDESG*A*W
						LRVPPNLIALTVQRSLPDLALPA
						QNCPPCRSMLEPAPYILLGMLA
		Ì				TWPACPG\HEVG*SHSAHPDEP
						ETLQTVSR*YRRFGRPVH*SVH
		_				VVGRYPHQACQCYLSSTAE
25560	55928	Α	25701	1	769	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25561	55929	A	25702	1	3707	MVRSAVVAGIAQAALPQSVVA
						WEYLVEDYDRIRNDIEAVLPEF
					ļ	ADYNQRIRHPGGFHLINAAAER
						RWMTPSGKANFITSKGLLEDPS
						SAFNSKLVMATVRSHDQYNTTI
				ŀ		YGMDDRYRGVFGQRDGYRDN
						CEEIAQLAEDCGNLFAVTVFRC
						PAGANLQGNRNVHCIDDLGKD
						RFNDIRNVQAAELLAEMAISSA
					ł	QRRMRAAKKVVRKKLTSGPAL
						PGKLADCTAQDLNRTELFLWK
						GEQNALLRGFPAVRLHSLL
25562	55930	A	25703	1	369	LPSHGAGLGTCSLPCLSLPPTP
						WAPVQPEPPRRAPPPAPWRPVP
						LTTQGLRN/DEHRVQDWQAAP
						PAAPLKVCKYTNQHPVFSTRFV
						NAPIDTLYLAALVRTWRTFMSS
						SRIVNTPIGTLYLAQ
25563	55931	A	25704	1	444	MRLHSSALGRSMGLGAVEQGA
				}		ALVGEAPAAQEPTEAGEGSGM
						AGCSPKACPAGRQLRPGPA\AA
						PSAGPPSPRPPGTPAGPQAPRAA
						PVPARASPSTPPCKLRERAAAF
İ						A/EPRKGLPQCSGGLKGSSSAA
		1				KVGAQAEEAPRASESCEDC
25564	55932	Α	25705	1767	2130	YTGQRLRRVYWVPQQCQPTCA
			}			ALDFSPSLSCLPA/AAGLRTYSQ
						PCLSLPPTPWAPVQPEPPQ*APP
		1				PAPRRP\AHRPPKG*GVQAHGA
					:	G\RQAAPPAAPVRDPLG\KPAGL
						LSLVGTWRTFMS
25565	55933	Α	25706	654	832	RRCARFLAGP*LPSHGAGLGTC
						SPPCLSLPPTPWAPVRPEPPRRA
		١.				PPPAPRRPVLCVFS
25566	55934	В	25707	1	537	
25567	55935	Α	25708	1	455	HCGSVIGGFLVSLTLRTKLRTL
		1				AVSVTALTVVCLEFIPSDVRMR
		1	1			SVSSFWWVRSLAGSRVKLQTF
						AVTVTALKAASLELFVPPGGLV
		l				VSLASGVKLQTAAAGK/RCLPV
		1				LRHAPALLSPWVVDGTGHRGA
1						GGGAHRGGSGRPGAHGGGGRL
25568	55936	Α	25709	1	314	SACREVWRERHEREPGLRGAL
		1				AGQLEFRVGVGLVRPALGGAG
						QPGAALDFSPGLSCLPA/AAGL
						GTCSPPCLSLPPPPWAPVQPEPP
						RRAPPPVHGAQSHRPPKG

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25569	55937	A	25710	144	519	HPGQRLRRVYWVPQQCQPIGA ELDFSPSLSCLPA/AAGLGTCSP PCLSLPPPPWAPVQPEPPQRAPP PAPW/WLSPIDHPRAEECECTA QDWQAALPAAPVWDPLEMSG LFDRAEKRYIRSFARKDSM
25570	55938	A	25711	271	743	ARTWNVPKVCVRIKANSHSIFT GLSCLPAGQGSGPAARHA*ASD PLRGLLCGPSLLDE/PPPPAPWR PVPSTTQGLRSAGEQRGTGRQL HLSAAPVRDPRGEAIWAPESGR SAASILKPARPPAHREERTTPDA PP*EL*HSPRRSAASLREDPWLH S
25571	55939	A	25712	1043	1348	GPARNRAQRRRAGTAGGPITPS AAAGPGAKPLIARRRQGWPAA PSAGPAKPTPTRISSWPAS\QPA AAVPARASPSTTLFKLREWAPA LASPERGSHSATVG
25572	55940	A	25713	22	226	NTRRWTEMTFDQVVRIFSIGNL QTVLQNRQPGGAIARCTGHIDP VTRFRPRAR*GSSHRNKAVDTQ RH
25573	55941	A_	25714	166	714	
25574	55942	A	25715	1	462	

	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25575	55943	A	25716	1	924	MFAIISYSSLAAVLLTATLTAAG
						IISFPVALCLVIGANLGSGLLAM
						LNNSAANAAARRVALGSLLFK
						LVGSLIILPFVHLLAETMGKLSL
						PKAELVIYFHVFYNLVRCLVML
						PFVDPMARFCKTIIRDEPELDTQ
į						LRPKHLDVSALDTPTLALANAA
						RETCALATPWTDDGRKYAYSA
						ASGGRRSATKVMVVVTDGESH
						DGSMLKAVIDQCNHDNILRFGI
						AVLGYLNRNALDTKNLIKEIKA
						IASIPTERYFFNVSDEAALLEKA
						GTLGEQIFSIEDMDLGDEVYTV
						GRPHPMIDPTLRNQLIADLGAK
						POVRVLLLDVVIGFGATADPAA
			:			SLVSAWQKACAARLDNQPLYA
					•	IATVTGTERDPQCRSQQIATLED
						AGIAVVSSLPEATLLAAALIHPL
						SPAAQQHTPSLLENVAVINIGLR
						SFALELQSASKPVVHYQWSPV
İ		İ				AGQGKWLANPELLEADADAEY
				İ		AAVIDIDLADIKEPILCAPNDPD
						DARPLSAVQGEKIDEVFIGSCM
						TNIGHFRAAGKLLDAHKGQLPT
						RLWVAPPTRMDAAQLTEEGYY
						SVFGKSGARVSSIPCAVPCVWA
ŀ						RVADGATVVSTSTRNFPNRLGT
						GANVFLASAELAAVAALIGKLP
ļ.						TPEEYQTYVAQVDKTAVDTYR
						YLNFNQLSQYTEKADGLLKPRF
						RPWQRKILDTLATYHEQHRDEP
						GPGRERLRRMALPMEDEALVL
25576	55944	Α	25717	1	417	MGVLNNWLSEEESLWIQSRIHL
						RALRYYSNWRQYFAGYTFGRQ
						YWQSPEDDHLPLLREFLARYER
						PMKNCWKILDIEETTDVDIIRRA
						YLALLPSFHPETDPQDFKQLRQ
						AYEEALRIAQSPAKSVWQPEEY
						EVAEHEILLAFRALLASDSERFL
						PSAWQRFIQQLNYCSMEEIDEL
						RWSLCTIAMNTAHLSFECVVLL
						AERLRWLQEENTGEIDEEELGS
						FLYAIAKGNVFNFQTILHLPVA
						RRPDICTQHNDQSRCEGYQILS
						DKRGHQHGGGITALYQCGNAD
						PRAKGERLFFDAPA*CASSARV
						CVLSLAGASKKSRSPFARGSAL
						PHWYRAVMPPPCW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25577	55945	Α	25718	1680	2058	YRAYAPAFLPLSPSCPPLWRHC
						GSGRGENRRRDSSAHGPYAPRR
						QPDMPAHRQS*SFV/PASCSAC
ŀ		1				MDEPHKRLTVTAGTECGTSASS
		l				AALRAILKPCSSVCSSFFLLLLL
						PPPPPSSSSSSFFFLF
25578	55946	Α	25719	1115	3549	NPDRLLQLNLILETSK*QQMGD
						TRKKRS/NLTVAPIISPLKRYEQ
						HTELSRHINVVNLGDRNRRQQL
		İ				ILDQGKSSQRNIYLSHVAQKIPG
		l				RATYALSHSVDMITIQLGTLLR
						CAPPHRRRYAGRFFCRSAGNFL
ļ		İ				NVQGFDAVLVAVKHDLLLCLT
						IAPSLIVCTRLRSPWCGALRRCS
ŀ						TDGRSDLASSGVMFSIDTESAL
						TRWCLSLPHGALGKIIAEGLLS
						VIASKASAIVTTVAVVPVTRRSS
					}	LVNWHSGGSGLWRCNRTDERD
						QQASQGTTRMGRTQRNYSPTR
		į				QAIHKTGSPTMATTSNTEQPPH
						EKPNTLTQHPRNPDRTIHPKAT
		ŧ				HNELTQDTPQRDAKQNGEKTQ
}	,					RKKNCLSELNDAEDQAERFQD
						RLMLKLQVTTKPCSMTRLRDC
						AGIWSAANRWSGIGIDRMIMLF
		l				TNSHTIATLFSSRRCAHRNKFH
						LMNEAVRRLLRSSFRKSVLRRD
						ASFHDNQRVHSLQLLKERKKSL
						IHGRICAAKASLFQTRRYRWQK
		1				APLFSAQFRGRNRAVTHNRWV
						TTTTAIERTRARGLRPNSGRGF
						HSSPAWQLRHRKCRRCARRYH
		i				TVYWIKRRRSVARASTVVSGRI
						TSRRGENRRRDSSAIAHMLHAA
	,	1				KQTCLRIAVMIIRAASCSACMD
						EPPSDLTVTAGTDAGLAPAGYA
						LNERROLLHALTKSTALRTAHR
						GPNRTGWLNRRIVRFVMTALF
25579	55947	Α	25720	606	1562	
25580	55948	Α	25721	688	762	
25581	55949	Α	25722	492	737	SLPSGATLPPPALLLASAPDTA*
						WRCRER*YHLPAYAALSPAVA
						HRASLYSTLPSSVPWRRQCAGF
L						RARRSPEQAWAYPAR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25582	55950	A	25723	335	903	WVHDLPARKGSSARNIMLKSA PLRGHTRTRRKKMNIIEANVAT PDARVAITIARFNNFINDSLLEG
						AIDALKRIGQVKDENITVVWVP GAYELPLAAGALAKTGKYDAG IALGTGIRGGTAHFEYVAGGAS NGLAHVGQDSE\IPVAFGVLTT ESI/EQAIERAGTKVGNKGAEA
						ALTALEMINVLKAIKA
25583	55951	A	25724	3644	4545	SEAWPWRTAGTCLLCLNTT/AH VDKAIESRTVVADVLAKFENAL TGKLLTVSFQAHEAVIHGHHPA PEENLQVLAALRLQYLQGDYT LHAAIPPLEEVYSLQRLKARISQ STKTFTPCERLEKRRTSFLEGTL RRSFRTGSVVRQKVEEEQMLD MWIKEEVSSARASIIDKWRKFQ GMNQEQAMAKYMALIKEWPG YGSTLFDVECKEGGFPQELWL GVSADAVSVYKRGEGRPLEVF QYEHILSFGAPLANTYKIVVDE RELLFETSEVVDVAKLMKAYIS MIVKKRYSTTRSASSQGSSR
25584	55952	A	25725	1	735	
25585	55953	A	25726	147	504	STCPASAPPRPSAGPRILSGSSAS GSPLGSSSASSPAVHKG*RFWL TG*CGP*VSAGNK\LFERWDGS VQSIIPLQILESQGSKNLEVFFRG WMVAMDNRFVGLKGDSQQLS GQRIFKLG
25586	55954	Α	25727	1	639	
25587	55955	Α	25728	1	1247	

SEQ ID		Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25588	55956	Α	25729	1	2376	MAEVEEKKQRIFRKFTYRGVD
		İ				LGQLLDMSFEQLRQLYGARQL
						RRLNHGLWRNAEAQAAFAAE
	į					APMLGQEGGADHREAGSGEDA
						PAGYDHPSQDGGQQGGRLQRQ
						DLQPGGDQAGDDRPRPGRVLH
						HLQAQRGKKPM/ISTVTFGQ*P
						DPPLRAGQRL*RC/RLLIYGRGK
						CWALSGNP/RSGKTTLLKSISAR
·						LTPQQGEIHYENRSLYAMSEAD
						RRRLLRTEWGVVHQHPLDGLR
						RQVSAGGNIGERLMATGARHY
			1			GDIRATAQKWLEEVEIPANRID
ł				}		DLPTTFLRATHTVKMFSIPGYSS
						PGQLLDPETNINIGTSYLQYVY
İ						QQFGNNRIFSSAAYNAGPGRVA
ļ						TAIVLTLYIIYMVGFFATSGELT
						YEVWIGFFASAFTKVFTLLALF
						SILIHAWIGMWQVLTDYVKPLA
						LRLMLQLVIVVALVVYVIYGFV
						VVWGMRAALQISQSGQTCALL
						SKVFPTRSHTVSAQGGITVALG
1						NTHEDNWEWHMYDTVKGSDY
						IDAGRKRQEEGDWNSGVGDPS
						DAGDRKHQLKAAQLRPEAIKQ
						RRIANRLKRRTQFPRHLKGFVN
						TLKPIHGGCSVGTKCPQMASLP
						EGLHHPVKLVFLGKPGCLLTDR
						PLKGPNTAKPVAVDLNASATAI
						TSYSLYGGSMILLFLASTLYHAI
		ŀ				PHQRAKMWLKKFDHCAIYLLI
						AGTYTPFLLVGLDSPLARGLMI
25500	55057		0.5720	210	650	
25589	55957	Α	25730	219	652	SASWREAICLSRCRLPRSATAR
						GAGRGGCGLADRRASRQGKNL
						EAESAQEQNGHQHRIHESQHPC
						QGGAPVSHHQAAVRLRESQIQ
		1				GAAEKR*PTGDVIHPGQPVSGG
						/LK*YPSIPTCLLTTRTASLLKPP
2.55.5	4.50.50	ļ	0.550:	1000	2100	GVRTSVCWQQLPR
25590	55958	Α	25731	1902	2100	RKFFSSSSGRS*PVRCSKL*SSID
						A*PLERIKRSRSYQVGSVGLCL
						RKSFHSTSAISAMPIGAPG
25591	55959	Α	25732	3223	3669	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			ļ	sequence		
25592	55960	Α	25733	1	4325	MPEPPTHSMGSCAAGASLTSTA
1					İ	PCSTAPSPIDHLRAKECERTAQ
		1				DWQAAPPAALVRDPLAALVRT
		l				WRTFMSSSRIVNTPIGTLCLAQ
						GFQWFSVLSQVHASTDQEIQE
						MHDEQANPQNAVGTLDVGLID
						SVCASDSPDRPNSFVIITANRVL
						HCNADTPEEMHHWITLLQRSK
						GDTRVEGQEFIVRGWLHKEVK
						NSPKMSSLKLKKRWFVLTHIPG
1						LLQEFREDALNWGPDEKIFKET
						ELVNDMDKINGRIERAE
25593	55961	A	25734	501	2871	TGCCCLRKTDCRRRESARGVH
23373	33701	 	25754	301	2071	AVYRRICARSMLLYRESVRPKA
						VTARVAVEAGIADYWYKYVG
			İ			LNGAIVGMTTFGESAPAELLFE
						EFGFTVDNPLASRAVRLRLPFN
						NDQVEAAVGWKLAVERHNGP
						TALILSRQNLAQVERTPDQVKE
			-			IARGGYVLKDSGGKPDIILIATG
		İ				
						SEMEITLQAAEKLAGEGRNVR
						VVSLPSTDIFDAQDEEYRESVLP
						SNVAARVAVEAGIADYWYKY
						VGLKGAIVGMTGYGESAPADK
1						LFPFFGFTAENIVAKAHKVLGV
i		1				KAGSHIPRKKYDVPGKKSFSPV
	İ					KYSTIGSPSPERPVSITTIPNSFVI
						ITANRVLHCNADTPEEMHHWIT
	ŀ	1				LLQRSKGDTRVEGQEFIVVEKL
		1				IRGLAMEDSRNMFALFEYNGH
						VDKAIESRTVVADVLAKFEKEP
]			VGKHLPTYDGQIAMGLESTAS
İ						VTRKHSSPSSLQNALSCETATSL
		1				IERRVRMALGTGDRRGLNTWL
						ARLPMEAKEKDEWRYWQADL
		1				LLERGREAEAKEILHQLMQQR
	1					GFYPMVAAQRIGEEYELKIDKA
		1				PQNVDSALTQGPEMARVRELM
		1				YWNLDNTARSEWAN\LLKNKS
		1				KPDRAHLPGYASTTQWWILSV
		1				QATI\AGNLGDHLKERFPLANN
		1				DLSKRYTSGKKIPQSYAMAIAR
		1				QKSAWNPKVKSPVGASGLMQI
1						MPGTATHTVKMFSIPGYSSPGQ
25594	55962	Α	25735	1	1195	
	1	<u> </u>	1	I		

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25595	55963	A	25736	1931	2676	FCGNTHQTYLGWVGGVANSEA *GEKWGTPDLVG/AERTETIQR LLGVCPEQGEGKIYIDGKQVDI RNCQQAIAQGIAMVPEDRKRD GIVPVMAVGKNITLAALNKFTG GISQLDDAAEQKCILESIQQLKV KTSSPDLAIGRLSGGNQQKAIL ARCLLLNPRILILDEPTRGIDIGA KYEIYKLINQLVQQGIAVIVISS ELPEVLGLSDRVLVMHEGKLK ANLINHNLTQEQVMEAALRSE HHVEKQSV
25596	55964	A	25737	1491	1667	TNGQWRAFYC*MRSGRNIRRR GEDISGGAGVSPRESPE*REVPE MGPGGAANRGTKRV
25597	55965	A	25738	419	823	VTLVAITRPIHVNRLRQYLVAIS LNETFGPSCKPSRSPCSSLSTCC WNAGVMHKK*VQGGRLCSYR N*SICLVVISPVVMGKRCIS*RC TAVLAALTVTVPSGVVAAHSV MLPRLPMKRSSIVPLPSNWRTS
25598	55966	A	25739	591	968	VKQCKQADEH*EQSLIPLERRR TTPLSVPQL/GKALTTVSFCASG GTSVNSLSHTS*ECMASAVAVK FTFPNLAVNFCTAAMAGPKVA LTSTLARIQAGSLARTGGRAYR WSRSTMLAKSFWCLMAL
25599	55967	A	25740	764	1005	QARPRAPRRAPYPILIRSSIITLIY /DGQRLGHLDDGTDSWNHVPT LNGQCTLVLIHEYVDTRGPEIK TILVISWWNILVFH
25600	55968	A	25741	463	786	
25601	55969	Α	25742	3	646	
25602	55970	A	25743		3008	MTMLQIVGALILLIAGFAILRLL FRALISTASALAGLILLCLFGPA LLAGYITERITRLFHIRWLAGVF LTIAGMIISFMWGLDGKHIALE AHTFDSVKFILTTALAGGLLAV PLQIKNIQQNGITPEDISKEINGY YCCFYTAFFLMACSDQRRLRG AMDKRYKFILVGFGEVFVFNLE SLDSGKKIHLLRRSHEEVMGSV MRTGTIDKGILPFIHHTRGNEIL FIPALFILFSLGGAVFGMGEEAV AFAIIIA

NO:	SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
25603 55971 A 25744 2 3494				1	I .		
25603 55971 A 25744 2 3494 TITNLRPAAPGICEMAQGLSA GEYTGASIFVAEYSPDRRRGF GSWLDLRSIAEIELGAGGVOFF TIVGEANFLDWGWRIPFIFIAL GIIGLYLRHALEDTPAFQQHW KLEGODREGLODGPKVSLEK TKYWRSLLTCIGLVIATNVTY MLLTYMPSYLSHNLHYSEDH ALIIIAIMIGMLFVQPVMGILS RFGRRFVLLGSVALFVLAIP ILINSNVIGENLLPAMFPTHIR ALLLEMKN		sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
GEYTGASIFVAEYSPDRRRGI					sequence		
GEYTGASIFVAEYSPDRRRGI	25603	55971	ĪA	25744	2	3494	TITNLRPAAPGICEMAOGLSAG
GSWLDLRSIAEIELGAGGVGI TIVGEANFLDWGWRIPFTAG GIGLYLRHALEDTPAFQQHV KLEQGDREGLQDGPKVSLKE TKYWRSLLTCIGLVIATNVT MLLTYMPSYLSHNLHYSEDF ALIIIAIMIGMLFVQPVMGLLS REGREPFVLLGSVALFVLAPI LINSNVIGLNLLPAMFPTHIR ALLLEMKN 25604 55972	į						1
TIVGEANFLDWGWRIPFFIAL GIIGLYLRHALEDTPAFQUM KLEQGDREGLQDGPKVSLEK TKYWRSLLTCIGLVIATNVTY MLLTYMPSYLSINLHYSGEN ALIIIAMIGMILFVQPVMGLIS RFGRRPFVLLGSVALFVLAIP, ILINSNVIGLNLLPAMFPTHIR ALLLEMKN							
GIIGLYLRHALEDTPAFQQHV KLEQGOREGIQDGPKVSLET TKYWRSLLTCIGLVIATNVTY MLLTYMPSYLSHNIHYSEDF ALIIIAIMIGMLFVQPVMGLLS RFGRRPFVLLGSVALFVLAG RFGRRPFVLLGSVALFVLAG LILINSNVIGLNLLPAMFPTHIR ALLLEMKN 25604 55972							i l
KLEQGREGLQDGPKVS.KE TKYWRSLLTCIGLVIATNVT MLLTYMPSYLSHNLHYSEDF ALIIIAIMIGMLFVQPVMGLLS RFGRRPFVLLGSVALFVLAIP ILINSNVIGLNLLPAMFPTHIR ALLLEMKN							i I
TKYWRSLLTCIGLVIATNVTY MLLTYMPSYLSHIALHYSEDH ALIIIAIMIGMIGHVQPVMGLLS RFGRRPFVLLGSVALFVLAIP, ILINSNVIGLNLLPAMFPTHIR ALLLEMKN 25604 55972		ŀ					``
MILLTYMPSYLSHNLHYSEDH ALIIIAIMIGMLFVQPVMGLLS RFGRRPFVLLGVALPVALIP. ILINSNVIGLNLPAMFPTHIR ALLLEMKN 25604 55972							t i
ALIIIAIMIGMLFVQPVMGLLS RFGRRPPVLLGSVALFVLAIP, ILINSNVIGLNLLPAMFPTHIR ALLLEMKN 25604 55972							I I
RFGRRPFVLLGSVALFVLAIP. ILINSNVIGLNLPAMFPTHIR ALLLEMKN							1
ILINSNVIGLNLLPAMFPTHIR ALLLEMKN							· ·
ALLLEMKN			i				1
25604 55972		ı					
25606 55974	25604	55972	Α	25745	1	277	
25607 55975	25605	55973	A	25746	902	1006	
25608 55976	25606	55974	A	25747	2	1265	
GHLRPVERQCSPDKRRFIAAI	25607	55975	Α	25748	409	525	
REIRGKQRAGHIFQLLSRCLL	25608	55976	A	25749	91	431	NHKPGNIDVARRIQRGFAGDQI
LNHCQRRAAHFRFQLSNQRH QLLPV/HYHAAEREYPAGACI RWLL			İ				GHLRPVERQCSPDKRRFIAADG
QLLPV/HYHAAEREYPAGACIRWLL	i						REIRGKQRAGHIFQLLSRCLLQI
RWLL							LNHCQRRAAHFRFQLSNQRHQ
25609 55977							QLLPV/HYHAAEREYPAGACLV
25610 55978		:					RWLL
25611 55979 A 25752 I 2786 MAAVIEQIRRAVLALVTGVV GDIPVVWDIVWNATAAFIAV SLLLDESGFFEWAALHVLRW YGPGRLPFNRIGLIRRITRRIRG LLFGLVTFILLLNRSQNPAQD LLAFRARTGKQTAQFIHHLPR VFTDKTGSSNGLAPQQCSAGELILNEKLAKQLVTAANWV MQSDEGEINPVDILRWPGVM AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPF LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H./RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAVGYFKVHVLG*RSVTPVTDIVKLEFTRLRLPGYTKSIE						I	
GDIPVVWDIVWNATAAFIAV SLLLDESGFFEWAALHVLRW YGPGRLPFNRIGLIRRITRRIRG LLFGLVTFILLLNRSQNPAQD LLAFRARTGKQTAQFIHHLPR VFTDKTGSSNGLAPQQCSAG GELILNEKLAKQLVTAANWV MQSDEGEINPVDILRWPGVM AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPE LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H /RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAVG YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE			 				
SLLLDESGFFEWAALHVLRW YGPGRLPFNRIGLIRRITRRIRG LLFGLVTFILLLNRSQNPAQD LLAFRARTGKQTAQFIHHLPR VFTDKTGSSNGLAPQGQCSAGELINEKLAKQLVTAANWV MQSDEGEINPVDILRWPGVM AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPE LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H /RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAVG YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE	25611	55979	Α	25752	1	2786	1
YGPGRLPFNRIGLIRRITRRIRG LLFGLVTFILLLNRSQNPAQD LLAFRARTGKQTAQFIHHLPR VFTDKTGSSNGLAPQGQCSAG GELILNEKLAKQLVTAANWV MQSDEGEINPVDILRWPGVM AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPE LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H //RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE]						
LLFGLVTFILLLNRSQNPAQD LLAFRARTGKQTAQFIHHLPR VFTDKTGSSNGLAPQGQCSAG GELILNEKLAKQLVTAANWV MQSDEGEINPVDILRWPGVM AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSF APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPF LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H /RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAVG YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE	1		1		1		
LLAFRARTGKQTAQFIHHLPR VFTDKTGSSNGLAPQGQCSAGELILNEKLAKQLVTAANWV MQSDEGEINPVDILRWPGVM AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPE LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H //RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV/G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE	1		1		1		· · · · · · · · · · · · · · · · · · ·
VFTDKTGSSNGLAPQGQCSAGELILNEKLAKQLVTAANWVMQSDEGEINPVDILRWPGVMAQEQDLDAIAAEILAALDGTIDFIVARETEGQSGLKRVYHSFAPDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRWVSSSPLETWNKRWAKISPAPFLLPISRLEKSEGDWLPETVISANMPSSLSLIISSL*FKVRDV*HVRI*TLRGHYRVINWPNFNIVVQGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\GVFKVHVLG*RSVTPVTDIVKLEFTRLRLPGYTKSIE							1
GELILNEKLAKQLVTAANWV MQSDEGEINPVDILRWPGVM AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPE LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H //RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							
MQSDEGEINPVDILRWPGVM AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPF LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H /RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							
AQEQDLDAIAAEILAALDGTI DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW VSSSPLETWNKRWAKISPAPE LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H //RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							·
DFIVARETEGQSGLKRVYHSE APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW. VSSSPLETWNKRWAKISPAPE LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H. /RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\GYFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							1 -
APDIREFTRDAIP 25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW. VSSSPLETWNKRWAKISPAPF LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H //RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							
25612 55980 A 25753 5 402 EIFSVVWIIMTRGDVVTISRW. VSSSPLETWNKRWAKISPAPF LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H. /RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							DFIVARETEGQSGLKRVYHSPG
VSSSPLETWNKRWAKISPAPF LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H /RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							
LLPISRLEKSEGDWLPETVISA NMPSSLSLIISSL*FKVRDV*H /RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE	25612	55980	Α	25753	5	402	EIFSVVWIIMTRGDVVTISRWR
NMPSSLSLIISSL*FKVRDV*H //RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE					1		VSSSPLETWNKRWAKISPAPFS
/RI*TLRGHYRVINWPNFNIVV QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							LLPISRLEKSEGDWLPETVISAF
QGIGKRLANSWLVFTLFHRI 25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE					İ		NMPSSLSLIISSL*FKVRDV*HFF
25613 55981 A 25754 48 219 PETCGHLWAYVWPSCAAV\G YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							/RI*TLRGHYRVINWPNFNIVVS
YFKVHVLG*RSVTPVTDIVKL EFTRLRLPGYTKSIE							
EFTRLRLPGYTKSIE	25613	55981	Α	25754	48	219	PETCGHLWAYVWPSCAAV\GL
							YFKVHVLG*RSVTPVTDIVKLL
	L						EFTRLRLPGYTKSIE
25614 55982 A 25755 1 912	25614	55982	Α	25755	1	912	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	<u>.</u>	
25615	55983	A	25756	1	1857	MRVCARACVRTRTRMCVYAH
23013	33703	ľ` .	23730	•	1037	TCVCVRTYAYVRVRVRVHVRA
		1				RVRVCAYARTRVRNSLSILPFIQ
		1				LTLATPIHHIHQEEFNIRGIVPVL
	ļ	1				RRVKPDLAIGIDITPSCDTPDLH
						DYSEVRINQGVGITCLNYHGRG
						TLAGLITPPRLIRMLEQTALEHN
						IPVQREVAPGVITETGYIQLFLP
						GWEIGFSPLALLLAFLCSTSPGF
						GDPDGLGVIAYQDTVRPNAAT
	<i>'</i>	İ				
						AISELNALAVKGVILTGDNPRA AAAIAGELGLEFKAGLLPEDKV
						KAVTELNQHAPLAMVGDGIND
						APAMKAAAIGIAMGSGTDVAL
		İ				ETADAALTHNHLRGLVQMIEL
						ARATHANIRQNITIALGLKGIFL VTTLDDRVVAGSAGRYGGDGA
						i
		İ				GDSECVKIVAQEIRQTDRNIER
						DRSPRPSGERVRVRGKGGIEAN
						QPLSTAFTNQITIRQSIRLFSNQF
						VFHKGISRVVAGSSAIISNVSPG
		1				CILRTPNCRRGFPISCTGEGKAA
						YGWQRDGGHAEYLLAEEKDLI
						LLPDALSYEDGAFISCGVGTAY
						EGILRGEVSGSDNVLVVGLGPV GMMAMMLAKGRGAKRIIGVD
						MLPERLAMAKQLGVMDHGY*I
			ŀ			LPDVY/V*IGVARVSWMNGRID
						SELRTRVRAYAHTRTRARTCTR
	İ					TRTRTYAYVRTHTHVCAYTHM
						RVRVRTHARAHTR
25616	55984	A	25757	3	1180	SKLGTRRSVVWA*SPSTSPTLW
23010	33904	^	23737]	1100	CSTFSAAGHSSMKRMNEFVDL
						LPAQQRMKGENWYRGTADAV
						TQNLDIIRRYKAEYVVILAGDHI
						YKQDYSRMLIDHVEKGARCTV
						ACMPVPIEEASAFGVMAVDEN
						DKIIEFVEKPANPPSMPNDPSKS
						LASMGIYVFDADYLYELLEEDD
	-					RDENSSHDFGKDLIPKITEAGLA
						YAHPFPLSCVQSDPDAEPYLAR
						CGYAGNFMESEPRSGLIRVSCM
						PAGPPLPLPAARSEAPKAAGTV
				1		ASVPSIAPARLRPVPDPVELVLV
				1		AAEFITPGDPTPRLHGSGFIDIR
						QIHHQTRSHLEGVKTGIRFLNH
						FSGNPQGGIAHVNGVARFQVK
						QCHQAWGQQYAARLRFQARGI
25617	55985	A	25758	16	543	SLQIAIHRVDIIHRFDVRQL
25618	55986	A	25759	1	3387	
23010	122300	<u> </u>	23133	<u>l' </u>	3301	<u></u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25619	55987	Α	25760	1688	2234	LSVGKTFPVLVPAAFRKVSATG
						AAVPGTPSILALPSYSTTPFGVC
						TSASMNVPVLTLRIRTRVTGEV
		1				AAIKPFSMANAPTPDSILPQLGV
		ŀ				VSTRCS*TITCANR*STSARGSL
						ERLIMATLL/WVAGTFD*SVWF
						GHDTDVVTLYRFHEALCYSVT
						LRTPHRRVLRFKSQHPGELACFI SPVA
25620	55988	Α	25761	905	4762	PPHNWMPSNATPGIAFVWCAY
						GAI/LPGDAPVPVVDDYRKVVR
		Ì				KDTKGLIARWKYFWMSVIALG
		ļ	Ī			VAFALYLAGKDTPATQLVVPFF
						KDVMPQLGLFYILLAYFVIVGT
	į					GNAVNLTDGLDGLAIMPTVFV
						AGGFALVAWATGNMNFASYL
						HIPYLRHAGELVIVCTAIVGAG
						LGFLWFNTYPAQVFMGDVGSL
						ALGGALGIIAVLLRQEFLLVIM
						GGVFVVETLSVILQVGSFKLRG
		<u> </u>				QRIFRMAPIHHHYELKGWP
25621	55989	Α	25762]1	1448	MCHVLLAGRQRRTAGPEHALT
						PPECGSAAIGPAVYKWAHATG
						VMIPDRPRSPHAGAEERHWHH
						PQPELISQRLGSFSSGPTKYIHEF
						QYLTLSYNLTWSDLNVILTFILP
		İ				LDEWERVFSLAQSHTDNCRLH
]				KPDLQEGIREVPQEDPQWNYQ
		İ				ENSPGIARRDYMISCLVEGLKK
		1				AAYKAINYDKLKETTQGTDKN
			ł			PAQSMACLAATMRHFAALDPE
		l				ALAPHRDVNHGIKLTCKTIRSSI
						DISREIRAPRECRSTEMASWHPP
						ADLTECPVESGYSVLSGRTDCQ YSHTVRRACLTTIDSRPAVRQL
	İ	l				LKIREVQLLSLLRGCVRSRRSGS
						~
						INAQYCRCLERVVTLPFFDSGPS LMNHAPHLYFAWQQLVEKSQL
						MLRLATEEQWDELIASEMAYV
						,
						NAVQEIAHLTEEVDPSTTMQEQ
						LRPMLRLILDNESKVKQVLQIR
						Q\DGLAKLVEQLRHLSKKHHLD
	J		<u></u>		L	TDSTSSSLPGVRTPYSPIRGGEE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25622	55990	A	25763	1029	1665	RPESISSVASKTRLGRSFHGAAR RTREYHSSTCNASIAAAATV\A AQGHPDTTSTPPASVDTTATNT QTPAVTAPAPAVDPQQNAVVS PSQANVDTAATPAPTAATTPDG AAPLPTDQAGVTTPVADPNAL VMNFTADCWLEVTDATGKKLF SGMQRKDGNLNLTGQAPYKLK IGAPAAVQIQYQGKPVDLSRFIR TNQVARLTLNAEQSPAQ
25623	55991	А	25764	658	1307	SNRLYTDVESINEIEGIYMKLRF ISSALAAALFAATGSYAAVVDG GTIHFEGELVNAACSVNTDSAD QVVTLGQYRTDIFNAVGNTSAL IPFTIQLNDCDPVVAANAAVAF SGQADAINDNLLAIASSTNTTT ATGVGIEILDNTSAILKPDGNSF STN\QNLIPGT\NVLHGLAFRAR CVSTANLRVPRPICFDPGSSYQA NTIGSGRCADCQPDA
25624	55992	Α	25765	167	232	
25625	55993	A	25766	441	686	
25626	55994	A	25767	206	331	
25627	55995	A	25768	674	900	VVPICTMLEEALERQNLTASLC G*LKKACGRSWQTSPIKRSLNG AKFSRTSIIMGFITAEKWSGWEI WSARNVTS
25628	55996	Α	25769	41	222	
25629	55997	A	25770	17	525	ESLECSGPSWNASGTQSGFYCH RIAPILPEKRLARMVEKTWGLG LRRRTGFRRQNLGGGTGTLVE CTSENS\KPSKSSFRKQRRGQRR EGH*SLRR*IRRERTERMQASR VTWNSFPQVPAAKKPSSLSESG *P*ATNYTREQDSMWNCVHHY WQPPTSVSRLVHLNSG
25630 25631	55998	A	25771 25772	698	2204	PYLRIRLTALISRSSTVMRILFAI SKRPIT*PKRPKPTTMTWGLSSL THGFSSSSSGPLNWRDSHLSTSF ISNGVVIMESVTVTSNNAIWSPS SSVAAVNTSRTPEAAIKRNTGR SK

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25632	56000	A	25773	3	891	RYRNQDDHELQIHTGTRFYVEL
						CGFRVNPPWLATDVTHAAMAL
		l				LTLVTTGLHIVGEWGKHATPPV
						PYSICSNPPRRAAYITVWRNRPC
		1				TLGDHLFSIAYPRGLRYDMGG
						GGEGTAWANVRQALARTTGR
İ		l		•		AQHWTKDNAKSSREARHPRQN
		i				KTKTHLGKPVLRWV/DPSFDQS
		l				KYDSIVWNPI/TYYPVPKPSTQV
						GQKV/LDKILNYTNTEMKEAIA
						H/DTSKEGLQFYEVVPVALVVA
						GTQMATGLRTMDTRLYFEGELI
						DAAPNKPVIKVVRQGEEPDWP
		ľ				SKGDAGDGEKVPSSLSESG
25633	56001	Α	25774	1	285	
25634	56002	Α	25775	1	302	SFSSFTQRTASVIISSTSTQSRLA
						TSPILAIARARTSRRCPEKPQLG
						YPDSAAHVFQQDRATKYVINR
						NSKKP*ICSACRSTVSTRQHRR
						WRGSLQPLSQ
25635	56003	Α	25776	307	473	
25636	56004	В	25777	67	809	
25637	56005	A	25778	44	301	
25638	56006	A	25779	1	1519	MINRLQHTVYTHKWNSYRTEP
		ŀ				DRRHTALRNSFCLVRLNDSSHS
		ł				RSLDSKQGHTEITFAATEHPPSP
		1				VSLRIHDVAFDDGRQTSRAPCF NLEQPGKLDCTKRLISDCWVM
						HPGESWHGFKDIPDNWSMLDPI
		ŀ				KISILAPGMGEDGELEETGVPA
						ALVTAWLGRHGIVPTRTTDFQI
						MFLFSMGVTRGKWGTLVNTLC
						SFKRHYDANTPLAQVMPELVE
						QYPDTYANMGIHDLGDTMFA
					}	WLKENYSGARLNEAYS/GLPSII
						ERHVVDAQGYRGGGMLCSCES
						NFCVSLLRIQAS
25639	56007	A	25780	461	789	HHVLSELQQLYTAYRSVDHIID
		-				HSLAIARAPQRRRCPEKPQLGY
						PDSLQHVFQQDRATKYVINGTS
						KKP*ICSACRSTVTHGHTDAGE
						EVWNPFAVLVPSGKDARVWG
25640	56008	В	25781	1	990	
25641	56009	A	25782	1	3066	
25642	56010	Α	25783	583	904	WGIRTTDFQIMFLFSMGVTRGK
						WGTLVNTLCSFKRHYDANTPL
						AQVMPELVEQYPGR*FTGVRK
						KSNN*FRQFGGVDTAGNNL\SEI
						FSASASAEIFPANSFCNRLA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	or peptide sequence	deterion,possible nucleotide insertion)
25643	56011	Α	25784	331	660	TGIQLPGAP*SQPWSTRRRAVV
						RPLYRVN*AVP*NR*VIRSKRA
						MPKRTDIKSILILGAGPIVIGQRL
						GWRDSDGVRLCGVLGSQENVC
	-					ELDEKGEERWSISGTSSEFTR
25644	56012	A	25785	1	798	MSDAEDGARTTLGSGNAVERL
		1				ADALSQQNVTVIKSTSLDDGFA
						ILSSNEAIDCLMFSYQMEHPDE
		İ				HQNVRQLIGKLHERQLNVPVFL
						LGDREKALAAMDRDLLELVD\
						EFAWI\LEDTADFIAG\RAVAAM
:						TRYRQQLLPPLFSALMKYSDI/Q
						SEYSWAAPGHQGGVGF\TKTPA
						GRFYHDYYRLLRVAWVLHKTE
		l				CRLINFPETPIFGNSFRYDIEVSN
ļ		ŀ				ESPDEEVKLRRHHLARCMKNF
					}	KTDIYFVSTFEPSTKSVDLLTVE
						TFAGT
25645	56013	A	25786	211	414	RVCECIQLRRIEIFRFMISSQPNL
						PEDLHPQIIAKPSQKRLIEQ*SSK
						LTVTKARRQGSRYKSSRFFS
25646	56014	Α	25787	1694	4974	LSLLSAK/PVYMVPSRNRYGIIG
		ŀ				PI/YPQEMQPETLQKKISE/SPLT
						KDKAGQKPSYCVV/TNCTYDG
						VCYNAKEAQD/LLEKTSDRLHF
						DEAWYG/YARFNPIYADHYAM
						RG/EPGDHNGPTASYIHVREGV
						GRLNFFRFNQAYMMH/ATTSPL
						YAICASNDVAV/SMMDGNSGLS
				-		LTQEDCWVMHPGESW/HGFKD
		l	[IPDNWSMLDPIK/VSILAPGMGE
						DGELEE/TGVPAALYSNLCLSSG
						TTGLSTEALLE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25647	56015	A	25788	11	1709	MSKPKYPFEKRLEVVNHYFTT
25011				ľ		DDGYRIISARFGVPRTQVRTWV
						ALYEKHGEKGLIPKPKGVSADP
				1		ELRIKVVKAVIEQHMSLNQAA
						AHFMLAGSGSVARWLKVYEER
						GEAGLRALKIGTKRNIAISVDPE
						KAASALELSKDRRIEDLERQVR
						FLETRLMYLKKLKALAHPTKK
1	l					LSASLTSMRTLKSVFSEIYHENR
						GRYGYRRVTLSLHREGKQINH
		1				KAVQRLMGTLSLKAAIKVKRY
						RSYRGEVGQTAPNVLQRDFKA
						TRPNEKWYTDVTEFAVNGRKL
		1				YLSPVIDLFNNEVISYSLSERPV
		1				MNMVENMLDQAFKKLNPHEH
						PVLHSDQGWQYRMRRYQNILK
		1				EHGIKQSMSRKGNCLDNAVVE
		ł				CFFGTLKSECFYLDEFSNISELK
		[DAVTEYIEYYNSRRISLKLKGL
						TPIEYRNQTYMPRVNCPLFDTL
		ŀ				RIPDIGGVVRARAIAKLLNDTD
						MAIIDKRRPRANVSQVMHIIGD
	1					VAGRDCVLVDDMIDTGGTLCK
						AAEALKERGAKRVFAYATHPIF
						SGNAANNLRNSVIDEVV/DLRY
						HSAER*NQITAERAYSDPVRKI
25648	56016	A	25789	2902	3271	SSAARHCAGCGDVRSVCRSGR
						ADAPRMHPGESWHGFKDIPDN
						WSMLDPIKISILAPGMGEDGE/P
						TRTTDFQIMFLFSMGVTRGKW
						GTLVNTLCSFKRHYDANTPLA
						QVMPELVEQYPAFVINQ
25649	56017	Α	25790	185	663	SPVPSSRPSTRHRLPDGSSSSQFS
						SAIAARKVVNSCILCSKICQN*F
		İ				NRRAASPLKRLP*SGASGMIT\P
						NQPAPAQ/PAK*LYTRLDEVKP*
						*KITHGNGVSFCPTG*A*RTGIS
						ASSRDLEVQSKKRSFPALNWPA
						VYCCSALGSAPKCKPIPFLRAT
		L_				V

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25650	56018	Α	25791	684	4208	NGLFWLFQPWLFADETRRRLE
25050	30010	1			1200	ERFRDRYQIIHHSSQVCHSDQA
		1				VYVLTQERVNERDDIVDIDLFV
		1				IDEFYKLAFRQLKSGDIDHQDE
						RVIELNIALSKLLKVSRQFYLTG
						PFVNSIRGLEKLGYPHTFVSTDF
						NTVALDVKTSASKRMTTKPSS
						KRWGKSRTCVDADHIKNGIGL
]						HFGALPRALQQYTADQFNAGK
						LRFLLCTSTHEGVNTIAKNVVIY
						DNRAGSTRTISADIINSVICGLN
						TLKSFDTRWALL
25651	56019	Α	25792	1	896	
25652	56020	Α	25793	231	721	IITAEKGRSREQQLAIL\PLNLAD
						MRQLQQQHSQTRLADTAADGL
1						RHFTAQQRLMPLQLQAIFVTGQ
1						RQLMLQRVGY/R/LHGSPWRKA
ŀ		İ				QTHLPVPGSTPEYRRSDPHGPA
		ł				LTGCSSHHNPVRARRGMTIAQL
						AANPDKEYRARSFAIARSRPLA
						SRSGYETVTPGC
25653	56021	Α	25794	1	933	MLEAAVCLCVFVSCSLAEGRA
						CCRVAVSIPVSVRARIHLLESDH
						LGRFREPKSIPRKDAQMDTFRT
						MVREPATFLDQVDGLQQSDDIL
						RLLPPELATLGITELEYEFYRRL
						VEKQLLTYRLHGESWREKVIER
		1				PVVHKDYDEQPRGPFIVCVDTS
						GSMGGFNEQCAKAFCLALMLI
						AIANKWRCY\IMLSS\TEIVRYE
						LSGPQGIEQAIRFLSQQFRGGTD
						LASCFRAIMERLQSREWFDADA
						VVISDFIAQRLPDDVTSKVKEL
						QRVHQHRFHAVAMSAHGKPGI
0.5.5.1	56022		05705	102	1100	MRIFDHIWRFDTGMRSRLLRR
25654	56022	C	25795	83	1108	
25655	56023	Α	25796	1	747	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25656	56024	Α	25797	25	1741	IMERLKRMSVFAKVVEFGSFTA
						AARQLQMSVSSISQTVSKLEDE
1						LQVKLLNRSTRSIGLTEAGRIYY
						QGCRRMLHEVQDV\HEHLYAL
						NNTPIGTLRIGCSSTMAQNVLA
						GLTAKMLKEYPGLSVNLVTGIP
						APDLIADGLDVVIRVGALQDSS
						LFSRRLGAMPMVVCAAKSYLT
						QYGIPEKPADLSSHSWLEYSVR
						TDNEFEL\IAPEGISTRLIPQGRF
						VTNDPMTLVRWLTAGAGIAYV
						PLMWVINEINRGELEILLPRYQS
						DPRPVYALYTEKDKLPLKVQV
						VINSLTDYFVETPTPLSSLTSLPT
						IEICCMVSIPGTNQRLRPFTGFA
						THRLQSDLLLQVMTISRGRFSR
						SARFNGPTPSGRRLIRVIISTESG
		1				SRSSNPRTTGCFEEHCDHYRAII
		ł				DSADGLPMVVYNIPALSGVKLT
						LDQINTLVTLPGVGALKQTSGD
						LYQMEQIRREHPDLVLYNGYD
						EIFASGLLAGADGGIGSTYNIM
						GWRYQGIVKALKEGDIQTAQK
	1					LQTECNKVIDLLIKTGVFRGLK
						TVLHYMDVVSVPLCRKPFGPV
						DEKYLPELKALAQQLMQERG
25657	56025	Α	25798	1	1005	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	}	
25658	56026	Α	25799	1	2392	MEMVAASKMRKSQDRMAASR
						PYAETMRKVIGHLAHGNLEYK
						HPYLEDRDVKRVGYLVVSTDR
						GLCGGLNINLFKKLLAEMKTW
						TDKGVQCDLAMIGSKGVSFFNS
						VGGNVVAQVTGMGDNPSLSEL
						IGPVKVMLQAYDEGRLDKLYI
						VSNKFINTMSQVPTISQLLPLPA
						SDDDDLKHKSWDYLYEPDPKA
						LLEQCSCMLRSPAWGITSTDTT
						RARTDLACPIWLLLDPYPKLMG
		ŀ				NAPKALASVDKRGVPVNTILVS
						ALVTALCVLINYLAPESAFGLL
						MALVVSALVINWAMISLAHMK
						FRRAKQEQGVVTRFPALLYPLG
						NWICLLFMAAVLVIMLMTPGM
						AISVYLIPPLQTNTFNSTTIAMA
						DYQMESLSAEINFAAAKLARA
						CADEWTARTPEKPRYVAGVLG
						PTNRTASISPDVNDPAFRNITFD
						GLVAAYRESTKALVEGGADLIL
		1				IETVFDTLNAKAAVFAVKTEFE
						ALGVELPIMISGTITDASGRTLS
		1				GQTTEAFYNSLRHAEALTFGLN
		1				CALGPDELRQYVQELSRIAECY
5						VTAHPNAGLPNAFGEYDLDAD
						TMAKQIREWAQAGFLNIVRGC
						CGTTPQHIAEMSPGRKRLTRAE
		1				SSSVPSTLPGKAWLEHALPLIAE
						QL/QGRRSAVFIPF\AGVTQTWD
						DYTAKTAAVLAPLGVSVTGIHS
						VVDPVAAIENAEIVIVGGGNTF
25659	56027	Α	25800	412	1115	LAGEVMDLLLLSNSTLPGKAW
						LEHALPLIAEQLQGRRSAVFIPF
						AGVTQTWDDYTAKTVAVLAPL
						GISVTGIHSVVDPVAAIENAEIVI
						VGGGNTFQLLKQCRERGLLAPI
						TDVVKRGALYIGWSAGANLAC
						PTIRTTNDMPIVDPQGFDALNLF
						PLQINPHFTNALPEGHKGDPRL
						FR\IRELLVVAPELTIIGLPEGNW
						ITVSKGHATLGGPNTTYVFKAG
		1		<u> </u>		EEAVPLEAGHRF
25660	56028	Α	25801	1	360	MDHAIAGIAVQFRGGNLLRFK
						AFQQRVKYRMCQAERAINRLF
						NIAVKRLTGNRLDDKSKQHIIDI
						AVDIPKWSDHLHIIRRKHHDPT
1						QDSGTHLPAVADDGFRTSVRN
						RSA*HIRYLTRC*KALNRNKLPP
}						RN*TAIPAMA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	• · · · · · · · · · · · · · · · · · · ·
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
25661	56029	A	25802	1032	1233	LVQFLRICFHILQRF/LPSH*RQK
						DESLRALPVSFLCWRTDSDFPA
		ļ				DISYQNYR*YNREPYLPRPDSG
25662	56030	Α	25803	1	1394	MTRDGLANKALAVARTLADSP
						EIRQGLQKKPQESGIQAIAEAVR
						KRNDLLFIVVTDMQSLRYSHPE
						AQRIGQPFKGDDILKALNGEEN
						VAINRGFLAQALRVFTPIYDEN
						HKQIGVINDSRWSIIWSVLFGM
						LVGLIGTCILVKVLKKILFGLEP
						YEISTLFEQRQAMLQSIKEGVV
	İ					AVDDRGEVTLINDAAQELLNY
						RKSQDDEKLSTLSHSWSQVVD
	İ					VSEVLRDGTPRRDEEITIKDRLL
						LINTVPVRSNGVIIGAISTFRDKT
						EVRKLMQRLDGLVNYADALRE
						RSRLEHILHNQRVPFIMKLHHR
						MLRHFIAASVIVLTSSFLIFELV
						ASDRAMSAYLRYIVQKADSSFL
		l				YDKYQNQSIAAHVMRALAAEQ
					:	SEVSPEQRRAICEAFESANNTH
						GLNLTAHK\SRAYAAHYKPHPL
		ļ				TATQLWK\RSTITRF*SGSGRQP
						PPG*LRFRSWDGRREISLLSRSL
25663	56031	A	25804	3	219	
25664	56032	Α	25805	14	265	
25665	56033	A	25806	744	1566	FASWLRVFSITNCAAPVTSESC
						ALDLGSAEAKAWIGVENPHRA
						DVLTELRRSTVARVCTGRAGPR
						PRTQALLRFLADHSRSKDTVLK
						EVPEEWVKAQGLLEVRSEISDK
						NLYLTRPDMGRRLCAEAVEAL
		ŀ				KAQCVANPDVQVVISDGLSTD
		İ				AITVNYEEILPPLMAGLKQAGL
						KVGTPFFVRYGRVKIEDQIGEIL
•						GAKVVILLVGERPGLGQSESLS
	1	l				CYAVYSPRMATTVEADRTCIY
]				NIHQGGTPPVEAAAVIVDLAKR
						MLEQKAF\GINMTR
25666	56034	A	25807	596	745	
25667	56035	Α	25808	151	660	STTERLGDDFVRAANIILHCEG
		1				KVVVSGIGKSGHIGKKIAATLA
ŀ		1				STGTPAFFVHPAEALHGDLGMI
		1				ESRDVMLFISYSGGAKELDLIIP
						RLEDKSIALAPNSRTVIT*CWFS
						AGDGGLPGPDYGQDFAAHPAG
						AGALYKCRDLINDNILRTVSCQ
						SHDDGDIRGMAFARQ
25668	56036	Α	25809	314	583	
25669	56037	Α	25810	i	2982	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
<u> </u>				sequence		
25670	56038	Α	25811	120	790	EGLKTKGEKASPPSCLSFCKNE
		1				FVISSTDYALSQSQSGGVMHRQ
		l				SFFLVPLICLSSALWAAPATVN
		l				VEVLQDKLDHPWALAFLPDNH
1		1				GMLITLRGGELRHWQAGKGLS
						APLSGVPDVWAHGQGGLLDVV
						*APDFAQSRRIWLSYSEVGDDG
		l				KAGTAVGYGRLSDDLSKVTDF
						RAVFRQMPKLSTGNHFGGRLV
						FDGKGYLFIALGENNQRPTAQD
						HRVPSWYK
25671	56039	Α	25812	707	1141	ASHTATSPRPVRLSSSIASITLAV
						NATCGMASSRRIR*CTLFSKRA
		1				PSAPAGWERAKSSSLNPRACMT
						AIASASPIIRVLTVLEVGAKCIG
						QGSRSDSTELSPFIKMVPPNSLT
ļ		l				TALAVIPPFSLSDTLPEVLISLSLI
						YNTLF
25672	56040	Α	25813	215	2160	EINSITSRLSIIPRSPCSASAGWT
						KKAGVPVLASVAAIFLPMWPD
		l				LPIPETTTLPSQCKMILAARTKS
						SPR/RSNIMTHIRIEKGTGGWGG
						PLELKATPGKKIVYITAGTRPAI
						VDKLAQLTGWQAIDGFKEGEP
					1	AEAEIGVAVIDCGGTLRCGIYP
					<u> </u>	KRRIPTINIHSTGKSGPLAQYIVE
						DIYVSGGKEENITVVGDATPQP
				·	İ	SFVGPDYDTSEKLMIVRKKPIG
						VQMLYQVGTVSMLLYTRTIIQT
						KMTPRTIVTISHSVRNAGDSFFS
						IASNQPMPPTAKKIEPLAISLLS
						AEAPTRLSELKARIGEPRWSIEA
						IKPMPISTHKPNMQAITPPARRA
}						ILSPCACESRSRQEPCPPGCHCS
						CPNHSCRSRLKGVLSMEQYLL
						QQKHVGTPPGPFRPPDTNQPCW KTKPSQREEYTRRVGFTGHSNQ
						GAKIIRTHIICRRRTSFALERPGD
						GFQAVVGGTVLMGLPRTKNVG
						LPVTILGRVHRRSSERFPRTSES
						AINRKDAGPKDPVRQRLAYKK
						HPMERRHGPHVVARTFGRAIPT
						LGPHRTVLSTRFQVAKNPLGPI
						GPSPLAVLTWTVPRPKNGRRG
						GKQRARIICQSRREASCNNVCL ARSSGVFKGFSPVSSSGEHTGN
L	<u> </u>	<u> </u>	l			KYSAYSFSLCPLFVFLPLSGRLL

	SEQ ID NO: of peptide sequence		in USSN	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25673	56041	A	25814	11	613	RLSSVFVSKSLASWRSCNCSFS GPLVRLTIRP\LSPPDVRLLLSPS VVHAYNCPHQETQRHHTHHLT P/RLPNHGQIAISAMVYSSPATN/ SMLRQLLIQHVEQIGSVPLVMD AISLVEAHD/RSAAG*SRPLY*R AN*SSRY*VSYARKRVRQAKSR /HGKPSKKVLAKRAVPNRVCRC CNRVKRRCICQPKRRKCMTLPV RATR
25674	56042	В	25815	1	1920	
25675	56043		25816	247	1182	EAVMRQTKTGILLANLGTPDAP TPEAVKRYLKQFLSDRRVVDTS RLLWWPLLRGVILPLRSPRVAK LYASVWMEG\GSPLMVYSRQQ QQALAQRLPEMPVALGMSYGS PSLESAVDELLAEHVDHIVVLP LYPQFSCSTVGAVWDELARILA RKRSIPGISFIRDYADNHDYINA LANSVRASFAKHGEPDLLLLSY HGIPQRYADEGDSLRELYAVA NPNPGPGMGVLLAYMFFGRGS AKQSAGGSGLDGLLRRTPPITP GGYFSVFVWKSLGSWRSCNCS FSGPLVGLTIRPRFTAGRSPTSF AQRCTCL
25676	56044	В	25817	1	651	
25677	56045	A	25818	1	1647	
25678	56046	Α	25819	1	1506	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
<u> </u>	sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25679	56047	Α	25820	645	2161	LDRCALNVTAQPSIECQVANAC
						LSPKGEFEYLQIDAPTPQALLSE
						IEKCWHRHRNVWPDHTINLAL
	:					AIHGQVDPVTGVSQTMPQAPW
						TTPVEVKYLLEEKLGIRVMVDN
						DCQLHYCKTAILNWSRKMALS
						ROKFTFERLRRFTLPEGKKOTF
						LWDADVTTLACRATSGAKAFV
ŀ						FQSVYAGKTLRMTIGNINDWKI
	,					DDARAEARRLQTLIDTGIDPRIA
		1				KAVKIAEAESLQAESRKTKVTF
						SVAWEDYLQELRTGISAKTKRP
		1				YSTRYIADHINLSSRGGESPGLG
		l				LLLAFTLFGKGMSKRSAPGAMI
						IHFLGGIHELYFPYVLMKPLTII
						AMIAGGMSGTWMFNLLDGGL
		1				VAGPSPGSIFAYLALTPKGSFLA
						TIAGVTVGTLVSFAITSLILKME
						KTVETESEDEFAQSANAVKAM
		ł				KQEGAFSLSRVKRIAFVCDAG
		ļ				MGSSAMGATT\FRKRLEKAGL
		ł				AIEVKHYAIENVPADADIVVTH
		l				ASLEGRVKRVTDKPLYGPAVV
25680	56048	Α	25821	2	341	
25681	56049	Α	25822	218	469	LICAQGRRSPSRESTRQPKVLTL
						ACHNGSVSVVVLSPNSLYIEVV
						VPS*CNAATGPVVTCLYKGKFQ
				:		PILILLVTSTRVSSCI
25682	56050	A	25823	1	3966	
25683	56051	A	25824	2	728	
25684	56052	Α	25825	528	1123	DAEEGPDHRYLSSAHGGGSAS
		1	İ			QPPSCAVTACRWPWRGRGCRA
						GVWNQPTAAQGRSWPVGKTSC
						*GQGSTCKSQTWGFRGQRLPQ
		l				DAPAPPASLCASFHLVEAGASA
]	l				DSGDTRRMTIR/FASKTVARAK
						RIIRVLRFSPLWVATRSLASTAI
						KIACCASEPGSFLQLWKPRSMA
						PVHRCTWHEACPEGQRQMSCV
						SSTGL
25685	56053	Α	25826	1	492	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25686	56054	Α	25827	1740	3858	ADAAGTEKTATVSRYHFYLRY
						PRSGRSVIDVRSWWRFSIMDAL
						SRSIPRAISICARGKPVVTAKFK
						QGTMPEPSNKAIILPIRFFPGVV
						LMIIKKSGGRWQLSLLASVVIS
1						AFFLNTAYAWQQEYIVDTQPG
						LSTERYTWDSDHQPDYNDILSQ
						RIQSSQRALGLEVNLAEETPVD
:						VTSSMSMGWNFPLYEQVTTGP
			:			VAALHYDGTTTSMYNEFGDST
						TTLTDPLWHASVSTLGWRVDS
						RLGDLRPWAQISYNQQFGENI
						WKAQSGLSRMTATNQNGNWL
						DVTVGADMLLNQNIAAYAALT
						QAENTTNNSDYLYTMGRTRWL
			<u> </u>			TLIGTIITQFALGSVYTWSLFNG
	}					ALSAKLDAPVSQVAFSFGLLSL
						GLAISSSVAGKLQERFGVKRVT
						MASGILLGLGFFLTAHSDNLM
						MLWLSAGVLVGLADGAGYLL
						TLSNCVKWFPERKGLISAFAIGS
				,		YGLGSLGFKF\IDTQLLETVGLE
						KTFVIWGAIALLMIVFGATLMK
						DAPKQEVKTSNGVVEKDYTLA
						ESMRKPQYWMLAVMFLTACM
			:			SGLYVIGVAKDIAQSLAHLDVV
				,		SAANAVTVISIANLSGRLVLGIL
						SDKIARIRVITIGQVISLVGMAA
						LLFAPLNAVTFFAAIACVAFNF
						GGTITVFPSL\ICGSIIASLFGGFY
						VTFYVIFALLILSLALSTTIRQPE
						QKMLHFTYLTTSALFPAGPKRN
25687	56055	A	25828	2	356	
25688	56056	Α	25829	1	1307	MYETLEEVLRSSGDPADQKYV
						ELKARAEKALDDVKKRKLYC
						WRRRQICALRRISRSPYPGHQL
		ĺ				ECIASFDRNFEAMQKEMYGQF
						ENTFMMYLPRLCEHCLNPSCV
						ATCPSGAIYKREEDGIVLIDQDK
						CRGWRLCISGCPYKKIYFNWKS
						GKSEKCIFCYPRIESGQPTVCSE
		Ι,				TCVGRIRYLGVLLYELTAQQFF
						PVWPPDHFVHPF*TLYVLPAPP
						SR*CDRVQLMASLQSVARASRE
						YRWYGFSR*TPRKALALAQLRP
<u></u>						AESSPTAPDCN
		•	•			·_ ·· · · · · · · · · · · · · · · · · ·

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25689	56057	I A	25830	583	1369	RHQLNSIASPAGGRWKDIGWF
23007	30037	``	25050	363	1307	NFPQSNLCLKREKQDESCSLTQ
						ALPSELKVSADNVSLTGAVSLA
		l				SMLTEIFLLQQAQGMPEPGWG
						RITDSHQWNTLLSLHNAQFYLL
						QRTPEVARSRATPLLDLIKTALT
						PHPPQKQAYGGT\LPLPVRFMA
						GPDTNLANLGGALKFNWTLPG
						QPDNTPPGGELVFERWRRLSDN
						SQWIQVSLVFQTLQQMRDKTP
						LSLNTPPGEVKLTLAGCEERNA
						QGMCSLAGFTQIVNEARIPACS
25690	56058	ļ	25831	199	543	QUMCSLAGFIQIVNEARIFACS
25691	56059	A A	25832	1	642	EASIFRRLSVYDNLMAVLQIRD
23091	30039	^	23032	'	042	DLSAEQREDRANELMEEFHIEH
		1				LRDSMGQ*SARPGRCRAGAQ*
						CV*CR*PRSGQPRQTVRRAE*IS
-		l	1			DSQPVRGQFLHG/VRSPPESDCP
			1			MLSRRCSM*NSSISSFARSSRCS
						ADKSSRICSTAIRLS
25692	56060	A	25833	3	329	ADROGICOTAIRES
25693	56061	A	25834	1974	2195	
25694	56062	A	25835	1	615	
25695	56063	A	25836	2	166	,
25696	56064	Α	25837	2	189	STPGNWRFTTTYPLNCATRWK
						M*FLIVATMAPSVYWSLPRNIA
						AAKPTTPPTPSRRSGARGK
25697	56065	Α	25838	64	354	
25698	56066	Α	25839	1123	1845	
25699	56067	A	25840	1120	2097	
25700	56068	Α	25841	124	548	CRQMVGTRRGGEQGKEVIDGŸ
						GKPATFYQMQDNGKPVEGHAS
ļ						QMHYELAKDFVVLTGNAYLQ
1						QVDSNIKGDKITYLVKEQKMQ
						AFSDKGKRVTTVLVPSQLAKA
1						YKG\VAW*KTSA*PSTPGKLSV
		ļ				CWGQTVPVRPPLSTWL
25701	56069	Α	25842	77	514	PRA 4 CL PORVIDA CL 4 POVONA
25702	56070	Α	25843	2487	5738	RRAAGLPGRNDAGLARSHQWA
						GSADTGSEKQHELQLRIQGEPV
						SGQLNLAGSFDRKEERWKG\TL
						SNTRFQTPVGPWSLTRDIALDY
	· .					RNKEQKISIGPHCWLNPNAELC
					:	VPQTIDAGAEGRAVVNLNRFD
			1			LAMLKPFMPETTQASGIFTGKA
			[DVAWDTTKEGLPQGSITLSGRN
						VQVTQTVN\DAALPVAFQTLNL
1						TAELRNNRAELGWTIRLTNNG
						QFDGQVQVTDPQGRRNLGGNV
25700	56051	 	25011	529	222	NIRNFNLAMINPIFTRG
25703	56071	A	25844	538	777	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25704	56072	A	25845	sequence 489	2797	TRRRRTMIALIQRVTRASVTV EGEVTGEIGAGLLVLLGVEKDD DEQKANRLCERVLGYRIFSDAE GKMNLNVHQAAGSVLVVSQFT LAADTERGMRPSFSKGMSQLP GLSRETRESIAMYHLRVPQTEE ELERYYQFRWEMLRKPLHQPK GSERDAWDAMAHHQMVVDEQ GNLVAVGRLYINADNEASIRFM AVHPDVQDKGLGTLMAMTLES VAPYFSGSETGMMTLNRYRLR HMAKQGNRSAKRVEKLLRKPD RLISLVLIGNNLVNILASALGTI VGMRLYGDAGVAIATGVLTFV VLVFAEVLPKTIAALYPEKVAY PSSFLLAPLQILMMPLVWLLNA ITRMLMRMMGIKTDIVDMLLS VLDLEKM/TVDDIMLPRSEIIGI DINDDWKSIL/R/QLSHSPHGAIV LYRDSLDDAISMLRVREAWRL MSEKKEFTKETMLRAADEIYFV PEGTPLSTQLVKFQRNKKKVGL VVNEYGDIQGLVTVEDILEEIV GDFTTSMSPTLAEEVTPQNDGS VIIDGTANVREINKAFNWHLPE DDARTVNGVILEALEEIPVAGT RVRIGEYDIDILDKLSFCFRYSN
						HRRTNRTTIQRITFLHNAQYVT WRNVIRFHHCDGLMHIRVQWD VSFGDHFNAKLTHNIQHRLQRQ LNAFNHRRHIRVSFISHFQRTIQ AINHRQQFVDEFLQREFVGFFNI
25705	56073	A	25846	87	199	QPASVQTAGAGCRL*LHQRQW RECLVLDSKRRGDGVL

	GKSMDKELPWLADNAQ\LELK YKKGKTPLSHRRWPGEPVSVIT
sequence	GKSMDKELPWLADNAQ\LELK YKKGKTPLSHRRWPGEPVSVIT
	YKKGKTPLSHRRWPGEPVSVIT
25706 56074 A 25847 1167 3306	YKKGKTPLSHRRWPGEPVSVIT
23700 30074 A 23847 1107 3300	YKKGKTPLSHRRWPGEPVSVIT
	GSLIQTLGDELLQKAEKKKNIV
	WRYENFSLEWQSAITQAINLIG
	EHKPSIPARTMAALACIAQNDS
	QQLLDEIVQQEGLEYATEVVIA
	RQFIARCYESDPLVVTLQYQDE
	DYGYGYRSETYNEFDLRLRKH
	LSLAEESCWQRCADKLIAALPG
	INKVRRPFIALILPEKPEIANELA
	VPALREFLAATKMPATCTLKGL
	GAVEADYPYYLGMLGMHGTK
	AANFAVQECDLLIAVGARFDD
	RVTGKLNTFAPHASVIHMDIDP
	AEMNKLRQAHLRDEHSWRYD
	HPGDAIYAPLLLKQLSDRKPAD
	CVVTTDVGQHQMWAAQHIAH
	TRPENFITSSGLGTMGFGLPAA
	VGAQVARPNDTVVCISGDGSF
	MMNVQELGTVKRKQLPLKIVL
	LDNQRLGMVRQWQQLFFQER
	YSETTLTDNPDFLMLASAFGIH
	GQHITRKDQVEAALDTMLNSD
	GPYLLHVSIDELENVWPLVPPG
	ASNYKKHHKLKQTFGVKIIPDV
	HDPSQAQPVADVVNVIQLPAFL
	ARQTDLVETHGENRPGQMGNI
	VDKFKEGGNEKVILCDRGANF
	GYDNLVVDMLGFSIMKKVSGN
	SPVIFDVTHALQCRDPFGAASG
	GRRAQVAELARAGMAVGLAG
	LFIEAHPDPEHAKCDGPSALPL
25707 56075 A 25848 1	MATRASVTPMSLFSAGTCLLST
25707 50075 11 25040 1	SCVLSPVGDTAEESCWQRCAD
	KLIAALPGINKVRRPFIALILPEK
	PEIANELVGLECPRTHFHSKEW
	LKVVANDPTAVRKLEHYWSQD
	IFSDREASYMSHENHFGYAACA
	ALLREQGLAAIPRLAMYAHKE DCGSLLVQINHPQVIRTLLLVA
	DKNKPSLQRVAKYHKNFPHAT
	•
	LAALAELLALTEPPA/RPWLSN
05700 56076 4 05040 500	HRRQKAACTAKSTR
25708 56076 A 25849 823 1091	CVRFARINCSDRRSRCFAGFNH
	VLNKALGVHINHFG/YSACAP*
	CRYPPHAAGEFYPDPCRHKGTT
	GYRHRQGYPPPGEPPPRASWLD
	LR
25709 56077 A 25850 714 875	EFSSARISRTSRLKYTNGCCRL
	WSAFCRLRTATTVPPARP*QLR
	PDRSRAQCQ

	equence		09/540,217	4		
25710 5				codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
	6078	Α	25851	2730	2893	WPVGERLAPGDYPVI*TGQLCT
. 1						AAGD/EWRR*KVRRHQPLWRG
						FPNRRYMAWRSA
25711 5	6079	Α	25852	750	929	SFHPAGRRYLYRHSSRSGNITN
						GCCRLWSAFCRLRTATTVPPAR
						P*QLRPDRSRAQCPV
25712 5	6080	A	25853	2	2427	CRQHHRWHSGSTAVYRRVLITS
						KCWNVFIRTKTWTVSILTTSVV
						CASARRVCVPAPRAVSSRCLSV
						TTLIPSASTPW*LAHRISLAAR*
:						AFWFNCRIPAGIDNVKVLERIH
						PDKDVDGFHPYNVGRLCQRAP
						RLRPCTPRGIVTLLERYNIDTFG
						LNAVVIGASNIVGRPMSMELLL
				1		AGCTTTVTHRFTKNLRHHVEN
						ADLLIVAVGKPGFIPGDWIKEG
						AIVIDVGINRLENGKVVGDVVF
						EDAAKRASYITPVPGGVGPMT
						VATLIETRYRQGKMFDGSSIGG
			:			WKGINESDMVLMPDASTAVID
						PFFADSTLIIRCDILEPGTLQGYD RDPRSIAKRAEDYLRSTGIADT
			ļ ,			
						VLFGPEPEFFLFDDIRFGSSISGS
						HVAIDDIEGAWNSSTQYEGGN KGHRPAVKGGYFPVPPVDSAQ
			1			DIRSEMCLVMEQMGLVVEAHH
						HEVATAGQNEVATRFNTMTKK
						ADEIQIYKYVVHNVAHRFGKT
						ATFMPKPMFGDNGSGSPPSQPQ
						SQPTPPEILLQALLSAGCFYAVY
						YVTYKTRLRKRVADVPRRPLFT
						MNRVETNLTWVILMGIALVSV
						GIFFMHNGFLLFRLNSYSQIFSS
1 1						EVSGVALKRFFYFFIPAMLVVY
						FLRQDSKAWLFFLVSTVAFGLL
						TYMIVGGTRANIIIAFAIFLFIGII
						RGWISLWMLAAAGVLGIVGMF
						WLALKRYGMNVSGDEAFYTFL
25713 5	6081	A	25854	502	885	
	56082	A	25855	233	738	SNSCKRTKIISDVTSVFHAIFPAI
		l.,		1		KITAPNSPRLRVNDSATPLTSAG
		1				ESSGSTTLQKLCQRVAPSVSAA
						SSYSGPNLFQHRLHGTHPKRNA
						GKGHSHRNPQPCIGDFDIKLRQ
						PFTVKTLYVKEKGQR*GGDRV
						LPAQRVNPSAHQAACGLGSDS
						GLGSTPSADRKRR

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25715	56083	A	25856	1	2363	MRRQDTGRRGRKRRDAGRWQ
						WRYWGKGSFTPMNATWDVAG
		-			:	KGEWHDSTITLTDLSTGFDQLQ
						YGTMTVEKPRLILDKPIVWVRD
						AQHPSFSGALSLDAGQTLFTGG
						SVLPPSTLKFSVDGRDPTYFLFK
						GDLHAGEIGPVRVNGRWDGIR
						LRGNAWWPKQSLTVFQPLVPP
						DWKMNLRDGELYAQVAFSAA
						PEQGFRAGGHGVLKGGSAWM
						PDNQVNGVDFVLPFRFADGAW
						HLGTRGPVTLRIAKQRKEMRN
						NNLRQFKLLGPDVGFDSINDRP
						MAEELSKLLSKQNEENLLPKTI
						LYCLNPRDNEVLGTMIENGASF
						AANPLYFDPKNIVELAIEAGCN
						CVASTYGVLASVSRRYAHRIPF
İ			<u> </u>			LVKLNHNETLSYPNTYDQTLY
						ASVEQAFNMGAVAVGATIYFG
						SEESRRQIEEISAAFERAHELGM
				1		DGGWIGLMIKPLGRWSLIMEID
						EGFAVGMSPAELSAEQLLSKL
						WLWEGKAERYGWGRKSMDKE
						LPRLADNAQLELKYKKGKTPLS
						HRRWPGEPVSVITGSLIQTLGD
						ELLQKAEKKKNIVWRYENFSLE
					}	WQSAITQAINLIGEHKPSIPART
						MAALACIAQNDSQQLLDEIVQ
						QEGLEYATEVVIARQFIARCYE
						SDPLVVTLQYQDEDYGYGYRS
		l				ETYNEFDLRLRKHLSLAEESCW
		ŀ				QRCADKLIAALPGINKVRRPFIA
25716	56084	Α	25857	1	4440	MNRFDGAKQNVVGADAHHLA
		ŀ				DTAVKRNQSLFQLRASGHPRLP
						AGGGKAVFHGRFAAKKIEAVA
						FYFRHLIALLVVQMHFKLVKG
						NVDVVFTAQLIDSTVQLIDSTTT
						VTQFTHIQTQLMRSVEWLTDN
						GSCYRANETRQFARMLGLEPK
						NTAVRSPESNGIAESFVKTIKRD
						YISIMPKPDGLTAAKNLAEAFE
1						HYNEWHPHKAGTLTNEQWQQ
						VTAELHDRMMETVFFALDDAE
						QLFAHHQPTPVTSVDLLGQG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
] 				sequence		
25717	56085	A	25858	1	3705	MEEYGGVDVRLYRIPDPMAFL
						RQQKNLHRIVVQPQYLGDGLN
						NTLTWLWDNWYGKSRRVMQR
						TFSSQSRQNVTQALPELQLGNA
						IIKPSRYVQNNQFSPLKKYPLVK
						QFRYPLWQAKPFEPQQGSRGL
						YLVEAMVGGYRATTGGVVSDT
						VALSKVSSKELLVWTAGKKQV
				•		NEPGSEIFGLTALRITAENQDCA
						SLTPETFLPRIHVIKGVNISTATV
						CRQCEDAPCANVCPNGAISRDK
		·				GFVHCEARTLHLFAKT
25718	56086	Α	25859	123	923	TDSPYERGHLMSNLLGPRDAN
	1					GIPVPMTVDESIASMKASLLKKI
						KRSAYVYRVDCGGCNGCEIEIF
						ATLSPLFDAERFGIKVVPSPRHA
						DILLFTGAVTRAMRSPALRAW
						QSAPDPKICIS\YGACGNSGGIF
			•			HDLYCVWGGTDKIVPVDVYIP
						GCPPTP\AATLYGFAMALGLLE
						QKIHARGPGELDEQPAEILHGD
						MVQPLRVKVDREARRLAGYRY
						GRQ\VADDSFTQLGQGEEQVAR
						WLEAENDPRLNEIVSHLNHVVE
25719	56087	A	25860	1337	1516	KLKSKSAKRHKFITPILAWRILI
23,17	30007	`	23000	1337	1310	HYLQRVAV*WGSRLL*LFLITIP
						SRWRLLPHNTGKG
25720	56088	Α	25861	1	545	MARLAALKACETVYSMGVRSH
25,20		`		1		RRSPLEHLWQLKDQLVNEGEL
						VLETLVIDGDENTVLVPGDRYA
						QMRNVYFIPSALALKNWLKKC
			:			GFVDIRIADVSR/ITTTEEQRRTE
						WMVTESLADFLDPHDPGKTVE
						GYPAPKRARNRNRAEDHRORL
						RHRTRKKQTHGQRRRHRPEPA
						QRQPQTGTTD
25721	56089	A	25862	620	1117	νννι ν 1011 μ
25722	56090	Α	25863	1	1188	
25723	56091	A	25864	231	407	
25724	56092	A	25865	1	501	
25725	56093	В	25866	1	2373	
25726	56094	Α	25867	1	2211	

SEQ ID NO:	SEQ ID NO: of peptide sequence	t .	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25727	56095	A	25868	2093	3589	GGINGKNFWFFLSPFTPCVGRC HSRVQLANSHLVDVDETPPSSA AVHLYATDADSIGNCGTDREFC PCNPIRRHAFCCERLQNGYHRS GYAFHLGHYGDRKVITNFYSLI AKNHLSHWLETLPAQIANWQR EQQHGLFKQWSNAVEFLPEIKP YRLDLLHSVTAESEEPLSAGQI KRIETLMRNLMPWRKGPFSLY GVNIDTEWRSDWKWDRVLPHL SDLTGRTILDVGCGSGYHMWR MIGAGAHLAVGIDPTQLFLCQF EAVRKLLGNDQRAHLLPL/GIE QLPALKAFDTVFSMGVLYHRR SPLEHLWQLKDQLVNEGELVL ETLVIDGDENTVLVPGDRYAQ MRNVYFIPSALALKNWLKKCG FVDIRIADVSVTTTEEQRRTEW MVTESLADFLDPHDPAIFQIWP CTFMHAYHAFFDPVSHHRACQ NLTTFVPDTHQIAIRNTKACSIF VSFALRTTHSCAISHSSLEDPPAI
25728	56096	A	25869	231	1785	LFKIADRMEQNLELLATAGNLG DDEVHRYSELRTRTVPSYPPER SGEAKTAAQRAGTAFRRGRGA GVPFNLQQRSDRWCS*RSQQN A*RLIGLHGQNSRSVPQLPMES ASVA*RCGSIIEKTTLSSRPFYW CPGCQHYADRFGA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25729	56097	A	25870	1818	3311	RMAIQFRTLSLRWCWKISLVSS FTVVKAMTIRIVAMRQLLRQQ KQRTFVC*SS/TVDGVLSDGLIY MGNNGEELKAFNVRDGYGIRC ALTSDIEVAIITGRKAKLVEDR\ LPHWGSLTCIRGSQTN*SPLAIC WKNWRLP/QENVAYVGDDLID WPVMEKVGLSVAVDDAHPLL GTEIDAYIENADYQYNKKRLRE IDRRVRYLTKCLENLKIVDYSP QQEGKVFFGAWVEIENDDGVT HRFRIVGYDEIFGRKDYISIDSP MARALLKKEVGDLAVVNTPAG EASWYVNAIEYVKPRLNQTVR LLLEHEMGQVWISGEISNFTQP ASGHWYFTLKDDTAQVRCAM FRNSNRRVTFRPQHGQQVLVR ANITLYEPRGDYQIIVESMQPA GEGLLQQKYEQLKAKLQAEGL FDQQYKKPLPSPAHCVGVITSK TGAALHDILHVLKRRDPSLPVII YPAAVQGDDAPGQIVRAIELAN QRNECDVLRPCVWCRRVRCRR
25730	56098	A	25871	1	3465	QRIVEED VERI EV WERR VRERR
25731	56099	A	25872	1	3126	
25732	56100	A	25873		1722	MSSLSQAASSVEKRTNARYWI VVMLFIVTSFNYGDRATLSIAG SEMAKHIGLDPVGMGYVFSAF SWAYVIGQIPGFVDIFSGFGIIV ALFTLRFLVGLAEAPSFPGQSRI VGDWFPAQDRGTGVSIFTPFIL RKGDLRPIWVVILMAGQLHAL MSTLEDTPFSNKAGMRLRRWI NAAVMRLNPLACLATRSNQVN WLLLTGNISVYPVGSSEPTRR STPINSTPHFNKTILPINARYSPT LPSSDGTRWTTRIDDKPTVGHK FARYWDVELREIP\MRPG\QLFR DPKRMIEGCAENPL\GV\VPTFG VTYAGNYEFPQPLPDALNKFQ ADPGIDIDMHIDAASGGFLAPF VAPDIVWDFRLPRVKSISASGH KFGLAPLGCGWVIWRDEEALP QELVFNVDYLGGQIGTFAINFS RPAGQVIAQYYEFLRLGREGYT KSTQPARGSPPANNCQAQPETP DRAVIHPTDGYESAATIIVLSPP TASDSDPAHRDQRVVKTDAWS VVPGSTSEYPRRYKAEWFCQPF AVLPAILAWSAALWRYQPRAR RRKADYGCRALNSLKNELTTP

SEQ ID NO:	SEQ ID NO: of peptide sequence	I .	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25733	56101	Α	25874	1	2385	
25734	56102	Α	25875	1	1767	
25735	56103	Α	25876	1	2079	
25736	56104	A	25877	368	1261	TSPRARPAAQGSRGAFL/HLTE KGVNRFAFYGLPESSGKRWAT EREYAFRQLVAEEKYRGVVYQ GLETAPENWQHAQNRLADWL QTLPPQTGIIAVTDARARHILQV CEHLHIPVPEKLCVIGIDNEELT RYLSRVALSSVAQGARQMGYQ AAKLLHRLLDKEEMPLQRILVP PVRVIERRSTDYRSLTDPAVIQA MHYIRNHACKGIKVDQVLDAV GISRSNLEKRFKEEVGETIHAMI HAEKLEKARSLLISTTLSINEISQ MCGYPSLQYFYSVFKKAYDTT
25737	56105	A	25878		868	PKEVFAIVNSEVML MTSLKNSMKWDEERFGLEYDL DIYMIVAVDFFNMGAMENKGL NIFNSKYVLARTDTATDKDYLD IERVIGHEYFHNWTGNRVTCRD WFQLSLKEGLTVFRDQEFSSDL GSRAVNRINNVRTMRGLQFAE DASPMAHPIRPDMVIEMNNFYT LTVYEKGAEVIGM\TPPLFGQE NFQNVILTCALEDPTRKVVLKP LCRPPLSLCNRRKRVMCRIFTSS ASTLRLSRRCAVCWNSRITVSM RSSRRVTSVWLSAPTPIILSPAIF IVRWWLLDSNPLIYYKAWSCW CSRK
25738	56106	А	25879	2097	2512	NTPVRPDVGT*TEEHGGAESGE *RNSRELRENDKA*LHQYHAQP DGKNLAEAFEHYNEWHPHSAL GYWRTVD/DMRGR*PQEPSLMI RAGRSSSPVQWQRIPLLIPGRKG DRMQKTVIPGSLFAGMPYAQPS IKTELAG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			:	sequence		
25739	56107	Α	25880	71	2613	QRKPTSSRKGLSARMMSGLTG
						TITTVSTGWCTTRGHNMKSRW
		l				SKVAIFTTR/SGRRVAKRVWRR
		1				ERDLTGWMSLSRKPQVTWYG
			,			WDGDRLTTIQNDRSRIQTIYQP
		1				GSFTPLIRVETATAVRRRRRWQ
		1	ŀ			WGIPAGTVQMLDRLESEILADR
		İ				VSEESRRWLASCGLTVEQMKK
ļ		l				TSIHASIVRHKLLTAEQALKLLG
		1				EMFVYHMPFNRALGMELERYE
			,			KEFAQLAFKNQPMMVGNWAQ
			,			SILHGGVIASALDVAAGLVCVG
		İ				STLTRHETISEDELRQRLSRMGT
						IDLRVDYLRPGRGERFTATSSLL
					•	RAGNKVAVARVELHNEEQLYI
						ASATATYMSKSMFLAVATILIS
						KSSLSRLRRPSTIVCGIPISSISAN
						ITPGRSLRSSSSTSKTLCTQFAV
						QFLSKLLYAEGFVHVHRQNRH
						LERRDSVRPYDASFVVVLLNRR
	ļ	i				SYHTRYPDTVATHRQDLVTAIF
						TLYGGFQCFGVLGTQLEDVTNF
						DTTFDQQPTLAIRA WIASHHVT
		ŀ				DICNFRGSDIAIPVDAEVVFTID
						VSTSSEITHRRNVDLFPDQLTVT
						RSQTFTAYERLSTALTVAQVCG
						VQRLCNYYSARLTPLPGPDSTR
						ESNHRLAQITQYARQLASSPSII
						DNRSRQHLNDVGLTAWDCVIIS
						QIIGFIGFQARTIATFQAYLGHP
						VRWLPGLEIQNYADASLFADES
						LRWRSSYEVEKLPEEHTKSSTA
25740	56108	Α	25881	71	3478	CCLSSHPSTTATALRSLSPVRK
						WPKISALIPWEWAMCSLLSHGL
		ŀ				MLSGRSLVAWCWTVLVQNAS
						TSGRSLSGRCLPCCKASSISLVD
						SALSFLLFTLRFLVGLAEAPSFP
						GNSRIVAAWFPARKGTGIINE\IS
						P\LANTALEGLGGSGDALCTQC
						EAEGFRHITYYLDRPDVLARFT
						TKIIADKIKYPFLLSNGNRVAQG
					1	ELENGRHWVQWQDPFPKPCYL
						FALVAGDFDVLRDTFTTRSGRE
						VALELYVDRGN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25741	56109	A	25882	90	629	PGDWGRRQLIGS*KTPGSVFKK GKSSTPN\DPFLKDKTQDRSGL ATFTMDGQI\RLFYQ\DISGNHS GK\QSLPPAQVIVSNSVDHLKIT GVEDHKPIFAGAGKPYQNLRQF IDEGNYTSGDNHTLRDPHYVED KAHKYLV/FEANTGTENGYQG EESLFNKAYYGGGTNFFRGSSR VDLQAC
25742	56110	Α	25883	1	3066	
25743	56111	Α	25884	104	547	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLMYVFCLPNTAIV MALSPRGWRSKFGMPVDSKGP PWLFKFLKNGLNFLLHSVGTRD LSRLSTILSPLYNTVAPGAN*CR ELKLVLDADDVLSTEVKRVITS SASNITPAFFCS
25744	56112	Α	25885	3	4288	
25745	56113	A	25886		2222	DFADFGTTIKQDFRLLGQTSVD RLLQLSQGQAVKGNQLLPVSLP QHTIPDVFIWMLSNNRRVAYA RIASKDLLYSPVAGQMGKHCG KIKTHFLKIPKQQQNEKYQVPQ FDQSTIKNIESAKGLDVWNSWP LQNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQKDFRLL GQTSVDRLLQLSQGQAVKGNQ LLPVSLVKRKTTLAPNTQTASP RALADSLM\SWHDRFPDWKAG RILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW* KEKPPWRPIRKPPLPARWPIH*C SWHDRFPDWKAGRKGSDAHRF GSWKFQLQRVSG\SATFTWGG KIR\LYSADYSGNHYGKQSLPS GQVNGSNSDDTLKINGVEDHK TILDGDGKTYQNVQQFIDEGNY TSGDNHTLRDPHYVEDKGHKY LVFEANTGTENGYQGEESLFNK AYYGGGTNFFRKESQKLQQSA KKRDAELANGALGIIELNNDYT LKKVMKPLITSNTIRKSDGTLQ EHDGICEIHVAKYAEIFGLTSAE ASKDIRQALKSFAGKEVVFYRP EEDAGDEKGYESFPWFIKRAHS PSRGLYSVHINPYLIPFFIGLQNR FTQFRLSETKEITNPYAMRLYES LCQYRKPDGSGIVSLKIDWIIER YQLPQSYQRMPDFRRRFLQVC
	1	1	0.500-	ļ.	2612	VNEINSRTPMRLSYRMGVRGK
25746	56114	В	25887	1	2640	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25747	56115	Α	25888	1291	1629	
25748	56115	A	25888 25889	1187	2925	NSLQRSHPNAANS/WHNKLWR SHSDSDLSDHHEPICKPGLELN KKDITTSADQIAEVKTMESHPPI PPVFVEHMVPQDANQKGLCTK ERMICLEFTSREFHAGQIEDELN LNDINGCSSGSTLEDPQFNDDSP EARKITRRWRIGEAADLVGVSS QAIRDAEKAGRLPHPDMEIRGR VEQRVGYTIEQINHMRDVFGTR LRRAEDVFPPVIGVAAHKGGV YKTSVSVHLAQDLALKGLRVL LVEGNDPQGTASMYHGWVPD LHIHAEDTLLPFYLGEKDDVTY AIKPTCWPGLDIIPSCLALHRIET
						ELMGKFDEGKLPTDPHLMLRL AIETVAHDYDVIVIDSAPNLEDP RVGVMARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSAYERGQ RYASRLQNEFAGNISALADAEN ISRKIITRCINTAKLPKSVVALFS HPGELSARSGDALQKAFTDKEE LLKQQASNLHEQKKAGVIFEAE EVITLLTSVL
25749	56117	В	25890	1	1954	
25750	56118	A	25891	1	454	MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEVYTK VFALDVAARHRAIR\VPRQQGD YRTRIWKFEDGLSNVLVIQLNK LIICVMCLVRDCDVLKTYFHL
25751	56119	A	25892	10	144	FLFIGKGFLKGIT*PGQIVQRG*E KKSNT*FRQFGGVDTAGNNLT

SEQ ID SEQ NO: of pe seque	otide hod	09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25752 5612	20 A	25893	888	892	TVDLDACTKGVLTFTTALLAG GANQAFAKENTKKAYKETYGV SHITRHDMLQIFKQQQNEKYQV PQFDQSTIKNIESAKGLDVWDS WPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGRVFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN YTSGDNHTLRDPHYV/EDKGH KYLVFEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVTDEIER ANVFKMNGKWYLFTDSRGSK MTIDDLWKFELENDDLEYLVE ENSKQKTIQDVIWLFLTAYTHI RGATQAFAKENNQKAYKETYG VSHITRHDMLQIPKQQQNEKYQ VPQFDQSTIKNIESAKGLDVWD SWPLQNADGTVAEYNGYHVVF ALAGSPKDADDTSIYMFYQKV GDNSIDSWKNAGRVFKDSDKF DANDPILKDQTQEWSGSATFTS DGKIRLFYTDYSGKHYGKQSLT TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN YTPGDNHTLRDPHYVKTKAMR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
25753	56121	Α	25894	1424	3807	HPLWKWLEGDMNMNIKKIVK
23733	30121	^	23034	1424	3007	l .
		ŀ				QATVLTFTTA/LLAGGATQAFA
İ						KENNQKAYKETYGVSHITRHD
						MLQIPKQQQNEKYQVPQFDQS
						TIKNIESAKGLDVWDSWPLQN
		l				ADGTVAEYNGYHVVFALAGSP
		1				KDADDTSIYMFYQKVGDNSIDS
		l				WKNAGRVFKDSDKFDANDPIL
						KDQTQEWSGSATFTSDGKIRLF
						YTDYSGKHYGKQSLTTAQVNV
						SKSDDTLKINGVEDHKTIFDGD
						GKTYQNVQQFIDEGNYTGDPL
		1				EAETAVINHKKRKNSPRIVQSN
		1				DLTEAAYSLSRDQKRMLYLFV
		1				DQIRKSDGTLQEHDGICEIHVA
						KYAEIFGLTSAEASKDIRQALKS
						FAGKEVVFYRPEEDAGDEKGY
		1				ESFPWFIKRAHSPSRGLYSVHIN
						PYLIPFFIGLQNRFTQFRLSETKE
						ITNPYAMRLYESLCQYRKPDGS
		1				GIVSLKIDWIIERYQLPQSYQRT
						PDFRRRFLQVCVNEINGAVIGIP
						CVSIRKPDGSGIVSIKIAWIIERY
		1				QPPQSYQRMPDFRRRFLQSRPA
1						CMHDWLCAEALAWSIQTASYL
		1				VTMQVNLTSLSSDTDRDLSVVS
		1				NSGWVSSGSLVRFNTIKTSSGEI
		1				KRTVPRILPDPDDPRSAIAEAPS
		İ				EMPGHEVPVEEHFPEAGTNSGS
						PQGARKGDESMTKASDSSSPSC
		l				SSGPRVPKGAAPGSQTGKKQQS
						TALOASTLAPANLLPKAVHLA
25754	56122	A	25895	3	2356	
25755	56123	Α	25896	1	2610	
25756	56124	Α	25897	1	2496	
25757	56125	В	25898	1	3198	
25758	56126	Α	25899	1	5274	
25759	56127	Α	25900	1	585	
25760	56128	A	25901	[]	2469	
25761 25762	56129	A	25902	1	1914	
	56130	A	25903	1267	2259	VI VTI IIMDI QWDINIQQVQQQQ
25763	56131	Α	25904	1367	1959	KLVTLHMDLSWR\NSGYQSQE
		1				T*K*PANRPVKRPH*GGI*\FSRD
						QKRMLYLFVDQIRKSDGTLQE
						HDGICEIHVAKYAEIFGLTSAEA
		1				SKDIRQALKSF/DGEGSIYSR*A
		1				HGAA*PSHRKDRESADLGSDG
						QNDKGH\QYLVFEANTGTENG
						YQGEESLFNKAYYGGGTNFFR
						KESHKLQQSAKKLDAELSNGA
						LGFIE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25764	56132	Α	25905	1	2418	
25765	56133	A	25906	3	1918	
25766	56134	Α	25907	1242	1463	
25767	56135	A	25908	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG
						AIQAFAKENNHKAYKETYGVS
						HITRHDMLQIPKQQQNEKYQVP
						QFDQSTIKNIESAKGLDVWDSW
						PLQNADGTVAEYNGYHVVFAL
						AGSPKDADDTSIYMFYQKVGD
						NSIDSWKNAGRVFKDSDKFDA
						NDPILKDQTQEWSGSATFTSDG
						KIRLFYTDYSGKHYGKQSLTTA
						QVNVSKSDDTLKINGVEDHKTI
						FDGDGKTYQNVQQFIDEGNEGI
						LPISEPPIKODFRLLG
25768	56136	Α	25909	610	2303	SLPNLDNAAICSSSSSPTRTR*SL
						SEGATQ\AFAKEKYPHKHTKKR
						SGVFHITRHDMLQIPKQQQNEK
						YQVPQFDQSTIKNIESAKALDV
						WDSWPLQNADGTVAEYNGYH
						VVFALAGSPKDADDTSIYMFY
						QKVGDNSIDSWKNAGRVFKDS
	i					DKFDANDPILKDQTQEWSGSA
						TFTSDGKIRLFYTDYSGKHYGK
						QSLTTAQVNVSKSDDTLKINGV
						EDHKTIFDGDGKTYQNVQQFID
						EGNYTSGDNHTLRDPHYVEDK
			,			GHKYRGPLESPSTHQAEFNPTS
						CVSSLGTLQGFPAPAWLALAHP
						VHPLKHKSGGSNRLSAAIWGIK
						RKPARVCPGTGIHASSQIQGEW
						RTECAVGPKAKAKATAGWRR
						GNNQHISSTYDINRADTQVRRA
						VNNYDIIVMSNSFNGQSEHQTY
						ESIVIDSAPNLGIGTINVVCAAD
						VLIVPTPAELFDYTSALQFFDM
						LRDLLKNVDLKGFEPDVRILLT
						KYSNSNGSQSPWMEEQIRDAW
						GSMVLKNVVRETDEVGKGQIR
						MRTVFEQAIDQRSSTGAWRNA
						LSIWEPVCNEIFDRLIKPRWEIR
25760	56137	Δ	25910	1	2103	DOTALI VOILER DREIRI RWEIR
25769	56137	A	25910	1	2103	LSIWEFVCHEIFDRLIKFKWEIF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25770	56138	A	25911	1	2124	MNMNIKKIVKQATVLTFTTALL
						AGGATQAFAKENNQKANKETY
						GVSHITRHDMLQIPKQQQNEKY
		l				QVPQFDQSTIKNIESAKGLDVW
		1				DSWPLQNADGTVAEYNGYHV
						VFALAGSPKDADDTSIYMFFKR
		ŀ				GAIFRVHKHAVNPMSPKCRRPG
						GRQAYPLVNWEDRNGRSQKTV
		l				HTEGDMNMNIKKIVKQATVLT
		ŀ				FTTALLAGGATQAFAKENNQK
		ŀ				AYKET/YPKQQQNEKYQVPQF
•		ŀ				DQSTIKNIESAKG\LDVWDSWP
		l				LQNADGTVAEYNGYHVVSALA
1						GSPKDADDTSIYMFYQKVGDN
						SIDSWKNAGRVFKDSDKFDAN
						DPILKDQTQEWSGSATFTSDGR
						RSLESTTTAARPIWRKDVGGDQ
						TQEWSGSAPFTSDGKIRLFYTD
						YSGKHYGKQSLTTAQVNVSKS
						DDTLKINGVEDHKTIFDGDGKT
						YQNVQQFIDEGNYTSGDNHTL
						RDPHYVEDKGHKYLVFEANTG
						TENGYQGEESLFNKAYYGGGT
						NFFRKESQKLQQSAKKRDAEL
						ANGALGIIELNNDYTLKKVMKP
						LITSNTVTDEIERANVFKMNGK
						WYLFTDSRGSKMTIDGINSNDI
		İ				YMLGYVSNSLTGPYKPLNTTG
						LVLQMGLDPNDVTWASLEPHE
						SFQWVRGLASSGVKLQTSVVL
						QLIKAMWTQRVSSSKVYCKEQ
						MNNASTMSKRTSAGCHCWQG
25771	56139	A	25912	1	3987	
25772	56140	Α	25913	1	2235	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25773	56141	A	25914	1	1950	MNMNIKKIVKQATVLTFTTALL
						AGGATQAFAKENNQKAYKETY
ł						GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
						VFALAGSPKDADDTSIYMFYQ
						KVGDNSIDSWKNAGRVFKDSD
			:			KFDANDPILKDQTQEWSGSATF
						TSDGKIRLFYTGSLNSSKTEKY
						QVPHIDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
						VFALAGSPKDADDTSIYMFYQ
						KVGDNSIDSWKNAGRVFKDSD
			:			KFDANDPILKDQTQEWSGSATF
						TSDGKIRLFYTDYSGKHYGKQS
						LTTAQVNVSKSDDTLKINGVED
						HKTIFDGDGKTYQNVQQFIDEG
						NYTSGDNHTLRDPHYVEDKGH
						KYL/VFEANTGTEEHPQPQ\ERP
						RTQSFTSAFAERRECIPNVPADT
						KLSKIKTLRLATSYIAYLMDLL
						AKDDQNGEAEAFKAEIKKTDV
					İ	KEEKRKKELASKCLDLEQLGAS
			<u> </u>			VEPTGNLRTKITKEKPRHTGPPE
						VVVPGCCPHRSRAYKSDKYAH
						TLTVTASQHAPPPPTHMEGFEL
						FHLPDLCSPSQDAQTTGRTQMK
						PDHSPRPSHRVPQAKGNNVVIT
						SYMTNRGFFEDKKATFAPSFLM
25774	56142	A	25915	1	2448	NIKGNKTSVVKNSILEQGQLTV
25775	56143	A	25916	1312	1974	
25776	56144	A	25917	2	1778	
25777	56145	A	25918	1366	2673	
25778	56146	В	25919	1	1938	
25779	56147	В	25920	1	2262	
25780	56148	Α	25921	1	2100	
25781	56149	В	25922	7145	7154	
25782	56150	Α	25923	2085	11232	VNSEGSEPADRKKPVHTEEAM
		1	ł			NMTIKKIVKQATVLTLTTALLA
						EGATQAFAKENNQKAYKETYG
						VSHITRHDMLQIPKQQQNEKYQ
						VPQFDQSTIKNIESAKGLDVWD
						SWPLQNADGTVAEYNGYHVVF
						ALAGSPKDADDTSIYMFYQKV
						GDNSIDSWKNAGRVFKDSDKF
						DANDPILKDQTQEWSGSATFTS
						DGKIRLFYTDYSGKHYGKQSLT
						TAQVNVSKSDDTLK\INGVEDH
0.5700	56151	 	0.500.4	1.52	202	KPILDGGGKTYQNVQQFI
25783	56151	Α	25924	153	293	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25784	56152	Α	25925	420	687	
25785	56153	A	25926	242	491	WLHVQPLHDEHHCWI*YPADT DGVRPAFQRSPALSPEHGCVPY TPARQGSVRSKGPCTSALLYVE CSIAAPDRKHSCHKSDQS
25786	56154	Α	25927	2	113	
25787	56155	A	25928	779	862	NSTLPRCASTTFARY*AIPIKVFS ILP
25788	56156	A	25929	282	443	FSAGFLNLRYAQKFPSSYPPV** CYRPIYYPASDPCRNRLLYPAD VPYQALLD
25789	56157	Α	25930	3	89	
25790	56158	Α	25931	614	823	
25791	56159	Α	25932	1229	1427	
25792	56160	A	25933	1965	2682	FAVPCRTSFGSIETVSHPGRDT* SA*AYRVQVDSHRPRLAHNVQ HRT*RGEVLLAGVPRHVAEREI ATLAGSFSLHEQNIHNLPRDQG PGNTVSLEVESENITERFFVVGE KRVSAEVVAAQLVKEVKRYLA STAAVGEYLADQLVLPMALAG AGEFTVAHPSCHLLTNIAVVER FLPVRFSLIETDGVTRQLLGVSY RILAMGHAEFLIQIADMRNDGG WRDFQFSGNLVMDEPNRSAQT YIKLVKSRLGTTKR
25793	56161	Α	25934	261	563	RHSRGRSALRQISPEC*IHVCSPP PVQQLHPGYGNAIPLSYGHRNQ PDESDDAPVPPGWCQRYNLHQ KSTAHCGGYTIHADLVKTRCW LAPHRLPPGPGR
25794	56162	В	25935	1	1329	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ł		sequence		
25795	56163	A	25936	761	3224	I RGGAVTAKAPPDISAISALTAV
23173	30103	ľ`	23730	, , ,		KHGNCSSLTPLLNPPGSDVIVC
						AEMDEQWGYVGAKSRQRWLF
		l				YAYDSLRKTVVAHVFGERTMA
						TLGRLMSLLSPFDVVIWMTDG
						WPLYESRLKGKLHSNEGDAVL
						LEIEQEVSSVDSSFNSTLGPTFN
		:				TRTIQNAVLVKTGETVVLGGLL
						DDFSKEQVSKVPLLGDIPLVGQ
						LFRYTSTERAKRNLMVFIRPTII
						RDDDVYRSLSKEKYTRYRQEQ
						QQRIDGKSKALVGSEDLPVLDE
			•			NTFNSHAPAPSSRWALAQRIGV
						SRVDMQQHVRRPPVNLSPKRE
						NVIAGYLSNSVARKQRHIQTGT
						VFHQLMNLLRDGINIIFMNFKY
						QFIVYLHFLLSPKWVMYNRKC
						VNGMLLIASVPATWMLSRYRS
						SHRWIAKEIPMGKTQPLPILLLG
		1				/GGRRIGLALA\WHFIIQKQPVIV
						SYRTHYPAIDGLINAGAQCIQA
						DFSTTDGVMAFADELLKSTHG
						LRAILHHASAWMAEKPGAPLA
						DVLACMMQIHVNTPYLLNHAL
						ERLLRGHGHAASDIIHFTDYVV
						ERGSDKHIAYAASKAALDNMT
						RSFARKLAPEVKRQTATRAGH
					İ	RGINQLSRYYRRALARQNQRR
						MVELRSLRFMYRHRPRSFVLW
					İ	QATRLHRLNIAVRHRKPDARPL
						PAIQRNTDIAIKQPKRAVITGNH
						HRSTFVPTRLAQTGSEIRRHAM
25796	56164	Α	25937	3	543	
25797	56165	Α	25938	209	343	LSPPMSSFLATVFRSIAWLLTAK
						SIRYRTT*RWIRCAAVWLTMD
25700	56166	<u> </u>	25020	547	640	
25798 25799	56166 56167	A	25939 25940	174	583	
25800	56168	A	25941	2001	2610	DVLV\RKHNGHWTVELYSDSIP
23000	20100		22771	2001		RLQINQHYASMCNNARNDGDS
					1	QFIRSNLQDAKWLIKSLESRND
					1	TLLRVSRCIVEQQQAFFEQGEE
		1				YMKPMVLADIAQAVEMHESTI
		1				SRVTTQKYLHSPRGIFELKYFFS
					1	<u> </u>
		1				SHVNTEGGGEASSTAIRALVKK
						LIAAENPAKPLSDSKLTSLLSEQ
		1				GIMVARRTVAKYRESLSIPPSN
	<u> </u>	1				QRKQLV
25801	56169	Α	25942	329	484	TRQLSLLVRMTL*AFVRKRRSS
		İ				LA*KPLWSWLSSVKSQPGWKL
		<u></u>	<u></u>		<u> </u>	MLARWKSF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25002	56170		25042	11	1785	
25802 25803	56170	A	25943 25944	2493	2696	
	56171	A		<u> </u>	1861	
25804	56172	A	25945 25946	1	700	
25805	56173 56174	A A	25947	456	2413	MPVIKVRENEPFDVALRRFKRS
25806	30174	A	23947	1	2413	CEKAGVLAEVRRREFYEKPTTE
		1				RSRYDLVDRNNNIVLEYRKKEL
						VRLTLTDPVTGKSGEVKSLVSS
						LQTKYALKGYNVEATALEAAG
}						GKVVTTGKDILVRKPTLDLPLE
						VRRKMWFKPFMQSYLVVFIGY
						LTMYLIRKNFNIAQNDMISTYG
						LSMTQLGMIGLGFSITYGVGKT
						LVSYYADGKNTKQFLPFMLILS
						AICMLGFSASMGSGSVSLFLMI
						AFYALSGFFQ\ST\GGSCSYST\IT
						\KWTPRRKRGTFLGFWNISHNL
						GGAGAAGVALFGANYLFDGH
				1		VIGMFIFPSIIALIVGFIGLRYGS
						DSPESYGLGKAEELFGEEISEED
						KETESTDMTKWQIFVEYVLKN
						KVIWLLCFANIFL\YVVRIGIDQ
						WSTVYAFQELKLSKAVAIQGFT
						LFEAGALVGNGCSYAQGMWG
						KTAETSDLQDLLIAALQGLSAW
ŀ						AVKAREYGIINHDVDSFAPRAF
						FSTLTNVNFDSPRIVGYAREAIA
	1					LREALKAQCLAVDANARVDNP
1						MADLQLVSDDLGELQRQAAEF
						TPNKDKAAIGENILGLRLLCLY
						GLKVFNGREDQLDSCYHGNRQ
						LRGSLRLLFLAFIRQRLRDLIITA
						HRVIRVNRQHAALGVKHCRLP
						GITGNRIQRQATQYRDRRGTGQ
		1				NQCMRGDMQQLFADIANVAN
						TFAQIIAGRGRKFGANLLHIAD
25807	56175	В	25948	1	3738	
25808	56176	Α	25949	1518	2124	DCFCGSRHDKLPSAHQCSAKPG
						SDRFWRSHADAAYAHDGGIQP
	ļ	1				VLCASRSNGCLQKPKCHTIVSG
						RCPLQQIGS\SVFPSGDAANVAS
		1				FSCACDNAGSAQHRTLLLGKQ
						FFNCRNAFHFNRNSRQTALKSG
						ISWVTFQLILKQQPRPVIMTKM
						AIGFRKV*SQRNIIRHLLVYIFKF
						ADGGCFVVIFLCLQRFIETGINN
					<u> </u>	KMG
25809	56177	C	25950	11	747	CAMPANA AND AND AND AND AND AND AND AND AND
25810	56178	Α	25951	168	332	CAWRAVCAAW/PTGASC/CNN
						DRFVFQILRSFEHDNSEDKPGP
	l					GMPPHGWRTQFWGG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	I .	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25011	56170		25052	11	2706	
25811 25812	56179 56180	A A	25952 25953	1	1062	
25812	56181	A	25954	1	855	
25814	56182	C	25955	1	2412	
25815	56183	A	25956	279	713	RCDAAAGAVLHSAGLLRHCGY
23013	30103		23730	2,7		WQRGKPDRWSRRPGNYADRIC RRWFCAGGVGDRQYELCQLLA
ļ						YTVSATRRGTGYCLYRDSRGR
						TGLPVV*HLSGAGLYGRCRFAG
		1				VRWCVRHYRRTATSGIPAGDY
		ŀ				GGRVRGRNAFCHPAVAP
25816	56184	Α	25957	1	769	MDFAETELEFIKFWGDIITNKLN
23010	30104	^	23737		1,0)	EALAAQGDNVVINLASDEYFKS
						VKPKKLNAEIIKPVFLDEKNGK
						FKIISFYAKKARGLMSRFIIENR
						LTKPEQLTGFNSEGYFFDEDSSS
						NGELVFKRYEQRAECRIVTRHL
						SFSGDVCLDHDRRDDHEELSY
						GGAAVAAVLVIEPNKLAFDGS
						GYLAWEGLICMQEIGKC/YRRT
						SGDCA*VAGRAQTG*VSGWAL
		l				SRGKNQPGVGCEAGARRHARE
						ARIGDERHRLAPROML
25817	56185	В	25958	1	2472	
25818	56186	Ā	25959	4300	4492	DCGGVRSQRPDQR*DWNR*GA
						GGESDS*SLATGGQAAEGVAV
						WRYSARWR*PLFAGRCARAGG
						D
25819	56187	В	25960	49	3000	
25820	56188	Α	25961	266	812	LLRWRPGALALGHKLVAGEIR
						QQRMDAWRAACLQNPQGILCC
						ARGGQRSHIVQSWLHAAGIDY
						PLVEGGYKALRQTAIQATIELA
		1				QKPIVLIGGCTGSGKTLLVQQQ
						ANG/VDLEGLARHRGSAFGRTE
						DELGKLAQTSTSSPAHWRETSK
						CGGFLCPIFLTNMRTPLPVCAT
25021	5(100	 	25062	761	974	VLPYLAIATV
25821	56189	A	25962	761	874	MAAVCCIEACTVIEACCICTIC
25822	56190	A	25963	2	304	MAAYGSGIFAQTYIEAFGISTIQ
						PASCSPVNQYITAAFVLFGNVA HALLIALQRRNRRHLQRRKGA
						VIVIAFNTSQGA/VPAFCCQP*S
						RYASPPCCSFSTA
25823	56191	A	25964	109	777	KTASFFCCSF3TA
25823	56192	A	25965	5	187	ITHKKPPPSWRSALLPAAGVFS
23027	30172	 		ľ		RRYMPALCE*HWAS*RMRAEA
						TETFSDCTMPIIGMMMS
25825	56193	A	25966	1	711	
25826	56194	A	25967	757	1026	-

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	1 ' '
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25828	56196	Α	25969	1	1065	MKVLEKRNNASSEPEEKNEIRA
						AREHAGFTLQELVCLGASGRK
						VQGEAANAEEEVAAGELDNIA
						KITNEGSYTEQQIFNEGYMWLS
						TLMKIKENKISCSWATQSHFQG
						SIDAGELEHLTPERVWKETESA
ļ						LTTRNPQVFFQVLRDCGALRVL
						FPEIDALFGVPAPAKWHPEIDT
						GIHTLMTLSMAAMLSPQVDVR
			:	1		FATLCHDLGKGLTPPELWPRHH
						GHGPAGVKLVEQLCQRLRVPN
						EIRDLARLVAEFHDLIHTFPML
						NPKTIVKLFDSIDAWRKPQRVE
						QLALTSEADVRGRTGFESADYP
						QGRWLREAWEVAQSVPTKAV
						VEAGFKGVEIREELTRRIAAG
						LRG*VSRSHPHLPNAEPKNH/AS
						NYLIPSMPGVNRSVSSNWR*PA
						RLTCAAE/HGFESADYPQGRWL
						REAWEVAQSVPTKAVVEAGFK
ļ			·			GVEIREELTRRRIAAGLRGMPT
25829	56197	A	25970	2373	2597	SADDKADSVA*YLRLASA*TNS
						CRPYRRPSAPVCRRAPAI*G*TP
						QNYGPPSSCPAGGFWRYPVDPP
						RFSGFVH
25830	56198	Α	25971	2616	2777	TSVRKRFSTLSGKPVAKAGRKR
						PPPCR*TPTANGHPKPCRPPVW
					:	CHPAPVARP
25831	56199	В	25972	1	1449	
25832	56200	Α	25973	1076	1477	CAVRRSITWCKLSSKTPVRPLR
						PSTYRDCLTVSIALTPPASEKVK
						RRPVPAVKSAMKVPPGAAQSR
		1				KRVWLVSPFPTCEFLASNSRGK
		1				KISVSLSALSPRWTS*PKARWA
		1				ARRLTTNLVVRH*TATSVLMK
						KK
25833	56201	Α	25974	1	3552	
25834	56202	Α	25975	196	493	KRCRFADRPGDPGRQGTPAATT
	1					FGGMSFVTILPAPIPELSPMVTP
	1					GLITT*LPIQTLLPIVIGKEYISPF
	}					FLNSWCTGCPVTERVTLGAIST
	<u> </u>					LSPIVTV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25835	56203	I _A	25976	1	3917	MTDKHQQHRYVAAPGPFVGD
			<u> </u>			KCQVAGDPLMLRRALSNLLSN
						ALRYTPTGETIVVRCQTVDHLV
						QVIVENPGTPIAPEHLPRLFDRF
		1				YRVDPSRQRKGEGSGIGLAIVK
						SIVVAHKGTVAVTSDARGTSGL
						DDFFIDVVYWVRRIKRKLSVYR
						RIPRMSYRELYKPDEQPLAIMV
						PAWNERASSAIWRAGGTTLDT
						KFLFVGLPGPILGSCKVPFEFLE
						VACPPSGGPVGPPWRRPCRGA
						AAAICASPAAIILAPT
25836	56204	A	25977	3	292	GDMQRLNSLFC/SVAYSVLEQP
23030	30201	` `	23777		2,2	DEDEGRDSINIVNPSGRPIIVSSG
						ATPAVREYAAHGFHLYGLROR
						VGEVRVDLQREQIYASKPCGST
						IGISLVVR
25837	56205	A	25978	2	181	SARRLR/RSKHRFRILNRRYSHA
2000.		1.		_	1.01	HS\MLGDMQRLNSLFC/SVAYS
İ						VLEQPDEDEGRDSINIVN
25838	56206	A	25979	1	2781	V EEQT EEEE CONSTITUTION
25839	56207	Α	25980	1	2554	
25840	56208	Α	25981	635	741	
25841	56209	Α	25982	91	501	LWIRLAKRSGKAIKERRDFIFRL
						CTHRVRQGTALLRLFQHSGGN
		ŀ				RLMKLDNQHLRLRISNHRAFHF
]				RHRTTVKQSQQTFRYPWLYRV
		1				RHWGQKPKTDNFHGLLARIFG
		l				NSRSKTWGENR*EHSVLEQPDE
						DEGRDEY
25842	56210	Α	25983	2153	3062	APVMPPERLPVIAVRQYPTANC
1						CSDCLAAASRFFLASVAAPEQT
						DADTRRSRVAVGRRKTRSNSA
						NQPRPRRDWRELQLMDRLARV
			<u> </u>			AQARASFAARETLRIGDAMEQ
		ĺ				MMEGLNKVMHGEPRQEKELR
						KLADDINVLYTAIKLYLARMPK
		l				EELAEEESRRWAEIIEMSLNLEQ
						ASDIVERMG\GELVDKSWAAR
						RAFSLDGLKELDALYEQLLSNL
						KLAMSVFFSGDVTSARRLRRSK
						HRFRILNRRYSHAHVDRLHQQ
						NVQSIETSSLHLGLLGDMQRLN
						SLFCSVAYSVLEQPDEDEGRDE
25843	56211	Α	25984	135	308	KLSLRLGIFPRPSLFPRPTPSPST
						PAPAS*PAPS*VSPSPRTATPSCP
						TSYSSFPCH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	:	09/540,217	, ,	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25844	56212	Α	25985	3	663	ARGKKPPRRGKEDFWDLSIATR
						VSVNPIKFPVEA*PFLKP\LQQV
						S\GPLGGRLPLPIPGNLLLQVAD
						GTLSLTGTDLEMEMVARVALV
						QPHEPGATTVPARKFFDICRGL
						PEGAEIAVQLEGERMLVRSGRS
						RFSLSTLPAADFPNLDDWQSEV
						EFTLPQATMKRLIEATQFSMAH
						QDVRYYLNGMLFETEGEELRT
						VATDGHRLAVCSMPIGQSLPSH
25845	56213	A	25986	1	1077	
25846	56214	Α	25987	1	1323	MHSGTFNPQDFGWQGLTLTPA
		İ				AAIHIRELEILDEYGIPNAWQGE
						TNFWGSTAVSIDRLAAYKDVD
						VLCFDHDNSKDMDALMATPL
						WQAMPFVRAGRFQRVPAVWF
						YGATLSAMHFVRVLDNAIGVIV
						ATALTWMNFSQALPRSQWAQ
						AAWSPDIDVIEQMIFHYSLLPRL
						AISLLVGAGLGLDVRYYLNGM
						LFETEGEELRTVATDGHRLAVC
						SMPIGQSLPSHSVIVPRKGVIEL
						MRMLDGGDNPLRVQIGSNNIR
						AHVGDFIF\TSKLVDGRFPDYRR
						VLPKNPDKHLEAGCDLLKQAF
						ARAAILSNEKFRGVRLYVSENQ
						LKITANNPEQEEAEEILDVTYSG
						AEMEIGFNVSY\VLDVLNALKC
						ENVRMMLTDSVSSVQIEDAAS
		İ				QS\AAYVVMPMRLEGSPPLGNP
						EFQKISSPCALYIALCSKARHHT
						GRYLGLCGL
25847	56215	Α	25988	211	475	GAIGVFTAGKLTRASVYHQAR
						RFMQRETVWLVEDEQGIADTL
						VYMLQQEGFAVEVFERGLPVL
						DKARKQVPDVMILDVGLPDISG
						FELCRQLLALHPALPVLFLTAR
		Ì				SEEVDRLLGLEIGADDYVAKPF
						SPREVCARVRTLLRRVKKFSTP
						SPVIRIGHFELNEPAAQISWFDT
						PLALTRYEFIVLKT\LLKSPGRV
						WSRQQLMDSVWEDAQDTTSH
						VVAFATILQGISRDLRRRILPYCI
						RCRRERCTGTALWQ

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
	<u> </u>	<u> </u>				
25848	56216	Α	25989	1661	2499	QMAHDEQWLTP\R\LQTAATLC
		ŀ				NQNAPRDGSPLWLGVDLGTCD
						VVSMVVDRDGQPVAVCLDWA
						DVVRDGIVWDFFGAVTIVRRHF
						DTLEQQFGRRFSHAATSFPPGT
	ļ	l				DPRISINVLESAGLEVSHVLDEP
	ł	i				TAVADLLQLDNAGVVDIGGGT
	1	l				TGIAIVKKGKVTYSADEATGGH
		l				HIFLTFAGNRRISLEEAEQYKRG
		l				HGEEIWPAVKPVYEKMADIVA
					:	RHIEGQGITDLWLAGGSCMQP
						GVAELFRKQFPALQVHLPQHSL
						FMTPLAIASSGREKAEGLYAK
25849	56217	Α	25990	915	1518	PSGHAPDLNGAPATAHQPGGR
						YPAPRSVRRATDNGYPAGDPLE
						WRSTAQVFVSSRRRVSLPNDRK
						TVLTRCWSAAH*FALPAPLCRD
	İ					RTGERKNRRFHTPTRCGRGFCP
						APAASRRCAGRRRGDASGRAY
						RRPAPSHCPVQ*RGHRKSTTTSS
						TSRRRPGQSARPYSGPEYRE*Y
	1					CSAQRFFHNDGSRPPVVRQAGR
						AQFP
25850	56218	Α	25991	1	1254	
25851	56219	A	25992	675	835	VRWCWIFPSQ*TLFQKRAGHA
						APSADVLHESCQHFLNLLNRLG
						RHYDFGEGEP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	l .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25852	56220	Α	25993	1	2255	MRESPTRDDSKNTVNTTIRIRIH
						NSYTEQLQIVTNSYCTKQWHV
						HHTAKPYAHIQRPATPDAQLTK
						MQEEEEVEPEPEMEAEVEPEPN
		l		<u> </u>		PEEAETESESMNQRDVRGTVRI
			•			VLKTFNNCRDTVFVAFEVNNT
						VSLLVATTDMTSGDTAIVVTTT
		1				GFAVFFQQRSKSAANEVQILAF
						FQGDVSFFPVATTTDTLSVTFN
						FPFNYQGVNDFDFDFKQFLHSS
						FDFCFGRVFSNFEYLHGARAHA
						CIPPSACIGEVLETSSFDIRVSVY
		l				RSSCVCVRLRESSTGDRYFGGL
				:		SLQMMRKATGLTDITSDTPGNT
				ŀ		DDQRWHPEHGLTQRMQKEQE
		İ		ļ		LVKEPEGAARDGDGEAEAWGE
				†		VKAKSSGCVGTRASSHLFRCNV
						CELHFKESSELLQHPCTPSGERP
						FRCGECQKAFKRPSG\LRQHER
		l				THSAERPFKCDLCPMGFKQQY
						ALMRHRRTHKTEEPFKCGLCE
		1				KGFGQPSHLLYHQHVHTLETLF
		l				KCPVCQKGFDQSAELLRHKCLP
		1				GAAERPFKCPVCNKAYKRASA
						LQKHQLAHCAAAEKPLRCTLC
						ERRFFSSSEFVQHRCDPAREKPL
						KCPDCEKRFKYASDLQRHRRV
		ł				HTGEKPYKCPNCDKAFKQREH
		Ì				LNKHQGVHAREQQFKCVWCG
		İ		İ		ERFLDVALLQEHSAQHSAAAA
		ł		į		AAEGAYQQTLHHPRRQQQQY
						WQLLCARNNVKLCMHILFSPH
25853	56221	Α	25994	98	596	YSGIIMAQSKLYPVVMAGGSGS
						RLWPLSRVLYPKQFLCLKGDLT
		İ				MLQTTICRLNGVECESPVVICN
1		1				EQPRFIVAHQMRQLNELSENIIL
						EPAGRTTAPTIAPAALAANRHS
						PESAPLMLVLATDHVIANEDAV
						RAPVK\NAIPYPKKGKLVTFGIG
		1				LDGRVPRYNM
25854	56222	A	25995	3	554	
25855	56223	Α	25996	1	222	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	· · ·
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25856	56224	A	25997	<u> </u>	1043	MKVKVLSLLVPALLVAGAANA
23630	30224	^	23991	l'	1043	AEVYNKDGNKLDLYGKVDGL
						HYFSDNKDVDGDQTYMRLGFK
						1
						GETQVTDQLTGYGQWEYQIQG NSAENENNSWTRVAFASLKFQ
						DVGSFDYGRNYGVVYDVTSW
						TDVLPEFGGDTYGSDNFMQQR
						GNGFATYRDTDVFGLVPTRLHP
						ARVCCALRELKDAGADRIWYI
						ADAFRAGLSVDGVFNLTNIDR
						WFLHINRAKDKNHMIISIDAEK
						AFDKIQQPFMLKTLNKLGIDGT
						YFRIIRAIYDKPTANIILNGOKLE
		İ				AFPLKTGTRQGCPLSPLLFNIVL
						EVLARAIRQEKEIKGIQLGKEEV
						KLSLFADDMIVYLENPIVSAQN
	:					LLKLISDFSKVSGYKINVQKSQT
						FLYTNNRQTESQIMSELPFTIAS
		İ				RRIKYLGIQ*IRY*WDVFQNNK
						SYL*QTHSQYHTEWAKTGSIPF
						ENWHKTGMPSLTAPIQHSVGSS
						GQGNQAGEGNKGYSIRKRGSQI
						VPVCRRHDCLSRKPHRLSPKSP
25857	56225	Α	25998	1	3339	
25858	56226	A	25999	1440	1880	AAQHASVYLYQNRIRGAVPPV
						RFFHADQRTRRDGADGKQRHA
						TETLCRIAEKISSSREQDWLHCD
						ERQSLYEWTW*PYSPHSGRSQK
						EKRQT*TAILDAYCADCFRCGR
						GVFARRERRTKRDRPGNAGTG
						GDCPCWLRRQYECVRL
25859	56227	A	26000	1	2277	
25860	56228	Α	26001	1	1845	
25861	56229	Α	26002	56	113	QQQPNPTRDQLQLAILHNIRGIR
						KIYG*IQSATREAG*GHSPQY
25862	56230	С	26003	1	2317	
25863	56231	Α	26004	3	2168	
25864	56232	A	26005	670	2541	
25865	56233	Α	26006	98	944	YSGIIMAQSKLYPVVMAGGSGS
						RLWPLSRVLYPKQFLCLKGDLT
						MLQTTICRLNGVECESPVVICN
						EQHRFIVAEQLRQLNKLTENIIL
						EPAGRNTAPAIALAALAAKRHS
						PESDPLMLVLAADHVIADEDAF
						RAAVRNAMPYAEAGKLVTFGI
					1	VPDLPETGYGYIRRGEVSAGEQ
						DMVAFEVAQFVEKPNLETAQA
						YVASGEYYWNSGMFLFRAGRY
1						LEELKKYRPDILDACEKAMSAV
						DPDLNFIRVDEEA/FLACPEESG
	. [<u> </u>		<u> </u>		DYAAMGRTGDAVVPLSLGAH

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25866	56234	Α	26007	3	417	
25867	56235	A	26008	507	717	WPEAEYLDNADAVLAMYHD/Q GLPVLKYQGFGRGVNIT/LGLPF IRTSVDHGTALEWRTCKPMVP DSIVSCIL
25868	56236	A	26009	5	378	MAVCSSLSPRRSPAFL/HDFTDV WTHHLVFGVNP*RGLIHGTALT DHVG/ENGNYSSD*IHGTALTD HVGKTETILPTKYANIYSINTSK DRFLTKPAFAEVVLFLHPRELQ TCSFFLSQNMLVKVGHQRHWF TEVDVTLTEITQLA
25869	56237	A	26010	I	469	MQKEYAYWMDGLKTCKPDNR KNALSNFGWYPSQPLLGRSRY ATTESWVEDIATAKSNPNRLPL KFTATCALPLRLAGFQ\PRWMD NPQQLNTLAPPASYRSI*TA*CL K*KNPRPRQQSCRR*RDGNQYE TLANARQKGIEKTCGTINKAG MPITT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25870	56238	A	26011		1854	CGGTLARACDGCLNGEFAA/LI TGPVHKGVINDAGI/PFTGHTEF FEERSQAKK/VVMMLATEELRV ALATT/HLPLRDIADAITPALL/H QPKYLDNADAVLAMY/HDQGL PVLKYQGFGRGV/NITLGLPFIR TSVGHG/TALELAGRGQ/ADVG SFIRPYSAIK*L*NAGASVRWLS ERRICRAITGPVHKGVINDAGIP LPVIPSFSKSVRRKRCDDAGD RRTSRGAGNDALPLRDIADAIT PALLHNRNILITPTPCWRCTRSG SSRAKIPGLRARCDITLGLPFIRT SVGHGQPLNWRDVANRCWQF YTPLFCHQMIVKPMHNRIPRAT YRGAVKSAIGLGCCCLKASATR CAYRWRRSGRRDQSRFRYFEIA GIRSRGINFIACPTCSRRNLMLS VRLTRWSNAWRYHHSDGRFD YRLRGECPGEALVSTLGVTGG NKKAASMKMGAQRPSGQQDM IDQLEARIRAKASQRTKRVELT FSRLKNNNVEKQDTALFALYQ RRLRCVRKVRRYVMAAVSAGC GGGVCAVSAYMPLNRLPNAQE ANNEYTSFENCIKCTVCTTACR
						VTLRNNDPKLPYLVKAGLKMK RVTRSPRRYCAAASATHRFNDE RAGKVQGMPDINKLPADRETC STLTCARSRQNQTNPYPANRAA NAYQVVLATKALEKVSMKSP WQHKVSSPAAVRHLPSITQRRT

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide seguence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
25871	56239	Α	26012	1	1504	MGIVASASVQAAEIYNKDGNK
		ł				LDVYGKVKAMHYMSDNASKD
		ł				GDQSYIRFGFKGETQINDQLTG
		1	,			YGRWEAEFAAWTDMFPEFGG
		ļ				DSSAQTDNFMTKRASGLATYR
						KTTSSAYRWPELNLQYHRCTS
						AARAMLLSGRPVMQINERTAV
		İ				RRQMTVYLRVERIHEIDPLVSL
						SHSMSVIPIDVERPIAAAPCTPG
ļ						LWRTKTPLRVPSTYPLRLPGRA
						RVVCHRTFRLHLCKDWVFMFS
						GLLIILVPLIVGYLIPLRQQAAL
						KVINQLLSWMVYLILFFMGISL
						AFLDNPRPYLADSVPDRQLLAP
						VNSISRYKTIEWLNYIATELHK
						GFTPLFRPDTPEEYKPTVRAHSE
						KKLQYVNEALKDEHWICGQRF
						TIADAYLFTVLRWAYAVKLNL
	1					EGLEHIAAFMQRMAERPEVQD
						ALSAEGLKGSRHLSAGARRLIL
						GIIVTFSLILALICVTQPFNPLAQ
						FIFLMLLWGVALIVRRMPGRFS
						ALMLIVLSLTVSCRYIWWRYTS
						TLNWDDPVSLVCGLILLFAETY
						AWIVLVLGYFQVVWPLNRQPV
						PLPKDMSLWPSVDIFVPTYNED
						LNVTPDELKQVLDVAAALKAL
						RAENISTKVFNSGLGISVFRDNS
						TRTRFSYASALNLLGLAQQDLD
						EGKSQIAHGETVRETANMISFC
						ADAIGIRDDMYLGAGNAYMRE
	560.46	_	26012	2000	2001	VGAALDDGYKQASGFSEPAMR
25872 25873	56240 56241	A	26013 26014	2903 123	3024 335	
25874	56242	A	26014	2634	2787	
25875	56243	A	26015	1477	2485	NPEQLMVKTQRVVITPGEPAGI
23673	30243	Α	20010	14//	2403	GPDLVVQLAQREWPVELVVCA
;						DATLLTNRAAMLGLPLTLRPYS
		ı				PNSPAQPQTAGTLTLLPVALRA
						PVTAGQLAVENGHYVVETLAR
						ACDGCLNGEFAALITGPG\HKG
						VINDAGIPFTGHTEFFEERSQAK
						KVVMMLATEELRVGLATTHLP
						VRDIADAITPALLHEGIAILHHD
						LRTKFGIGEPRILV\GGLNPHAG
						EG\GPMGTEEIDTIIPVLNELRA
						QGMKLNGPLPADTLFQPKYLD
						NADAVRPMYHDQGLPVLKYQ
						GFGRGVNITLGLPFIRTSVDRGT
						ALELAGRGK\ADVGSFITALNL
						AIKMIVNTQ
<u> </u>	<u> </u>	Ь	L			LUMANIA IA IA

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25876	56244	В	26017	1	3432	
25877	56245	A	26018	1385	2536	KSSQSHLITGMLEHVFVKSGDT
25077	30243		20010	1303	2550	PSR/LPELMNGAQALANQINT/F
						VLNDADGAQAIQLGAN/HVWK
						LNGKPDDRMIED/YAGVMADTI
						RQHGADGL/VLLPNTRRGKLLA
						AKL\PDASRTGETH/TVEWQAP
						AVAITRTATQARQSNSVDLDK
		1				ARLVVSVGRGITDSQTLRLYYI
	İ					RLPPSLMGMRLTVFLLPICGFH
						RVGPPTLLSVLATNRNRNAKVF
						AHKNAPKFRSHTASEQWKSSIA
						HNKGVHPRVTSHTHARHSLME
1						TDIPHNIHSGHASPADITRHRAQ
		1				VFNSVPKMASPIGDRVPTLHTQ
		l				HNSPANTGKAQSLLTCGPAAES
						CCRLIPRQMVSLVFRLKARLLLI
	ļ					TTELPKGLVPVATISGTGNFGN
						TQSANPYRPSENTDLSLS
25070	56246	A	26019	926	1293	LSPNPKEPSCRTRLKKSGFFTRI
25878	30240	A	20019	920	1293	SAGAEPLMAIPARLSNSLACGA
						RDSAAKE/GFVVVPVCVAVEA
						DIAELDDEERDEFMADVGFT\V
					,	GVKEVRAWTIPVGATAPQAAG
						KIHTDFEKGFIRAQT
25879	56247	A	26020	1	1278	KIII DI EKOI IKAQI
25880	56248	A	26021	678	1526	ERNTNTCEVVPNRKRAYASHD
-		-				MELSISPVGKGASKGEVNPADD
		1				IEVINTELALADLDTCERAIHRV
İ		ŀ				QKKAKGGDKDAKAELAVLEK
					ļ	CL\PQLENAGMLRALDLSAEEK
						AAIRYLSFLTLKPTMYIANVNE
						DGFENNPYLDQVREIAAKEGSV
						VVPVCAAVEADIAELDDEERDE
					1	FMQELGLEEPGLNRVIRAGYKL
						LNLQTYFTAGVKEVRAWTIPV
				,		GATAPQAAGKIHTDFEKGFIRA
						QTISFEDFITYKGEQGAKEAGK
						MRAEGKDYIVKDGDVMNFLFN
25881	56249	Α	26022	1177	1605	
25882	56250	A	26023	1	644	MDNHIALDFLLASECGSVYVY
					1	ATTHGRNMAGARALWRATGM
						TDADFGKPIIAVVNSFTQFVPG
						HVHLRDLGKLVAEQIEAAGGV
						AKEFNTIAVDDGIAMGHGGML
						YSLPSRELIADSVEYMVNAHCA
						DAMVCISNCDKITPGMLMASL
						RLNIPVIFVSGGPMEAGKTKLS
						DQIIKLDLVDAMIQGADPKIN/D
						YQSRGRRCPNRCFRCKNQAGS
25883	56251	В	26024	1	1944	
23883	20221	lR	26024	11	1944	

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25884	56252	Α	26025	1 '	1488	
25884 25885	56252	A	26025 26026	1	1488	MNKAHFVSNLGATKCCPLSFLP YRWRRVIAFVVAFYFRHLIDLL VVQMHFKLVKGNVDVVFTAQ LIDSTVQLIDSTTTVTQFTHIQT QLMIQRAGTKCRKEDFRHCVGI LEPEWYPIIVVRVVVDVSQFEV RSQSLIFAVGEGITCIYTQFITHA VVRLTVNFHVVAQLSSPDWNR PETLPVRSHVTSITQFEVVTGFQ TEAPSVGVGATVNVSTVAHGC RQVVVEVRVAQATINKDVVRE VSRRVDVGSLAVLIHLTRTVIH VTFSEACSRTDDPLSVVTVNFGI NTDHDAVNILIIVDGAVVAVEV TTEVAYPCAAVISQAMTRVGQ TSTNGVWTISSVNAFQIRTGAA RSLAPPWSLTEKVFCGTTMER MRAALEAIMPFTESSSATQAPY LPCGRECGLAVRQFFGRGEGIE TVAYLFRIIRVVRTRVLSIGGFS RTRISSTPVKIATLRQNRSDCHA AMIADTYRQVTPTDPFSRHPFS
						RVLRGLFFIIFKDTKAHNGIGMI GGVNRRADYLNLLEKVFGDRV SSPQWQATLKAIVPSYGRKLNG DVAATERELQYTSEVVGLNYD KPQAADNNRQHKVRAARSRRQ NRPDRGSQIADSTAGARCRFQT PTAGDGA*SAASTAAPI/MLNLL EKVFGDRVSSPQWQATLKAIVP SYGRKLNGDVAATERELQYTS EVVGLNYDKPQAADNNRQHK
25886	56254	Α	26027	1	2130	
25887	56255	A	26028	1144	1309	PGGSTPMAVEDPDFRSSERVLR FQPAVSVYGPEQPAV*DYAQTS YLRTRPRRSDP
25888	56256	Α	26029	1	3546	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25889	56257	A	26030	1097	3332	TRVLVLDHRLLRCLYATVCAG
						ASWGMNPVVCSQQIDPQFHTM
						LMICASEEAQRMQQASEDEFN
						RALNIAFDNRLGLCKVESARQV
						FPLTGRYARQFASHRLALVGD
						AAHTIHPLAGQGVNLGFMDAA
						ELIAELKRLHRQGKDIGQYIYL
						RRYERSRKHSAALMLADSFVR
						TTHALRRSHGGFPRLDDAAAL
						RFANRRTSCERNDDNTWSRSL
						YADLKNGTAQNIRAKFVFIGAG
						GAALKLLQESGIPEAKDYAGFP
						VGGQFLVSENPDVVNHHLAKV
İ						YGKASVGAPPMSVPHIDTRV\L
						DGKRVVLFGPFATFSTKFLKNG
						SLWDLMSSTTTSNVMPMMHV
						GLDNFDLVKYLVSQVMLSEED
						RFEALKEYYPQAKKEDWRLW
						QAGQRVQIIKRDAEKGGVLRL
						GTEVVSDQQGTIAALLGASPGA
						STAAPIMLNLLEKVFGDRVSSP
						QWQATLKAIVPSYGRKLNGDV
						AATERERKTLHVIFNDLRPEQC
						EAGKSPSRVQLQTWTNGGMLN
		1				APLSLRLTLVEKLASMLDPGHL
						ALTQIAQHLALLQKMDHRQHS
		1				AFPELPQQIAALYEWFSARCRW
	İ					KEKALTQRGLLVQAGDQSEQIF
						TRWRAGAYNAWSLPGRCFIVL
						EELRWGAFGDACRLGSPQAVA
						LLLGDLLEKATQHLAESINAAP
			:			TTRHYYHQWFASSTVPTGGEH
25890	56258	Α	26031	115	654	HATQTMTPWFLYLIRTADNKL
						YTGITTDVERRYQQHQSGKGA
						KALTGGSARSPLIKKALAEQLP
						GIPIAGGDDFGSVTAGLAR*RF
						HQRHGPCWSMKAESLQLCRAD
						CQRRFQPMSFGGHFRHYRLSVC
		1				WRYRFIRPEHKTAFTARFPVDN
						RLGQMVAKPFHLLNATTGNIC
						GCFNTKRP
25891	56259	A	26032	1	348	
25892	56260	Α	26033	1	906	
25893	56261	В	26034	59	910	
25894	56262	Α	26035	1	3684	
25895	56263	A	26036	1	2634	
			<u> </u>	٠	<u> </u>	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	•	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25896	56264	I _A	26037	1162	3478	LVRFGLLPLAYSARCFSARSED
23070	30201	``	20037	11.02	3 77 0	RPKDECETCCIKYPNGRNVLSQ
		İ				EIHQVFVLNGIQSMSGYVYNLG
į						NELASMQGLVDVVRLSPQGSS
						AREAFSHSLDLARLAEKRGYH
		}				RYWLAEHHNMTGIASAATSVLI
į		İ				GYLAANTTTLHLGSGGVMLPN
						HSPLVIAEQFGTLNTLYPGRIDL
						GLGRAPGSDQRTMMALRRHM
·						SGDIDNFPRDVAELVDWFDAR
						DPILEPTHNGRRLCSTVRHPRM
		ŀ				
ì						GYTPGVEPTTGPLGQGLANAV GLAIAERTLAAQFNQPDHEIVD
						HFTYVFMGDGCLMEEGWFTD
						DTAKRFEAYHWHVIHEIDGHD
						PQAVKEAILEAQSVKDKPSLIIC
						RTVIGFGSPNKAGKEEAHGAPL
		ŀ	i			GEEEVALARQKLGWHHPPFEIP
						KEIYHAWDAREKGEKAQQSW
						NEKFAAYKKAHPQLAEEFT\RR
						MSGGLPKDWEKTTQKYINELQ
	[ANPAKIATRKASQNTLNAYGP
						IMLPELLGGSADLAPSNLTIWKG
						SVSLKEDPAGNYIHYGVREFG
						MTAIANGIAHHGGFVPYTATFL
		ŀ				MFVEYARNAARMAALMKARQ
						IMVYTHDSIGLGEDGPTHQAVE
						QLASLRLTPNFSTWRPCDQVEA
						AVGWKLAVERHNGPTALILSR
		l	}			QNLAQVERTPDQVKEIARGGY
		1				VLKDSGGKPDIILIATGSEIEITL
						QAAEKLAGEGRNVRVVS\LASS
25897	56265	A	26038	1	1033	MNKSPKTRDIQEEELEVLLEEE
23697	30203	^	20036	1	1000	AAGGDEDREKEILIERIQSIKEE
						KQKGLGLAAGWTADVSSRRPG
						ASQLPPPPTHPIPQYRGWGPPD
			İ			QHLLSTLWTNVGSYKSGSFLQL
						GGWCMNLDMDLNSEESRWLF
						RRHWDTGGIKPHERKRAVAHL
						TLSEREEIRAGLSAKMSIRAIAT
		1				ALNRSPSTISREVQRNRGRRYY
						KAVDANNRANRMAKRPKPCLL
						DQNLPLRKLVLEKLEMKWSPE
						QISGWLRRTKPRQKTLRISPETI
						YKTLYFRSREALNHLNIQ\HLA
						RSHWLWPGERY\NRNGERGPV
						TLWTG/TPISDGSRTSVKRALGQ
						WGEHLSRRNAFFPLCATVV
	}		l	J		WUEDLSKKINAFFFLCATVV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25898	56266	Α	26039	797	1440	 PAMRLTAMRCISMKSRLPASR
						MQFCATVRWKYRCHREPTLSA
						QHGAFRSINPTPRNSRGNCWKK
		l				REMKWANWPIWCR*KN*RERS
						LSAICCASRK/TGQFVLPPARYH
		1				LRRSHSLRHGRRHTRKGERGTI
		1				NIVNGTPIHERSRNIDNRRSLGH
		1				WEGDLVSGGVGTVIGVVTGVII
		1				FTVINYGLTYIGVNPYWQYIIK
		1				GAIIIFAVALDSLKYARKK
25899	56267	A	26040	687	1106	GSLSLTALLPDTAEREEIRAGLS
230))	30207	` `	20010	007	1	AKMSI/RAIATALNRSPSTISRE/
						VQRNRGRRYYKAVDAN/NRAN
						RMAKRPKPCLLDQ/NLPLRKLV
		ŀ	ļ			LEKLNIQHLRRSHS/LRHGRRHT
						RKGERGTIN/IVNGTPIHERSRNI
		İ				DNSALVTVLR
25900	56268	A	26041	1	2851	MKTLIARHKAGEHIGICSVCSA
23900	30208	^	20041	1	2651	HPLVIEAALAFDRNSTRKVLIEA
1						TSNQVNQFGGYTGMTPADFRE
1						FVFTIADKVGFARERIILGGDHL
			:			GPNCWQQENADAAMEKSVEL
						AVVIDLWSRAVIGWSMSPRMT
		ŀ)
1						AQLACDALQMALWRRKRPRN VIVHTDRGGQYCSADYQAQLK
1						RHNLRGSMSAKGCCYDNACVE
						SFFHSLKVECIHGEHFISREIMR
						<u> </u>
						ATVFNYIECDYNRWRRHSWINS
25901	56269	В	26042	1	1048	LLSQKRNTQGRIEDGRQH
25901	56270	A	26043	323	1290	GTSMNTVGTPLLWGGFAVVVA
23902	30270		20043	323	1290	IMLAIDLLLQGRRGAHAMTMK
1						QAAAWSLVWVTLSLLFNAAF
		l				WWYLVQTE\GRAVADPQALAF
						LTGYLIEKSLAVDNVFVWLML
1		l				FSYFSVPAALQRRVLVYGVLG
1						AIVLRTIMIFTGSWLISQFDWIL
						YIFGAFLLFTGVKMALAHEDES
						GIGDK\RWCAGYA/VHLRMTDT
1					}	
				1		IDNEHFFVRKNGLLYATPLMLV LILVELSDVIFAVDSIPAIFAVTT
]
						DPFIVLTSNLFAILGLRAMYFLL
			}			AGVTKRFSMLKYGLAGILVFIG
						IKRLIVNFNLLQTRACLGGGWA
		<u> </u>				FGETLIIKPGEYRMKTAGG
25903	56271	A	26044	28	96	
25904	56272	A	26045]1	777	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	tocation of first codon for peptide		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
25905	56273	A	26046	77	532	KPSRPEISKGKSVKPAASRRARE
23303	302.3	ļ^^	200.0	' '	332	CAVQALYSWQLSQNDIADVEY
						QFLAEQDVKDVDVLYFRELLA
	ļ 					GVATNTA\YLDGLMKPYLSRLL
						EELGQVEKAVLRIALYELSKRS
		1				DVPYKVAIKEAIELAKSFGAED
						SHKFVNGVLDKAAPVIRPNKK
25906	56274	Α	26047	3	175	
25907	56275	A	26048	85	440	YSSSSLWAARKRRQMVLSARR
						FATSDRVCRCVLVWSAGTSRA
		İ				KSKSTGWLSMASKAIGVSS*TK
						TPTARRVSSSSLPCGMAIPLPIP
						VLPIFSRVRIASKTT*GSSLSCFA
						ARSLMTS
25908	56276	Α	26049	80	706	KLIQVAVVIGGGQPLGAFLCHG
						LAAEGYRFPVVDIQSDK\AANV
						AQEINAEYGESMAYGFGADAT
						SEQSVLALSRGVDEIFGRVDLL
					:	VYSAGIAKAAFISDFQLGDFDR
		1				SLQVNLVGYFLCAREFSRLMIR
						DGIQGRIIQINSKSGKVGSKHNS
		-				GYSAAKFGGVGLTQSLALDLA
		l				EYGITVHSLMLGNLLKSPMFQS
						LLPQ*KTKLGIK
25909	56277	A	26050	741	893	TGCSGKRSLQQRREERRRNPVQ
						KIRCTV*RVRNGRIRYCSPRAGF
						YSRYR
25910	56278	A	26051	269	987	MD A V CD D CD DDWG WD DD C
25911	56279	Α	26052	1	1268	MDAKCDRSRFPWLWPTKRPRG
						CFATFVPIGIPYDQTKTHLHTLS
						LVAKRLADKTICRRLRAAQSDE
						ELYQIITDTEGTPDEARCEEKQY
						MVLMIVSGRSGSGKSVALRAL
					•	EDMGFYCVDNLPVVLLPDLAR
						TLADREISAAVSIDVRNMPESPE
						IFEQAMSNLPDAFSPQLLFLDA
						DRNTLIRRYSDTRRLHPLSSKN
						LSLESAIDKESDLLEPLHGFPDY
						DTVGFSCKRRIDYVCRIKHSRRI
						RQVVLLNFAKSGAFSTTRGTDD
		1				KTRRSLLVTL/VAYFLCAR/EFS
		1				RM/MIRDGIHVRIIQINSKSGKV
						GSKHNSGYSAAKFGGVGLTQS
		1				LALDLAEYGITVHSLMLGNLLK
						SPMFQSLLPQYATKLGIKPDQV
						EQYYIDKVPFKRGCDYQDVLN
25012	56000	 	26052	1	160	MLLFYASPKA\SY\CTGQSINVT
25912	56280	Α	26053	1 .	168	LKVFILVIFTLSRE*EHAMFGFL
1						FLC*FAENDGFQLHPCPCKGHE
<u> </u>	56281	A	26054	2	253	LILFYGCIVFH
25913						

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25914	56282	В	26055	319	3780	
25915	56283	Α	26056	513	762	
25916	56284	A	26057	375	550	GVGLCGRSSIRRNM*CK**G*/L SPKIALMACGRRHTRSLFMTSK DLSRMMRLQKEIRL
25917	56285	A	26058	662	1033	EPKRASGCMWPVGAHCHHPLL LLACQQKLGPPSHQASSRS*NIQ TLDRLCMSSWIPQEHSSSQSWH RSCFLNVTRPWSFYSPVGKNR WMGPFWSFSLDALLLFFTLHSY VAWPVEMMALNLLG
25918	56286	В	26059	1	2034	
25919	56287	A	26060	369	515	HAKPPGGLGHCSLCPSHYSCIH G*KGPRYVSVSCSRGWKPEAT KAFMW
25920	56288	Α	26061	352	2631	
25921	56289	В	26062	10	351	
25922	56290	A	26063	321	537	EPLDTGRGTSHTRACHGVGYW GRDSVRRYT*CK*RINGYSTPT WHMHEYVTNLHIVHMYPRTYS IIIKKMSD
25923	56291	A	26064	788	912	VHTHLSERTRKCLPPPAPS*WV TCHHGDCCLPTRLRAPQGP
25924	56292	Α	26065	1348	1799	
25924 25925 25926	56294	A	26065 26066	543	741	ATYPSAHYPDHNRGEFLWPSL GLGKELDTFWSSLRVFGSPVSA VSRELVRKFSLGGTVDSTGSLP VCGDISPVSDVA/ACTREPLRFR LQVGDRYITLMDLPGVGESGA RDTEYAALYREQLPRLDLVLW LIKADDRALTVDEHFYHQVIGE VYRHKVLFVISQSDKAEPTSGG GQLSTAQKQNISRKICLLHELFQ PVHPVCAVSVRLQWGLKVMA ERMIKCLPREATSPVVSQLHPSF RTTVVREQARSDFGETVGAVL DSISAFPLIPAPVRAVIQAVRTT VVSFAASVTLLLLPLRSTPVEKS PTCILPASETFPLLVVMLNPVAS LLTLTSPVLDTSCPTHSLSAAQP NLIQLSGNNNISFVVNRAVVTN VLNTMRTACNSQATIQIYNADI ARDFGTRGIFSINSGFSTVYSRRI GHQSPEVTGEAMALTLSSQPSC IDDGLVAVNLDTDGLRIGDARQ KAITAGYPVVDTDDKCRIRRLR RIRHEQCADENSYQAYNYCRP VGRIRHLCRIRQSMPDATLSRLI

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	deletion, \=possible nucleotide insertion)
25927	56295	A	26068	3	373	VYTGLKPRTIDAQYTPINVV/W KFLSLTHHAYSPLLVVINKAKF DGLSPEFQQALVSSAQEAGNY QRKLVAEDQQKIIDGMKEAGV EVITDLDRKAFSDALGNQVRD MFVKDVPQGADLLKAVDE
25928	56296	A	26069	I	1107	MGAFTGKTVLILGGSRGIGAAI VRRFVTDGANVRFTYAGSKDA AKRLAQETGATAVFTDSADRD AVIDVVRKSGA*ILILKRRSISSA FNSRASPKTPIPAFTTRISNAPLL RTTSMTASLSALSVNTAVAPVS CARRLAASFDPA
25929	56297	Α	26070	39	254	
25930	56298	Α	26071	1432	1845	
25931	56299	A	26072	674	1614	AVIVVAILVSKSTGAWVAFSIR MPSITFSHNSVVAGVASARKDS SPSYGDPLESAIPKLNVKRSRSG LSKSLLTLTSCSTIWINWITGQT PLKPCSVTGSVVPKAWRSPSTL TTMTTR*PFTLPA/LDTFISRPAG CTYANECHAPESATIRNDVAAR PCNCAQCAALDCVSVFVTIRHS CSSVYSAPGILVAALQAGHKPV ALVGGATGLIGDPSFKAAERKL NTEETVQEWVDKIRKQVAPLP DRKNISPADSRLSPDGRYRGYV HPAPPIPDSHLIRHHRCVIYQWR QCLAQFRLNGWAASRSQSICRI GCD MSSSCIEEVSVPDDNWYRIANE
25932	56300	A	26073		3476	MSSSCIEEVSVPDDNWYRIANE LLSRAGIAINGSAPADIRVKNPD FFKRVLQEGSLGLGESYMDGW WECDRLDMFFSKVLRAGLENQ LPHHFKDTLRIAGARLFNLQSK KRAWIVGKEHYDLGNDLFSRM LDPFMQYSCAYWKDADNLESA QQAKLKMICEKLQLKPGMRVL DIGCGWGGLAHYMASNYDVS VVGVTISAEQQKMAQERCEGL DVTILLQDYRDLNDQFDRIVSV GMFEHVGPKNYDTYFAVVDR
25933	56301	Α	26074	200	1100	
25934	56302	A	26075	1	2061	
25935	56303	A	26076	1	3294	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
-				sequence		
25936	56304	Α	26077	1	2064	MNYSLKQLKVFVTVAQEKSFS
						RAGERIGLSQSAVSHSVKELEN
						HTGVRLLDRTTREVVLTDAGQ
						QLAFRLERLLDELNNTLRDTGR
						YGATTERSARYSASLPAPTSGR
						SEPAALVQNSSSQPSSLKENIM
						KLRSVTYALFIAGLAAFSTFFLA
						\AQSIRCGYETSQADSQHSGAK
						KFNDLLQERPKGELKLKLFPDS
		1				TLGNAQAMISGVRGGTID\MEM
						SGSNYFAGLSPVMNLLDVPFLF
						RDTAHAHKTLDGKVGDDLKAS
						LEGKGLKVLAYWENGWRDVT
						NSRAPVKTPADLKGLKIRTNNS
						PMNIAAFKVFGA\NPI\PMPFAE
		l	ļ			VYTGLETRTIDAQEHPINVVWS
						AKFFEVQKFLSLTHHAYSPLLV
						VINKAKFDGLSPEFQQALVSSA
						QEAGNYQRKLVAEDQQKIIDG
						MKEAGVEVITDLDRKAFSDAL
		ł	,			GNQVRDMFVKDVPQGADLLK
						AVDEPGWAERDIWAFAPAFFY
						PLFISDFNRVRLEFVGHYQDVC
ł						EKPASTTLWLDVGRSSGLDLTY
						QTLNVKNDLSHFPVPFFDPSDN
						RTNTLPMVFAGAPDVGLQQAS
						AIVASWFGSRSGWRGQNFPVL
		ļ				YNQLPDRNAIVFATNDKRPDFL
		1	}			RDHPAVKAPVIEMINHPQNPYV
1		1				KLLVVFGRDDKDLLQAAKGIA
1		1				QGNILFRGESVVVNEVKPLLPA
						GSQPVWSSSASESRCCFYA
25937	56305	Α	26078	1	480	LGNTKTVKGWLAQLPAKYHQ
					ł	RATCMFDRHGLLALLAGRFLA
						FVRTLLPTMAGISGLPNRRFQFF
İ						KAKLR\WLS*PTRIAAALAFMP/
						FMDDHHPRLMQTVILQILQRRG
						TGDRLKIMVERRYAHVGFCRQ
						LLDAQVFGVFILNPFQHAANQT
						EVSLATDQRQ
25938	56306	Α	26079	1	2184	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25939	56307	A	26080	1429	2152	NLFREVVFPTHCPVCGSDVERV
			İ			EGEAVARCTGALICGAQRKESL
				•		KHFVSRRAMDVDGMGDKIIDQ
						LVEKEYVHTPADLFKLTAGKLT
						GLERMGPKSAQNVVNALEKAK
						ETTFARFLYALGIREVGEATAA
				-		GLAAYFGTLEALEAASIEELQK
		ŀ				VPDVGIVVASHVHNF\LPKKAT
		l				AMSSASCWRKVFTGLRRSLSTR
						KRLTARLLVKPWCLRAASGTP
•		l				LKRASLLMFSGCFSHTSGLAMY
25940	56308	A	26081	1	2448	
25941	56309	A	26082	125	741	AHLNRTRWKVCWIR*RKISPW
		`				AKRNTKTVKG\WLAQLPAKYH
						QRATCMF\DRHGLLALLAGRFL
						AFVRTLLPTMAGISGLPNRRFQ
		ĺ				FFNWLSGLLWVSVVTSFGYAL
		İ				SMIPFVKRHEDQCRNGVFGKR
				:		KGGIAAALILTRLRRRFVSSWK
						RFRELRRKSSQADDMNVFGILE
						DFTHQFIGGAFLRADISGAAKM
		l				SCLAKAQASSSMH
25942	56310	A	26083	1066	1359	
25943	56311	Α	26084	256	952	RLKRCSTGKSMAVIQDIIAALW
			ŀ			QHDFAALADPHIVSVVYFVMF
ĺ						ATLFLENGLLPASFLPGDTLLIL
						AGALIAQGVMNFSGLRIAVLDP
						RNQVRGGGLSIFKGRWLGNPK
		1				TVKG\WLAQLPAKYHQRATCM
	ļ	1				FDRHGLLALLAGRFLAFVRTLL
		1				PTMAGISGLPNRRFQFFNWLSG
	İ	1				LLWVSVVTSFGYALSMIPFVKR
1		1				HEDQVMTFLMILPIALLTAGLL
		1				GTLFVVIKKKYCNA
25944	56312	В	26085	1	1290	
				<u> </u>	<u></u>	<u> </u>

SEQ ID			SEQ ID NO:	1	•	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
25945	56313	I A	26086	1	1839	MRCQNA WWIMQHSSGSERLSS
23943	130313	A	20080	1	1039	` `
						VLLHFRRTNLADSNDRIQYHSL
						RFFDEDGAQWLVILGDVLNHG
						PRNALPDGYAPRKVAERLNEV
						AHKVIAVRGNLRQRVDQMLLI
						SRAINRLVASNWNRRSAQMRC
						PISGKNLAWIPVQLPVYWQNN
						CRRLLMRSHRKHGSGTNLPGE
						LMAIKLIAIDMDGTLLLPDHTIS
						PAVKNAIAAARARGVNVVLTT
						GRPYAGVHNYLKELHMEQPGD
						YCITYNGALVQKAAD/GYDDY/
						RF/LEKLSREVGSHFHALDRTT\
						LYTAN\RDISYY\TVHEFLRCHQ
İ						FPLVVCDGGRMTPRAMFLFSSA
						HILMPLNYHNSHINTLFPVAGT
						LMVEPTESESKVELDRFIDAML
						AIRAEIDQVKAGVWPLEDNPLV
						NAPHIQSELVAEWAHPYSREVA
						VFPAALVTGGSRGIGRATALLL
						AQEGYTVAVNYQQNLHAAQE
		İ				VMNLITQAGGKAFVLQADISDE
						NQVVAMFTAIDQHDEPLAALV
		1				NNAGILFTQCTVENLTAERINR
<u> </u>		1				VLSTNVTGYFLCCREAVKRMA
						LKNGGSGGAIVNVSSVASRLGS
		1				PGEYVDYAASKGAIDTLTTGLS
		1				LEVAAQGIRVNCVRPGFIYTEM
25046	56214	ļ_	26097	12	1275	HASGGEAWTRRSR
25946	56314	Α	26087	2	1275	VNFSPKSSQIHHALRTVAGRFA
						VKSIDYFWHDSCNASKRFHIWE
						SIMLELLFVIGYLVMLMVTGVS
						LLGIIAALVVATAIMFLGGMLA
		1				LMIKLLPWLLLAISVVWVIKAI
						KAPKVPKYQRYDRWQLAVRRS
						PLLPDHTISPAVKNAIAAARAR
						GVNVVLTTGRPYAGVHNYLKE
						LHMEQPGDYCITYNGAL/VYRK AAGWLAPLAAKLLKLMDELI
						· ·
						GFLEKLSREVGSHFHALDRTTL
		i				YTANRDISYYTVHESFVATIPLV
					1	FCEAEKMDPNTQFLKVMMIDE
					1	PAILDQAIARIPQEVKEKYPVLK
						APNLQQPHGSSGSSFHREIFFSS
					İ	RSEDKRRGGLVVSGISLLVVSA
				1		GPWVRNANEPLGQLKTWFSLS
						HTLTLTYTRAPACRLTSTQTEP
						RARPCLSPLSSEPRDRSLTPRLG
0.50.4=	56017	<u> </u>	26000	1	1.500	QRFIYLAVQ
25947	56315	В	26088	1	1509	
25948	56316	Α	26089	1	1323	_

SEQ ID NO:	of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25949	56317	В	26090	1	5073	
25950	56318	Α	26091	249	531	CWAMRMDSKVGVITPIRMWSA
	1	ŀ				SGPFAMGTLVPTFAAVTDIPTK
						SVTTCLRQICERWQAPSTR*SRF
						ASLSQPAPRFTPSPITLALVLLP
						ARRC
25951	56319	Α	26092	3	1038	LVLFGVAETYPVANDFAAGAG
						AYVRGRYAAGVRAWPTIITRK
						TMKTLVVALGGNALLQRGEAL
ŀ						TAENQYRNIASAVPALARLARS
						YRLAIVHGNGPQVGLLALQNL
						AWKEVEPYPLDVLVAESQGMI
						GYMLAQSLSAQPQMPPVTTVL
						TRIEVSPDDPAFLQPEKFIGPVY
						QPEEQEALEAAYGWQMKRDG
						KYLRRVVASPQPRKILDSEAIEL
		1				LLKEGHVVICSGGGGVPVT\ND
						GAGSESVIHKDLAAALLAEQIN
						ADGLVILTDADAVYENWGTPQ
						QRAIRHATPDELAPFAKADGSM
						GPNVTAVSGYVRSPVQMHHRQ
						FQPVIIHIATNQIDHHRRIIHHWL
25952	56320	Α	26093	I	3639	MKRLIVGISGASGAIYGVRLLQ
						VLRDVTDIETHLVMSQAARQT
						LSLETDFSLREVQALADVTHDA
						RDIAASISSGSFQTLGMVILPCSI
						KTLSGIVHSYTDGLLTRAADVV
						LKERRPLVLCVRETPLHLGHLR
						LMTQAAEIGGNTGEIDEEELES
						LLYAIAKGNVFNFQTILHLPVA
						VQNDTIDFYQMFARIWSSHPQ
						WLTLYLAQHRAVIIPDDAKLHR
						NLLRWYSAGRLDIPELLDYAQS
						WRETEPDNEDAPY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25953	56321	A	26094	1	1260	AWARQDRRLSVKQWGKPPVD
	20321	1	2009 1	ļ. •	1200	ETIPAKEQVRILRKLFDRYYGE
[VAGRGDGFCSPHVARYVGRVA
						G*RPCRLGPGHPTNRTPFVAPL
ĺ						LEALDIAKYFSVVIGGDDVQNK
						KPHPDPLLLVAERMGIAPQQML
						FVGDSRNDIQAAKAAGCPSVG
						LTYGYNYGEAIDLSQPDVIYQSI
						NDLLPALGLPIAKIRNRKMTKPI
						VFSGAQPSGELTIGNYMGCTEA
						DRQFAFNFNNFVLIQLLTNGGP
						DRLGTTTPAGYTDLLVNYTYRI
						AFEGGGQDFGLAAAIATLIFL
						LVAIMFPLLMVVAISLRQGNFA
						TGSLIPEQISWDHWKLALGFSV
						EQADGRITPPPFPVLLWLWNSV
						KVAGISAIGIVALSTTCAYAFAR
						MRFPGKATLLKGMLIFQMFPA
						VLSLVALYALFAPRVRAALCY
25954	56322	A	26095	l	3240	
25955	56323	Α	26096	494	792	ATRLRHGVTSVGGDGGLQLTV
						MDKLDVILLMSV/NPGFGGQSFI
						PQTLDKL/REVRRRIDESGFDIR
						L/EVDGGVKVNNIGEIAA/AGA
						DMFVAGSAIFDQPDAR
25956	56324	Α	26097	1624	2390	RTSERRWHAKALLKLFSAHHA
						GFVCCKEEEERLATGKVGWLP
						VETLLAQQHIEGHYQVDPSLFK
						PNADCPVRVSGMSMKDIGIMD
						GDLLAVHKTQDVRNDPLLVPL
						FTLIREGKLAANWPLEQDELLT
						RLQKSCDMTQVSADYNALFIG
						DECAVPPYRSAWVEGATEAEV
						RAFLSERGMPLADTPADHIGTL
						LLAASWLEDQSTEDESEALETL
						FKRGA/LPKSLCLWGKAPAPHG
						SPVGGFSKGPKTWAPHEGAS
25957	56325	В	26098	1	534	
25958	56326	A	26099	67	399	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	1	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25959	56327	A	26100	8	1016	PESRRKAVMTQPVLDIQQLHLS FPGFNGDVHALNNVSLQINRGE IVGLVGESGSGKSVTAMLIMRL LPTGSYCVHRGQISLLGEDVLN AREKQLRQWRG/ARVAMIFQEP MTALNPTRRIALQMMDVIRHH QPISRREARAKAIDLLEEMQIPD AVEVMSRYPFELSGGMRQRVM IALAFSCEPQLIIADEPTTALDVT VQLQVLRLLKHKARASGTAVL FISHDMAVVSQLCDSVYVMYA GSVIESGVTADVIHHPRHPYTIG LLQCAPEHGVPRQLLPAIPGTV PNLTHLPDGCAFRDRCYAAGA QCENVPALTACGDNNQR\GAC WYPQQEVISV
25960	56328	A	26101	3	102	ISRLNTQQHFG*RTRQISPHSPQ GCSRCPLHS
25961	56329	A	26102	290	490	SSLNSCMAVWDKTRLIRQ*LV MWSY*SPSPCR*PAGYRHMKL RSTSLVLSTPSRLFLAVIPPVVVI
25962	56330	Α	26103	1	3255	
25963	56331	A	26104	119	634	
25964	56332	A	26105	1640	1770	HLDSNRRVHDSTCNWCCNLS* QRLLWSG*WSELCCSVPRQKR A

SEQ ID	1 .	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ļ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
25965	56333	A	26106	281	2108	RESLKQKVGGRPQLSPFPPPDS
20,00		` `	20100			WALDPGGGRARETPRGVSNAT
						KEPISVAQHGN/GGDKEIRRELK
		1				YYAHLGRRLKDWSGIPRYHGT
	,	1				VETDCGTGYVYDVIADFDGKP
						SITLTEFAEQCRYEEDIAQLRQL
	1	-				LKQLKRYLQDNRIVTMSLKPQ
						NILCHRISESEVIPVVCDNIGEST
						LIPLATWSKWCCLRKQERLWK
		Ì				RFIAQPALAIALQKDLQPQATE
						ASGAENMASIASGNIARTDPDM
						LSIPLSKKICCFGDRIIEIPETIDQ
						PVRFWVLTGPVVDMGIYACYL
		İ				SSPOWGWYAERDAEIENETVR
		İ				REVEELRQASETDLQPGTIEYE
						RHRLTRAQADAQELKNARDSA
						EVVETAFCTFVLSRIAGEIASIL
						DGIPLSVQRRFPELENRHVDFL
						KRDIKAMNKAAALDELIPGLL
						SEYNRADRQYAGGSRVAARFA
						ASPRVAVLSVITGLIPRHVCAPY
			<u> </u>			LLCGDPCCLSTPEDMTPRFRRY
						AVRSGNRSTPGLDHRCDACQR
						SAYELADLRCRPPPSTLFLLPEA
						DKNDFSDALPAVADAMYAAPP
						RRKAAPSKPEKAVVSPLRSVRK
				1		ARHGSVCSLRPDQYAVRNLPA
					ĺ	YRSCSSPDLQFMVWCALA
25966	56334	A	26107	1	2880	1 RSCSSPDLQFMV WCALA
25967	56335	В	26107	61	5101	
25968	56336	A	26109	80	561	IRPLPPRFKTESRSLPGPCLQPGT
25700	30330	``	20107		301	FLWSRNRRVLGFPSMNGEDMG
		l			}	LLFLCSEWERSSEGWLCNREGG
		1				SGHSIEPHCCTFLHLTHRSLAFS
				1	1	LLAGVSCTCASSCKCKE\CKCTS
						CKKSECGAISRNLGLWLKVGR
		İ				EPKAVPEVRASGEPAFLCPCRL
		ł				SLPV
25969	56337	A	26110	1	277	· · · · · · · · · · · · · · · · · · ·
25970	56338	Α	26111	902	1006	
25971	56339	Α	26112	2	1265	
25972	56340	Α	26113	409	525	
25973	56341	Α	26114	91	431	NHKPGNIDVARRIQRGFAGDQI
				1		GHLRPVERQCSPDKRRFIAADG
				i		REIRGKQRAGHIFQLLSRCLLQI
						LNHCQRRAAHFRFQLSNQRHQ
						QLLPV/HYHAAEREYPAGACLV
	<u></u>	L		<u> </u>		RWLL
25974	56342	Α	26115	3	71	
25975	56343	A	26116	li .	1212	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	3	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25976	56344	A	26117		2786	MAAVIEQIRRAVLALVTGVVHP GDIPVVWDIVWNATAAFIAVIII SLLLDESGFFEWAALHVLRWG YGPGRLPFNRIGLIRRITRRIRQR LLFGLVTFILLLNRSQNPAQDIQ LLAFRARTGKQTAQFIHHLPRM VFTDKTGSSNGLAPQGQCSAQ GELILNEKLAKQLVTAANWVK MQSDEGEINPVDILRWPGVMA AQEQDLDAIAAEILAALDGTLD DFIVARETEGQSGLKRVYHSPG APDIREFTRDAIP
25977 25978	56345	A	26118	48	219	EIFSVVWIIMTRGDVVTISRWR VSSSPLETWNKRWAKISPAPFS LLPISRLEKSEGDWLPETVISAF NMPSSLSLIISSL*FKVRDV*HFF /RI*TLRGHYRVINWPNFNIVVS QGIGKRLANSWLVFTLFHRI PETCGHLWAYVWPSCAAV\GL
237,0			20117			YFKVHVLG*RSVTPVTDIVKLL EFTRLRLPGYTKSIE
25979	56347	Α	26120	1	912	

3498

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1	İ		sequence	1	
25980	56348	A	26121	1	1857	MRVCARACVRTRTRMCVYAH
23980	30348	A	20121	I	1037	TCVCVRTYAYVRVRVRVHVRA
ĺ		İ				RVRVCAYARTRVRNSLSILPFIQ
		į				LTLATPIHHIHQEEFNIRGIVPVL
			İ			RRVKPDLAIGIDITPSCDTPDLH
						DYSEVRINQGVGITCLNYHGRG
						TLAGLITPPRLIRMLEQTALEHN
						IPVQREVAPGVITETGYIQLFLP
						GWEIGFSPLALLLAFLCSTSPGF
						GDPDGLGVIAYQDTVRPNAAT
						AISELNALAVKGVILTGDNPRA
						AAAIAGELGLEFKAGLLPEDKV
		İ				KAVTELNQHAPLAMVGDGIND
1		1				APAMKAAAIGIAMGSGTDVAL
						ETADAALTHNHLRGLVQMIEL
						ARATHANIRQNITIALGLKGIFL
						VTTLDDRVVAGSAGRYGGDGA
]				GDSECVKIVAQEIRQTDRNIER
						DRSPRPSGERVRVRGKGGIEAN
						QPLSTAFTNQITIRQSIRLFSNQF
			ı			VFHKGISRVVAGSSAIISNVSPG
		1				CILRTPNCRRGFPISCTGEGKAA
						YGWQRDGGHAEYLLAEEKDLI
ĺ	:					LLPDALSYEDGAFISCGVGTAY
						EGILRGEVSGSDNVLVVGLGPV
					11 13	GMMAMMLAKGRGAKRIIGVD
						MLPERLAMAKQLGVMDHGY*I
						LPDVY/V*IGVARVSWMNGRID
:						SELRTRVRAYAHTRTRARTCTR
						TRTRTYAYVRTHTHVCAYTHM
						RVRVRTHARAHTR
25981	56349	A	26122	3	1180	SKLGTRRSVVWA*SPSTSPTLW
23701	150517	'				CSTFSAAGHSSMKRMNEFVDL
	}					LPAQQRMKGENWYRGTADAV
ľ						TONLDIIRRYKAEYVVILAGDHI
						YKODYSRMLIDHVEKGARCTV
		-				ACMPVPIEEASAFGVMAVDEN
						DKIIEFVEKPANPPSMPNDPSKS
						LASMGIYVFDADYLYELLEEDD
						RDENSSHDFGKDLIPKITEAGLA
		1				YAHPFPLSCVQSDPDAEPYLAR
						CGYAGNFMESEPRSGLIRVSCM
						PAGPPLPLPAARSEAPKAAGTV
						ASVPSIAPARLRPVPDPVELVLV
						AAEFITPGDPTPRLHGSGFIDIR
					1	QIHHQTRSHLEGVKTGIRFLNH
]			}			FSGNPQGGIAHVNGVARFQVK
						QCHQAWGQQYAARLRFQARGI
		\perp				SLQIAIHRVDIIHRFDVRQL
25982	56350	Α	26123	16	543	
25983	56351	A	26124	1	3387	<u> </u>

NO:	SEQ ID SI	EQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
AAVPGTPSILAL TSASMNVPVLT AAKEPSMANA VSTRCS*TITCA ERLIMATILI/W GHDTDVVTLYE LRTPHRRVLRFS SPVA	NO: of	f peptide		in USSN	location of first codon for peptide	codon for last amino acid	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
KDTKGLIARWK VAFALYLAGKE KDVMPQLGLI AGGFALVAWA' HIPYLRHAGELY GNAVNLTDGLI AGGFALVAWA' HIPYLRHAGELY LGFLWFNTYPA ALGGALGIIAVI GGVFVVETLSV QRIFRMAPIHHI 25986 56354 A 26127 1056 1373 1301 SSGTDAGRRYR RRVNRQPAPQQ SSPFSLPAVKLP LAEVRYDSAIS SFSTGSITVTL 1305							LSVGKTFPVLVPAAFRKVSATG AAVPGTPSILALPSYSTTPFGVC TSASMNVPVLTLRIRTRVTGEV AAIKPFSMANAPTPDSILPQLGV VSTRCS*TITCANR*STSARGSL ERLIMATLL/WVAGTFD*SVWF GHDTDVVTLYRFHEALCYSVT LRTPHRRVLRFKSQHPGELACFI SPVA PPHNWMPSNATPGIAFVWCAY
25987 56355							GAI/LPGDAPVPVVDDYRKVVR KDTKGLIARWKYFWMSVIALG VAFALYLAGKDTPATQLVVPFF KDVMPQLGLFYILLAYFVIVGT GNAVNLTDGLDGLAIMPTVFV AGGFALVAWATGNMNFASYL HIPYLRHAGELVIVCTAIVGAG LGFLWFNTYPAQVFMGDVGSL ALGGALGIIAVLLRQEFLLVIM GGVFVVETLSVILQVGSFKLRG QRIFRMAPIHHHYELKGWP
RRVNRQPAPQQ SSPFSLPAVKLP LAEVRRVDSAIS SFSTGSITVTL 25988 56356 A 26129 362 595 25989 56357 B 26130 I 1305 25990 56358 A 26131 I 2022 MISKRSERSFGY SSSEGFFNLHSL STATSTMGIVLE RVALCGGDDYL CSRFGWQVRPS ENQQHLHRGKE CGAACGSLRGE SSQQGKKESG RHDSAHRPKE VKFWRVKCVCV VVCVDGDTYCV PTLRGPDSALGE 25991 56359 A 26132 3 236 25992 56360 B 26133 I 4638 25993 56361 A 26134 1501 1914 SAFSRALTGROI NGAECLLYHVC VGAAVGFSHIEI LADLFVHVARR	25986 5	6354	Α	26127	1056	1373	
25989 56357 B 26130 1 1305	25987 5	56355	A	26128		301	SSGTDAGRRYRPRQRPSKSRNN RRVNRQPAPQQSSRN/SLRPSTT SSPFSLPAVKLPSAP/V*SAGMR LAEVRRVDSAISTVDSR*CPTAS SFSTGSITVTL
25990 56358 A 26131 I 2022 MISKRSERSFGY SSSEGFFNLHSL STATSTMGIVLF RVALCGGDDYI CSRFGWQVRPS ENQQHLHRGKE CGAACGSLRGE SSQQGGKKESG RHDSAHRPRKE VKFWRVKCVCV VVCVDGDTYCV PTLRGPDSALGE 25992 56360 B 26133 I 4638 25993 56361 A 26134 1501 1914 SAFSRALTGRQI NGAECLLYHVCV VGAAVGFSHIEI LADLFVHVARR	25988 5	6356	Α	26129	362	595	
SSSEGFFNLHSL STATSTMGIVLE RVALCGGDDYI CSRFGWQVRPS ENQQHLHRGKE CGAACGSLRGE SSQQGGKKESG RHDSAHRPRKE VKFWRVKCVC VVCVDGDTYCV PTLRGPDSALGE	25989 5	6357	В	26130	1	1305	
25992 56360 B 26133 1 4638 25993 56361 A 26134 1501 1914 SAFSRALTGRQI NGAECLLYHVC VGAAVGFSHIEI LADLFVHVARR							MISKRSERSFGYGVGLVRRQDF SSSEGFFNLHSLRIDINKCLGVRI STATSTMGIVLPEQIKLACNGIQ RVALCGGDDYLTSVDSFDVMF CSRFGWQVRPSSFCSPVFTWVT ENQQHLHRGKDNLSLKNNNSA CGAACGSLRGEKSDPPSARNNP SSQQGGKKESGQQPSLKDPHIL RHDSAHRPRKEKPRQPVNASLV VKFWRVKCVCVHNDHKRPACS VVCVDGDTYCWTEAYPAMGL PTLRGPDSALGERPE
25993 56361 A 26134 1501 1914 SAFSRALTGRQI NGAECLLYHVC VGAAVGFSHIEI LADLFVHVARR					1		
! ! ! ! !	25993 5	56361	A	26134		1914	SAFSRALTGRQHFNNCAFTRFS NGAECLLYHVCQTAFLVARRR VGAAVGFSHIEIVIVPLHLLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRRSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
25995	56363	В	26136	4	2040	
25996	56364	A	26137	804	947	LPCHCSCPWDGDVQPSPTPRQ WT*GERLH*QSEALPGVCCAPG HGPL
25997	56365	A	26138	1	734	SVHIGHQFFQFQSTSLNICPPLH RLFIAFQMNIRRNAAARHAKFQ RLQAQVSIFEDDMSRKIANRQA TAMLNAPPFEANIGIHNVPFIGF EAVIRQHFARRLNAFFALLLFR PFRLFCPFPGINANQRSQVRQPQ LPRLDITFQFWSWLSGGVDQRT VDIVCHQWRSALDRKEYYPAE TTMPTALHSRLCIIVGKIKRPVI VLFREANQARVGLFE/H*STAA RPFWSAAPAGPALPLRVANAPS
25998	56366	Α	26139	2	309	
25999	56367	A	26140	472	885	SAFSRALTGRQHFNNCAFTRFS NGAECLLYHVCQTAFLVARRR VGAAVGFSHIEIVIVPLHLLQQP LADLFVHVARRLSSTMGIRDQR PLPG*LLNNITRWRRSAPVDQT HSQSAGFAVTPENAFVASSGPS RHRHQR
26000	56368	Α	26141	1	2469	
26001	56369	A	26142	1175	1435	
26002	56370	A	26143	218	443	AMARWKMLCTKSPPCVCLPGY P\G*RLAGPHHHHEFPPPAGAAS TGPPIVQDHQSLAGRSRRHDDS RHLGRCHHH
26003	56371	À	26144	1	2031	
26004	56372	A	26145	1419	1875	TFCSPRSQPGSLKRRLRAGAGN CPLYSTGNGPLQRAICCAQPT*L HGRVPSHVPATFSSFQLWSFTV GACIHRSMYIISRSRCPFDPKTK TATMLGITSFVMERCQLFILSRA FTSGQPTCYYPTASSNTWFSST RHCQVINLHSNSMHISL
26005	56373	A	26146	218	441	AMARWKMLCTKSPPCVCLPGY P\G*RLAGPHHHHEFPPPAGAAS TGPPIVQDHQSLAGPRRHDDSR HLVRCHHH
26006	56374	A	26147	1196	1462	LNTLVVAVRDGLKMTTVIANN VTSVSVLKIARNVTRKTILPPAA AANVTPYWLIRTIC*KRRYD*K TRWYYAVAACLCNMGTTRKA NG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26007	56375	Α	26148	45	443	APSDPKRDFPLPHGADSAMAE
						YDRCHRAVLSQGGQWPTALSA
						GDHAAYSLHAALVQPERRCHG
						RCPVRNRLHAPVCPIIPG*RPAG
		1				SHHHHEFPPPARAASTGPSIVQ
						DHQSLAGRSRRHDDPRHFGGC
						ннн
26008	56376	Α	26149	581	957	TSWISFSRTTPSTVSPYSTVDAN
						GIIWSARNRLASVNNIASWLSFF
ļ						SNPLYLAITKPNCRLMMRNGCS
•						TPGPGCWLSCIRC*WAVCSCVD
<u> </u>						AASRFLPCRGARRSASPHPPRQ
						APRRCGALW*PASAETNCSSPC
						SRLPS*LRGCCFKVLTLPGRSAI
						SQSTSTSASSSALWRPLVAGIG
26009	56377	В	26150	1	3924	
26010	56378	Α	26151	597	856	
26011	56379	В	26152	1	2781	
26012	56380	Α	26153	2809	2989	RCGYVRE*LAKSLQSNHFQWR
						MPQHQTAYCRS*AWYRHVAH
						ERLPAQTDNRHQHADRWNG
26013	56381	В	26154	1	2802	
26014	56382	Α	26155	4493	5470	IQRRNHRRDGWCLASLPAGTD
						HAGARAEEAGSWHSGGPHRVR
						ARSVSTPFAPIV\NTATSLKPVR
						QLLDAALKIDHRRTLPKYSFGT
						FRRWYRSVAAQQAQYKDQVA
		1				FFHGCFVNYNHPQLGQDLIKVL
						NAMGTGVQLLSKEKCCGVPLI
						ANGFTDKARKQAITNVESIREA
						VGVKGIPVIATSSTCTFALRDEY
1						PEVLNVDNKGLRDHIELANRW
						LWRKLDEGQ\TLPLKPMTLKVV
						YHTPCHME*MGWTLY/TLELLR
	1					NIPGLE/LTVLDSQ/CC/GIPPIRV
				1		VIHMFRQIEESGADLVVTDCET
						CKWQIEMSTSLRCEHPITLLAQ
						ALA
26015	56383	Α	26156	2467	3465	

SEQ ID NO:	SEQ ID NO: of peptide sequence	l l	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26016	56384	A	26157	5758	7019	LKEGLLEPLAVTERLAIIRWRRP TMNDTSFENCIKCTVCTTACPV SRVNPGYPGPKQAGPDGERLRL KDGALYDEALKYCINCKRCEV ACPSDVKIGDIIQRARAKYDTT RPSLRNFVLSHTDLMGSVSTPF APIVNTATSLKPVRQLLDAALK IDHRRTLPKYSFGTFRRWYRSV AAQQAQYKDQVAFFHGCFVN YNHPQLGKDLIKVLNAMGTGV QLLSKEKCCGVPLIANG\FTDK ARKQAITNVESIREAVGVKGIP VIATSSTCTFALRDEYPEVLNV
						DNKGLRDHIELATRWLWRKLD EGKTLPLKPLPLKVVYHTPCHM EKMGWTLYTLELLRNIPGLELT VLDSQCCGIAGTYGFKKENYPT SQAIGAPLFRQIEESGADLVVTD CETCKWQIEMSTSLRCEHPITLL
26017	56385	В	26158	1	2247	
26018	56386	A	26159	882	2372	HAVHESPPECRSNQQRPTRTCR TIIDIMEMYHALHVSWSNLQDQ QSIDERRVTFLGFDAATEARYL GYVRFMVNVEGRYTHFDAGTH GFNAQTPMWEKYQRMLNVWH ACPRFLFDLDGTLVDSLPAVER AWSNWARRHGLAPEEVLAFIH GKQAITSLRHFMAGKSEADIAA EFTRLEHIEATETEGITALPGAIA LLSHLNKAASGVTNKGFLTVD EIRRVTRAFARLGTEKVRLTGG EPSLRRDFTDIIAAVRENDAIRQ IAVTTNGYRLERDVASWRDAG LTGINVSVDSLDARQFHAITGQ DKFNQVMAGIDAAFEAGFEKV KVNTVLMRDVNHHQLDTFLN WIQHRPIQLRFIELMETGEGSEL FRKHHISGQVLRDELLRRGWIH QLRQRSDGPAQVFCHPDYAGEI GLIMPY\DKDF\CATCNRLRVSS IGKLHLCLFGEGGVNLRDLLED DTQQALEARISAALREKKQTH FLHQNNTGITQNLSYIGG
26019	56387	A	26160	68	399	NKVKPRGDSV/PGSPHSPRLLSP PPLPGLLLWR/PLEEPFSPPLHC GSPFLGWPRPGGRGLGG/PPHSE QPASLSLPPTPRAPVRPEPPRRA PPPAPRRPVPSTTQGLRNASAP

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	in USSN	location of first	codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	detetion, (=possible nucleotide insertion)
26020	56388	Α	26161	207	479	PWSDGAGPLPSLPHPDGRG*SV
						NSPQVLL**GSGE/PRASDSPLP
						QLCGVSPHRPTWGSALWGGEQ
						CTSEMGETIDPPGPHTFSKNFCF
26021	56389	В	26162	1	453	ELQ
26021	56390	A	26163	1	379	
26023	56391	A	26164	11	1054	MFLQAAQKAWNPHLLLVRTQ
20023	30371		20104	1	1054	AASTHGRRADPHVGRCGETPQ
				ļ ·		SWGKGESLALAPLSLTKAALED
						CSQISPSHQGTLLCLLILDLRTG
		1				KLSLEHTEEPSDVPSHLLYRWSI
						SSAITEVFQALASSDSTSQPVNV
						HTKEDMKVQDIALVLPSRKSR
		1			,	NACRTTTSTCKALLMRQLAAR
						VILONCVSKSSRGIHVPOKNLT
						LPVRGDSVLAGSPHSPRSLSAPP
						LPGLPLWRHLKSPSAHRCTVGG
						PFLGWPRPEPAPSACREALAAF
						P/PGQGSGPAAR\QPEPPPPPWA
						PVQPESPRQAPPPAPRSPVPSTT
		-				QGLRSTGTKHRDWQAAPPAAP
						VRDPLGEASWAPESGGDVENL
26024	56392	A	26165	2	362	EMSRLYRSRDRD/GVCLQ/IEVK
		-				MVSRTEANIDDSLIGGNASAEA
						PEGEGTESTVITGVDIVMNHHL
		-				QETSFTKEAYKKYIKDYMKSIK
						GKLEEQRPDRVKPFMTGAAEQI
						KHILANFKNYQ
26025	56393	Α	26166	35	359	
26026	56394	Α	26167	22	459	
26027	56395	В	26168	102	431	
26028	56396	Α	26169	85	674	RRRRLPSVAIMIILPGPSSSHDE
						MF\SDISKIR\EIADGVCAWKVE
						G\KMV\SRTE\GTID\DSLIGG\NA
						SAERPRGAKGTERHQLITGV\DI
		1				VMTP\HL\QETKFSQKEASKK\YI
						K\DYMKSIKRET*KNRRPEKSK
						TFL*PGAAEQIKHILANFKN\YQ
				1		FFI\GENMNP\DGMVALLDYP*D
						WVVTPYMIFF*GWV*KWEKC
26029	56397	A	26170	1	1640	
26030	56398	Α	26171	1	1527	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26031	56399	A	26172	61	2560	PGFCHPRKAYSSYGQRSKGSQK
20031	30377	`	20172		2300	MKASSGRCGLVRWLQVLLPFL
		l				LSLFPGALPVQIRYSIPEELAKN
		l				SVVGNLAKDLGLSVRDLPARK
		1				LRVSAEKEYFTVNPESGDLLVS
						DRIDREQICGKQPLCVLDFDTV
						AENPLNIFYIAVIVQDINDNTPL
						FKQTKINLKIGESTKPGTTFPLD
						PALDSDVGPNSLQRYHLNDNE
						YFDLAEKQTPDGRKYPELILKH
			}			SLDREEHSLHQLVLTAVDGGDP
		l				PQSGTTQIRIKVTDANDNPPVFS
						QDVYRVTLREDVPPGFFVLQVT
						ATDRDEGINAEITYSFHNVDEQ
						VK:HFFNLNEKTGEITTKDDLDF\
		1				EIASSYTLSIEAKDPGDLAAHCS
						IQVEILDDNDCAPEVIVTSVSTP
						LPEDSPPGTVIALIKTRDRDSGE
ŀ						NGEVYCQVLGNAKFILKSSSKN
						YYKLVTDGALDREEIPEYNLTI
		ŀ				TATDGGKPPLSSSIIVTLHISDV
						NDNAPVFQQTSYMVHVAENNP
		İ				PGASIAQISASDPDLGPSGQVSY
						SIVASDLKPREILSYVSVSAQSG
						VVFAQRAFDHEQLRAFELTLQ
						ARDQGSPALSANVSLRVLVGD
						LNDNAPRVLYPALGPDGSALFD
						MVPRAAEPGYLVTKVVAVDA
		-				DSGHNAWLSYHVLQASEPGLF
		1]		SLGLRTGEVRTARALGDRDAA
1		İ				RQRLLVAVRDGGQPPLSATATL
						HLIFADSLQEVLPDLSDRREPSD
26032	56400	Α	26179	47	325	ATMRLSVCLLLLTLALCCYRA
		1				NAVVCQALGSEITGFLLAGKPV
						FK\FQLAQFKAPVEAVASNMEA
						INCVDTM\AYEKRVLITKTLGKI
						AEKCDR
26033	56401	A	26180	1	3747	
26034	56402	Α	26181	2776	2874	
26035	56403	Α	26182	89	369	
26036	56404	Α	26183	382	555	
26037	56405	A	26184	2	67	
26038	56406	В	26185	1	444	
26039	56407	Α	26186	1129	1275	
26040	56408	Α	26187	61	313	WIPHQGYRWSCLPVPRCALAFL
				1		SPWVVDGTGHRGAGGGAGWG
				}		GFGRTGAHG\GVGGSGMAGCR
						SRAHSGGVGMTMTWQIIPEVP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26041	56409	A	26188	61	433	WIPHRGCRWSCLPVPRGALAFL SPRVVSGTGRRGAEGGARRGG SGRTGAHGVGGRLRHGGLQVP SLAPREGSCTCGG\GSGAREEQ NLGFPREPRSGGGARGSDGICG
0.6040	56410	ļ. —	26100	207	500	MRVMFRKWILFCPSSR
26042	56410	Α	26189	297	599	
26043	56411	A	26190	370	585	
26044	56412	Α	26191	222	799	
26045	56413	Α	26192	346	634	
26046	56414	В	26193	206	955	
26047	56415	Α	26194	281	549	
26048	56416	Α	26195	1981	2337	TRVDMIHYGLRKGPGETPS*SL
					·	RSFRAGQTGASRARGLTLLSSH SSALRKGSPKHFCTLCWQTFLA WCVWKVAFSPSRCQTQFDLGK STQWTLEILTDPKSHLFSRKQQ PQARAPAVFPAPLKGCHVGAR GSHCQGFQGCFRPSVAPLILGT DGFSLLEKLWTFKTC
26050	56418	A	26197	165	374	RVTVQWL*YLRPRMP*N*PRPR SGKPFIDSTHSSHR*RQRNAVSL FSPVMSALRRCSVHRRLPDGGV VA
26051	56419	A	26198	357	981	HWRGDVLRRSHRRTALQSRYF CGIYRSP/YKAR/MQIQFFDPQQ MEAAQKRLTEESDILNALENHQ FAIWLQPQVEMTSGKLRGISKQ LVGFTNRQNGATKLLVQYFTH RQIDCAGTADQPNPAGKVDDC GVTGNVTDRQQGKQHGQAKE NELQNACAFQRAEEHKQRKYA PQTQVDTKELCIWRIGQTQFRH QQNRNQRHAERTNHFGVR
26052	56420	Α	26199	1	2601	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26053	56421	Α	26200	1	1236	MGPGDLPRGLATFWTELGLLS
		l				WARELARMPAVEMPPRSCPGR
		l				SRLSCSIGVAMFYGDLTAEQLY
						SRAISAAFTARHKGKNQIQFFD
		ŀ				PQQMEAAQKRLTEESDILNALE
						NHQFAIWLQPQVEMTSGKLPG
		1				KSAAIMLPLSVNLSALQLMHPN
						MVADMLELLTRYRIQPGTLILE
						VTESRRIDDPHAAVAILRPLRN
						AGVRVALDDFGMGYAGLRQL
						QHMKSLVRLTKSEVSSETDQDE
						LPLAKVSEVDEAKRQWLQGMR
						HPVDTVTEPEPAEILAEFIRQHS
						AAGQLVARAVFLSPPYLVAEEE
						LSVLLESIKQNGDYADIACLTG
						SKDDYYYSTQAMSENYAAMSL
						QVVEQDIFSP\IAHAVRFECQTY
			İ			PRPYKVAMLMQAPYYFQEAQI
						EAAIAAMDVAPEYADIRQGIVG
26054	56422	Α	26201	l	1161	
26055	56423	Α	26202	1	1038	
26056	56424	Α	26203	1	1472	MVRLCIRLPIRVYAKVVDKNAL
						SLWMRERSDLWVQPKVDGVA
						VTLVYRDGKLNKAISRGNGLK
						GEDWTQKVSLISAVPQTVSGPL
1	İ	1				ANSTLQGEIFLQREGHIQQQMG
						GINARAKVAGLMMRQDDSDTL
						NSLGVFVWAWPDGPQLMSDRL
					ļ	KELATAGFTLTQTYTRAVKNA
						DEVARVRNEWWKAELPFVTD
				1		GVVVRAAKEPRIPPLATGPGRV
						AGGLEISTCSSGCRSEGNEPGKI
						SVVASLAPVMLDDKKVQRVNI
						GSVRRWQEWDIAPGDQILVSL
						AGQGIPRIDDVCPSDPAILSDIVP
						SW/VTTQW/LKKRAVSSRMMK
						NQ/VKKGSETGYFDKDEARFQK
		l				EGFRVVPPAALRQGAFIARNTE
						LRPSYVNIGAYVDEGTMVDTW
		1				ATVGSCAQIGKNVHLSAGVGIG
						GVLEPLQANPTHEDNCFIGARS
		1				EVVEGVIVEEGSVISMGVYIGQ
						STRIYDRETGEIHYGRVP/AGKV
		1				DAKTRGKVGINELLRTID
26057	56425	A	26204	240	455	RLHPPYYRGWIFEEVPVISMGV
						YNGQSTRIYDR/ETGEIHYGRVP
		1				AGSVVVS\KVDAKTRGKVGINE
		1	1	1	1	

SEQ ID NO:	SEQ ID NO: of peptide sequence	L	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26058	56426	A	26205	197	1043	YEKSLTMQQLQNIIETAFERRA EITPANADTVTREAVNQVIALL DSGALRVAEKIDGQWVTHQWL KKAVLLSFRINDNQVIEGAESR YFDKVPMKFADYDEARFQKEG FRV\VPPAA\VRQGA\FIARNTVL MPSYVNIG\AYVDEGTMVDTW AT\VGSCAQIGKNVHLSGGVGI GGVLEPLQANPTIIEDNCFIGAR SEVVEGVIVEEGSVISMGVYIG QSTRIYDRETGEIHYGRVPAGS VVVSGNLPSKDGKYSLYCAVIV
26059	56427	A	26206	1	406	KKVDAKTRGKVGINELLRTID MGKKNWNTLGEGVCSCRMFL PDANTLAKNSACSAASAVQAA DRPDSQEAEALEHMAHSRCAL RCQTLVIVHVSLMRVSWYHSVI IVVPLTEPLLESLVRCRLRSRRD DVPVAPAVSATPRREP\SVLRIA ERTNA
26060	56428	A	26207		2574	MWAFRGKRPVTLKILHVPITNL RKNITSTRGLTKESSQGKLVRA QEEYTPAREIAKMG\GNPCRPG GIVFAGER*DVTSPYV*TSTRGL TKESSQGKLVRAQEEYTPAREI AKMGWQSLPARRYCLCWRKIR RYITLRLNIAYAGGYKAPVEDI ALWMETDGACDHVDFTWNIPS KCQGPMDIVSRPVFWHAHGIV LFAGARNLNPTLTRIPPYLWLL TLRTGYAAAGMQALALDSRGS PDAVVLSTQHSEEIDQ
26061	56429	Α	26208	1	3771	
26062	56430	A	26209	239	451	LPPTAWMSTTNLTSAMLSVRG NVPMTLPARRRVNLPSSLICTCF HKPA*RISMPKPVW*KARIISGN STS
26063	56431	Α	26210	1	2079	
26064	56432	Α	26211	1573	2562	
26065	56433	A	26212	275	643	SSRTALFTGSAVPGCAPPSGRSL FPQCLQSKLARSFPIRCSRSGAA ILFRRLSFSPGTELILEDR/IVKRF MRENSRGPQVPAGLPMTEEQL KKLGGRQLRALGKLMPGEEE\S VLRIAERTNA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	The state of the s	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26066	56434	A	26213		899	MGRTTRRDAAQAPGTRRSGDS RGYPYVTRPEGTDADDPQKDK AALGSHRVAGQPELFSIDELTR RDPHSASGAWTARYTVSTIAAF ALVIANRLYTIEEEATTPSGCGP ASSSTSSRGVDMCLRNLCMHG YDATIPLTLIAADSMDEYNKPD LSHVISQGQRADDLTRQTAGEF AEQFNLHLFPQTWVTDIDAEAR VVKSQNNQWQYDKLVLATGA SAFVPPVPGRELMLTLNSQQEY RACETQLRDARRVLIVGGGLIG SELAMDFCRAGKAVTLIDNAA SILASLMPPEVSSRLQHRLTEM GVHLLLKSQLQGLEKTDSGIQA TLDRQRNIEVDAVIAATGLRPE TALARRAGLTINRGVCVDSYLQ TSNTDIYALGDCAEINGQRD*SS ARRVVPGRFPGAVRWRQLPHP LRYCAGGPALPECQNPFFPAPV
						TEISTADERPSPSTDAASGCLLP VALTTPEYWQRCRLA
26067	56435	A	26214		1264	MDYMVPVGMDWLCRETAGM RVSIKKGSVVFPLNPELVMKVV RQRSTIVTPSGFKAGAFNFERFK EASNQTLGSTFLYSLSCPKPNL GSQPLDFDTKKSYTLKVEAAN VHIDPRFSGRGPFKDTATVKIV VEDADEPPVFSSPTYLLEVHEN AALNSVIGQVTARDPDITSSPIR LYRIPGDDAKCVQFNREGVKA LKAKPVEKAAPAPAAAAPKAA PTPAKPMGEQLALYRMAGSNA DRIQGRMDPTRGQSAAEWLQT AEEADIAWVLKTYGEERFAKRI ARAIVERNREQPMTRTKELAEV VAAATPVKDKFKHPATRTFQA VRIWVNSELEKIEQALKSSLNV LAPGGRLSIISFHSLEDRIVKRF MRENSRGPQVPAGLPMTEEQL KKLGGRQLRALGKLMPGEEE\S VLRIAERTNA
26068	56436	В	26215	64	663	
26069 26070	56437 56438	A B	26216 26217	27	791 1638	
26071	56439	A	26218	1	375	STKKQRGEIHHPDGHGIAQDRH LPRTSVDQRPLRQTNHPAGL*Q ANG*GVFKRCRAHSATT**KDD E*NESAENAA*GGKVEGTDVT GDLLHENPAITPDKCEHNQATD CQWVALSCGRHERSSV

SEQ ID	1 -	1	SEQ ID NO:	1		Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26072	56440	Α	26219	213	407	TTCCCTNLSIPLANKYRSLSPQS
						DWRLSMPR*NRYVQKAPARAN
						KTSPMKAPPANIALGVNVAR
26073	56441	Α	26220	l i	1179	
26074	56442	Α	26221	176	569	WPMRHTFSEAHAAQRAGGKNP
						GHDTADYATNAVHTEDIAGIIH
						PQQAFEHGNAPQARQTSYHAD
						NQRAANPNVAAGWRHADQTG
						NRARTRPQQ*RLTTQRPFTEDP
				:		AKNCRRRCDHSIHKCQCRDFIR
						RAR
26075	56443	Α	26222	1442	2309	
26076	56444	Α	26223	155	2929	HLHWFVFSGWFTVTRLAFGEG
						NNFFGNINWLMLKNIELTAVM
						GSIYQYIHVAFQGSFACITVGLI
						VGALAERIRFSAVLIFVVVWLT
						LSYIPIAHMVWGGGLLASHGAL
İ						DFAGGTVVHINAAIAGLVGAY
						LIGKRVGFGKEAFKPHNLPMVF
}						TGTAILYIGWFGFNAGSAGTAN
					-	EIAALAFVNTVVATAAAILGWI
						FGEWALRGKPSLLGACSGAIAG
						LVGVTPACGYIGVGGALIIGVV
						AGLAGLWGVTMLNAC
26077	56445	A	26224	2	1064	
26078	56446	Α	26225	1849	2515	MEGHLWIRIDLSQSAVSHSVKE
j						LENHTGVRLLDRTTREVVLTD
						AGQQLALRLERLLDELNSTLRD
		İ				TGRMGQQLSGKVRVAASQTIS
						AHLIPQCIAESHRRYPDIQFVLH
						DRPQQWVMESIRQGDVDFGIVI
						DPGPVGDLQCEAILSEPFFLLCH
					1	RDSALAVEDYVP\ALPLPEGSPL
						VVKRITPVVERQLMLVRRKNR
						SLSTAAEALWDVVRDQGNAL
						MAAA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26079	56447	A	26226	102	1655	RKQMNYSLKQLKVFVTVAQEK
20077	150447	^	20220	102	1055	SFSRAGERIGLSQSAV\SHSVKE
			ļ			LENHTGVRLLDRTTRAVVLTD
						AGQPLALRLERLLDELNSTLRD
						TGRMGQQLSGK\VRVAASQTIS
		İ				AHLIPQCIAESHRRYPDIQFVLH
		İ				DRPQQWVMESIRQGDVDFGIVI
						DPGPVGDLQCEAILSEPFFLLCH
			ı			RDSALAVEDYVPWQALQGAKL
			ļ			VLQDYASGSRPLIDAALARNGI
						QANIVQEIGHPATLFPMVAAGI
						GISILPALALPLPEGSPLVVKRIT
						PVVERQLMLINVIQTLRFAFIFR
						LSRRQHFAKVTPLLHRHGDYF
						VFIGFDYGTANCSVAVMRDGK
	ł					PHLLKMENDSTLLPSMLCAPTR
						EACGRVDVIEVSKSKVRKNTY
		1				AMRYVAGQPAERILPPGSFASI
	İ	l				GQALPPGEPLSTEERIRILVWNI
						YKQQRAEWLSVLKNYGKDAH
						LVLLQEAQTTPELVQFATANYL
						AADHVPAFVLPQHTSGVMTLS
						AAHPVYCCPLRERKPILRLAKS
						ALVTVYPIFPYLSNS
26080	56448	Α	26227	159	290	
26081	56449	Α	26228	562	774	VLRMIT*SKSQFAQDMCRNVLL
						INNFGRIQHDPAIFHFQRNEAVP
						LWTVSAQEVKKDFTSGLRHGS
						VRGDL
26082	56450	Α	26229	50	409	GYASQALILASIPAASRPSSARIS
						S*VPCGIKKSGRPMFSTGTGLR
						WAISTSFTPLPAPPIMAFSSTVTS
						ASWLAAISRINASSSGFTKRIST
		l				SVAFSDSATFAASSTNSRNAPPP
						VEM
26083	56451	A	26230	405	626	
26084	56452	Α	26231	1	1528	
26085	56453	В	26232	1	1755	
				1	1	L

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26086	56454	A	26233	152	2099	GNRLLVVSFIAFSKNSTHFKGIF AMRIILLGAPGAGKGTQAQFIM
						EKYGIPQISTGDMLRAAVKSGS
						ELGKQAKDIMDAGKL\VTDELV
				1		IALVKERIAQEDCRNGFLLDGF
						PRTIPQADAMKEAGINGHYVLE
						FDVPDELIVDRIVGRRVHAPSG
		1		-		RVYHVKFNPPKVEGKDDVTGE
		ŀ		ł		ELTTRKDDQEETVRKRLVEYH
						QMTAPLIGYYSKEAEAGNTKY
						AKVDGTKPQIYRGSLYVSDQIG
						HTIVNPDGVVCDCGRYGCLET
						VASLSALKKQARVWLKSQPVS
						TQLDPEKLTTAQLIAAWQSGEP
						WITSWVDRSANAIGLSLYNFLN
						ILNINQIWLYGRSCAFGENWLN
						TIIRQTGFNPFDRDEGPSVKATQ
	ŀ				}	IGFGQLSRAQQGVDLGNMIITS
		ŀ				GQIPVNPKTGEVPADVAAQAR
ł						QSLDNVKAIVEAAGLKVGDIV
			1			KTTVFVKDLNDFAPVNATYEA
						FFTEHNATFPARSCVEVARLPK
į						DVKIEIEAIAMLYTGYHYNDAP
						SAVRYPRGNASGVELTPLEKLP
						IGKGIVKRRGEKLAILNFGTLM
						PEAAKVAESLNATLVDMRFVK
						PLDEALILEMAASHEALVTVEE
						NAIMGGAGSGVNEVLMAHRKP
1						VPVLNIGLPDFFIPQGTQEEMRA
						ELGLDAAGMEAKIKAWLA
26087	56455	Α	26234	935	1020	
26088	56456	Α	26235	145	373	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	1	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26089	56457	A	26236	530	1865	RGNKRLDLMFKQSHASMYIKQ
l				•		PEQLDYQLNLKEVITAVFISMV
						VLNISPTLY/PDKPSPKDKYVAY
						AINIPDYELAADVYNINVTSPSG
		İ				QQETFKILINLEHLRQTLERKSL
						TAVQKSQCEIITPKKPGEAILHA
						FNATYQQIRENMSEFARCHYG
						YIQIPPVTTFRADGPETPEEEKG
						YWFHAYQPEDLCTIHNPMGDL
						QDFIALVKDAKKFG\IDIIPDYTF
						NFMGIGGSGKNDLDYPSADIRA
	ľ					KISKDIEDPVTKERKQIHPEDIH
						LTAKDFEASKDNISKDEWENLH
	İ					ALKEKRLNGMPKTTPKSDQVI
						MLQNQYVREMRKYGVRGLRY
						DAAKHSKHEQIERSITPPLKNY
						NERVHNTNLFNPKYHKKAVM NYMEYLVTCQLDEQQMSSLLY
	}				}	ERDDLSAIDFSLLMKTIKAFSFG
					Į.	GDLQTLASKPGSTISSIPSERRILI
26000	56450	Α.	26237	14	2031	LIVLS*QHG/DLRQNRSGAEHFG
26090	56458	Α	20237	14	2031	LQRLMLHASQLSLTHPFTGEPL
						TIHAGLDDTWMQALSQFGWRG
						LLPENERVEFSAPSGQDGDPTL
						GLIKEVACELSGMMRRSQPWE
1						EAEESIPDRGESLLEVSGTPNAG
						WGAEGLAEREALLLCCCCGPM
1						GPDPLGLGSPGSVRGRSRLIHH
						AISGEALWEVTSEGLDMAAAR
						QFAIEKGAPALRAMTFIERAAM
ŀ						LKAVAKHLLSEKERFYALSAQT
		1				GATRADSWVDIEGGIGTLFTYA
						SLGSRELPDDTLWPEDELIPLSK
						EGGFAARHLLTSKSGVAVHINA
						FNFPCWGMLEKLAPTWSGRNA
						SHHQTSYRDGPLTQAMEFEDK
						AQQRDVETARHFTFFRIIANED
						KKTGFPRFQTIVITASHKTIDRT
						RYTYGAWRCYRPLLTVEEYRA
						TGSLITQPKFPPHKSSEVHRVPR
						NQGRFVAVNSTLPTEPATVAPV
						RNGNASRDTAKTQTAERPSTTR
						PARQQAVIEPKKPQATVKTEPK
		1				PVAQTPKRTEPAAPVASTKAPA
		1				ATSTPAPKETATTAPVQTASPA
		1				QTTATPAAGAKTAGNVĢSLKS
		1				APSSHYTLQLSSSSNYDNLNGW
		1				AKKENLKNYVVYETTRNGQP
		1				WYVLVSGVYASKEEAKKAVST
					[LPADVQAKNPWAKPLRQRHRD
	1				[LRGDERRDDRRSEYFNRQVIS
<u> </u>	1	1	<u> </u>	l	L	

SEQ ID NO:	SEQ ID NO: of peptide sequence	•	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26091	56459	Α	26238	732	1025	HEAKRTGRSYWFTAV*WLRG
						WRRMVARQNAKNCWHGTFFR
						VARVSLPISAHASSTHLSGSAH
						YVPPSAYRNSRRYSRGLCRCRV
						SSCDAATGVVVPQ
26092	56460	Α	26239	1905	3087	RVCSCDAGTLHWLQNLRCGLP
İ						VWCDGSGGTSGDPQQRRGSEC
		İ				TG*QSRSQ*MRPVQPS*RRPGV
						YGGLPDS\WLICVDRNKLEQLT
		1		-		PEKRRQAKLRAMKPDEFAQIQ
				,		QAVITQMLQHPQTLGEEASKLS
						KDFDRGNMRFDSRDKIVAQIKL
]						VTPQKLADFFHQAVVEPQGMA
		:				ILSQISGSQNGKAEYVHPEGWK
						VWENVSALQQTMPLMSEKNEQ
		ŀ				NLYDCGALFAPVTWTSGSAAF
						PRPLTVEELLVVTFTEAATAEL
						RGRIRSNIHELRIACLRETTDNP
						LYERLLEEIDDKAQAAQWLLL
						AERQMDEAAVFTIHSFCQRML
						NLNTNECCFQRTTKTIHRDSFK
						STPRAAKSCSGLLPALAPSQISS
						NTPIQPLSRFKFSGVTSPTSAAS
26093	56461	Α	26240	1	2235	
26094	56462	Α	26241	166	416	CHVVGPFRVRRNLISAQH\PLTL
						NS\RHTTTRAARRLLRYFGTPR
		1				YRHSIDIHMQLDMTTSRSLSSL
		}				RDQLHCRWLLPAERQAI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26095	156463	Α	26242	1	2084	MLFPLATSGAMEPFPFLAGTAG
20093	30403	^	20242	'	2004	ALVGGLQNIGSGVLASLSAMLP
						· ·
					i	QTGQPGVVDDLNGIVDRAVLA
1						AAGDADVASGAARLSARHRSI
	1		ļ			VISSMGERCCFIRSRITRICGHWI
	1					CPQGNEIPVVAVASHDTASAVI
			:			ASPLNGSRAAYLSSGTWSLMG
	İ					FESQTPFTNDTALAANITNEGG
						AEGRYRVLKNIMGLWLLQRVL
						QEQQINDLPALISATQALPACRF
						IINPNDDRFINPETMCSEIQAAC
	1					RETAQPIPESDAELARCIFDSLA
						LLYADVLHELAQLRGEDFSQL
	-					HIVGGGCQNTLLNQLCADACGI
ĺ						RVIAGPVEASTLGNIGIQLMTLD
	1					ELNNVDDFRQVVSTTANLTTFT
						PNPDNSLYTTDKGALRMTTQL
ļ		1				EQAWELAKQRFAAVGIDVEEA
		1				LRQLDRLPVSMHCWQGDDVSG
		ŀ				FENPEGSLTGGIQATGNYPGKR
						VMPVSYVPIWNSTLSLSGSNWF
		1				NRKALGSPARYDVLPKWWRN
						VVKPTRTRLYIGIAFYKVGEPS
						KIEPDWMINGGVPELKKQLDL
						NDAVPEISGTILFREDYRNKPQT
						QQAADPPIRAKAAEIAVAHAH
1	}	1				YLSIEFYRIVRIDPHAEEFLSNEQ
1				ļ		VERQLKSAMERWIINVLSAQIR
						PQPAVT\HYRGLATVEMPVATG
1	1					RYPTTRY\GLVELEPKTGRKHQ
						LRRHLAHLRHPIIGDSKHGDLR
						QNRSGAEHFGLQRMER
26096	56464	A	26243	1	2871	ZITTOGALIII GEQRINER
26097	56465	A	26244	690	824	
26098	56466	A	26245	950	1484	
20098	130400	JA.	20243	טכבן	1464	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
ł	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26099	56467	Α	26246	1	2625	MVAFYRHAGRMWPGIALSCSL
		1				GNIAASILLFSTSSLNMTWTTINI
						VEAVVGAVLLRKLLPWYNPLQ
						NLADWLRLALGSANSAGVNIS
1						TATVCRQCEDAPCANVCPNGAI
						SRDKGFVHVMQERCIGCKTCV
ŀ						VACPYGAMEVVVRPVIRNSGA
						GLNVRADKAEANKCDLCNHRE
						DGPACMAACPTHALICVDRNK
						LEQLSAEKRRRIPGNIRRIRSGR
						YRRPVTAGCDAVVSGRAGYAI
						HDGGNNSMAKNTSCGVQLRIR
						GKVQGVGFRPFVWQLAQQLSH
						GSRMRDGTCNLKYDEYSRSGS
						MQYNPLGKTDLRVSRLCLGCM
1						TFGEPDRGNHAWTLPEESSRPII
						KRALEGGINFFDTANSYSDGSS
						EEIVGRALRDFARREDVVVATK
						VFHRVGDLPEGLSRAQILRSIDD
						SLRRLGMDYVDILQIHRWDYN
						TPIEETLEALNDVVKAGKARYI
						GASSMHASQFAQALELQKQHG
						WAQFVKSDENDAPDRQSGSTG
						SQCKNCGADTEPQVAAGPGLS
						ELNPVHCPHLHYRAHFRADRH
		1				SVACSLLDTPVTGHQVAPTYRQ
						QVPRAGQVHDPSKHTRMPCEN
						IDPVRTIIRRISDPPVPASATLGA
1		ŀ				SKASRIRPRRSHSIPEITAKSRKP
						GGQPKWQVICWLDRDEKVVV
						MQTVRDQIGQHVFTAHRLDRP
į						TSGVLLMGLSSEAGRLLAQQFE
26100	56468	A	26247	1	1833	
26101	56469	A	26248	1	517	MRNKLSFDLQLSARKAAIAERI
20101	,	` `				AAHKIARSKVSVFLMAMSAGV
						FMAIGFTFYLSVIADAPSSQALT
						HLVGGLCFTLGFILLAVCGTSLF
		l				TSSVMTVMAKSRGVISWRTWL
						INALLVACGNLAGIACFSLLIWF
						SGLVMSENAMWGVAV\YTAPR
						AKCIIHLLNLSASALCAI
26102	56470	Α	26249	3117	3527	EAVHRLARYRDAPRRS**SPLL
20102	50470	<u> </u> ^	2027)	211/	3321	CASVYP*LEQVPLQAQAVVPLR
						VLQAGKPVVPVAVLNAQAAAL
		l				ARPVAKLAAATAVQAAADRQ
						AAAPAALDAEHVAAVPALQAA
						AGPVDAAAQTHKAVGTGVAA
						TDEQPHAPER
L	L	L			1	IDEQUIATER

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26103	56471	IA	26250	2	563	STTSSTTAFSATTAGTPSTGNTP
						SASPIWRRPNFWARKVYLLHW
		ŀ				FCHRQPSKEVLFHLALYRNNPR
						CKAVVHLHSTWSTALSCLQGL
		ŀ				DSSNVIRPFTPYVVMRMGNVPL
						VPYYRPGDKRIAQDLAERETH\
						NHAFLLANHGPVVCGESLQEA
						ANNMEELEETAKLIFILGDRPIR
						YLTAGEIAELRS
26104	56472	Α	26251	2	1481	PENQINKLKQAIPADYRSHQKC
		l		1		VNQPSSPTITPRLFAITVITDERG
						YATGSAGNLSL/LLPDGNLLAT
				}		PT/GSCLGN/LDPQRFSKVAADG
		ŀ				EWL/SGDKPSK/EVLFHLALYR/
						NNPRCKAVVHL/HSTWST/ALS
				}		CLQGLDSSNVIRPF/TPYVVMR
						MGNVPLDLAELAA/DNQAFLL
						ANHGPVVCGE/SLQEAANNME
						ELEETAK/LIFILGDRPIRYLTAG
						VCPLAKMLNGTGQYLSIKRCT
	İ					NNRSVRGTCSAPRAGPKGYGL
						MMMIDVLSASYSAYRSGDRTL
						LYSYHRASACADSTTLTVLISY
						TFHLVNSYSTVPPLEGSGTQPA
1						SPSFPTRVSDDHNRDFFFLLSPC
			ŀ			GLLQNLAQCIRQVGIQLDFGCV
						IISAQTETDGPLVCGRFEEGTPF
						SPQTPRDCDPNRSYSGNTQGVR
			}			GATSSPGSAISFEQTVNARSHVL
			ľ			RVTLTLGLTRPMLYVTGSLKWI
						NICILPISLKPLRYYIHLAAQFPT
						APISLGRSLHVVPHEEVAM
26105	56473	Α	26252	1	413	
26106	56474	Α	26253	3	247	
26107	56475	Α	26254	300	665	
26108	56476	A	26255	1	1854	
26109	56477	A	26256	1	1611	
26110	56478	Α	26257	942	1040	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
2(111	56470	<u> </u>	26260	1616	12679	DI AVEGDODEOLA CLAVIA UDC
26111	56479	Α	26258	1616	3678	PLAKTGRQREQLAGLAK/AHPS
						LTLHQDPVYVTRADAPVAGKV
					;	ALLSGGGTEHEPMHCGYIGQG
		1				MLSGACPGEIFTSPTPDKIFECA
					;	MQVDGGEGVLLIIKNYTGDILN
						FETATELLHDSGVKVTTVVIDD
						DVAVKDSLYTAGRRGVANTVL
		1				IEKLVGAAAERGDSLDACAELG
						RKLNNQGHSIGIALGACTVRSA
						GKPSFTLADNEMEFGVGIHAIL
						KGDIPEAEAILASIKPAGVVSRA
		İ				DVVLPNQFQALRKSFIPERPVP
						VMVTRLFELPVQISLGVYSLER
						PANPQPIAYLVLQPRRKANNQN
						ASTSAIIRATIGEPISCSVPSRGC
		ļ				EGGISVAETVPAMIIAIGITISEG
		İ				LDARYRHVNSEHDPSDRQAKF
						EWRYFGNLGKTVNDWRKNNK
						ADIKEDGNRRCRHTNQPHCRIE
		ļ	Ì			AVEYDDGRLCPLHGAHRGQSS
						DGELVKPTVKTQSLAVHYSIGK
]			LRHRPNHGAVYYQRLRSGMGL
			ļ			MNAFDSQTEDSSPAIGRNLRSR
		İ				LARKKLSEMVEEELEQMIRRRE
			ļ			FGEGEQLPSERELMAFFNVGRL
		l				RAGSVKTQRSGANKQRRTRCV
						SRPSADTIIGELSGMAKDFLSHP
						GGIAHFEQLRLFFESSLVRYAA
						EHATDSRDPRYRPKFYSISRSVP
						VSDNITLQQLLLSLNDQPARCK
		l				PSARCRLHGSHTSRYECNHRHG
26112	56480	Α	26259	185	775	IPEIFSGETHLKVSTLSKPTFSISS
20112	30460		20239	163	1//3	LIRCTTRFSSQLSLGIATMSHRK
						RVISALKSLSRLSANSLVFANQ
						· · · · · · · · · · · · · · · · · · ·
						VERSSLTNLGCTRCSG*SLFWQ
			1			RPALR*PFGLCPTVALTYLIVSP
						EW*KAVSVKCWRNRRLTLMTS
						PICTNSGTLTTAPVDRVAQVTF
						QSPECLQHMRLTIALRYFRVAL
						SRRLLVYASVCFTFSG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	,
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26113	56481	Ā	26260	301	1313	RLEHDGVCLHRANHRYPGCRL
		İ				HLDYVEPQLQHDDALRAAVM
						MFKQYLQVTKPGIIFGNLISVIG
						GILLASKGSIDYPLVIYTLVGVS
						LVVASGCVFNNYIDRDIDRKME
1						RTKNRVLVKGLISPAVSLVYAT
						LLGIAGFMLLWFGANPLACWL
						GVMGFVVYVGVYSLYMKRHS
						VYGTLIGSLSGAAPP\VIGYCAV
	İ					TGEFDSNAAILLAIFSLWQMPH
	Ì	ł				SYAIAIFRFKDYQAANIPVLPVV
						KGISVAKNHITLYIIAFAVATLM
						LSLGGYAGYKYLVVAAAVSV
						WWLGMALRGYKVADDRIWAA
		l				QSCSGFSIIPITALSVMMSVDFM
						VPDSHTLLAAVW
26114	56482	A	26261	3631	4078	CFLNFKTLLLVHLFRRVFLRIRL
	-	ĺ		İ		RHRKLHPVGLGGPVNKAAYAF
	1					CLGAMANGVYGPYAIFASVKM
						VSAFTVTASTMLAPR\WLLGLA
	1					GITEGAIPMAIEDPLRVIGSFVL
						GSMVTGAIVGAMNIINRTLRVE
				1		ASVTSAQIVQTIIRLRR
26115	56483	Α	26262	814	2126	CTGCRKQRLPVVQGFAAGLAA
į						NMIGSGFLGAVVGGLIAGYLM
İ						RWVKNHLRLSSKFNGFLTFYL
						YPVLGTLGAGSLMLFVVGEPV
						AWINNSLTAWLNGLSGSNALL
		1				LGAILGFMCSFDLGGPVNKAA
						YAFCLGAMANGVYGPYAIFAS
						VKMVSAFTVTASTML\APRLFK
					ł	EFEIETGESTLLLGLADITEGAIP
						MAIEDPLRVIGSFVLGSMVTGA
						IVGAMNIGLSTPGAGIFSLFLLH
		1				DNGAGGVMAAIGWFGAALVG
						AAISEGKRIFRYRDLIIVNSNQL
						FLHDHRFPRWEGLESVFFLLAA
						FQQDVGIWPPLGAMLGLATAV
						VLGFLLYWGGIRLNLGAFFKW
						TSLFILFVAAGLAAGAIRAFHEA
		1				GLWNHFQEIAFDMSAVLSTHSL
		1				FGTLMEGIFGYQEAPSVSEVAV
						WFIYLIPALVAFALPPRAGATAS
26116	56484	A	26263	1	525	
26117	56485	Α	26264	1	700	
26118	56486	Α	26265	1	1428	
26119	56487	Α	26266	254	475	RDQLVSELNQMLV*KSAFRMA
						ALITSRWPMVTHWFREVRRGN
						WRQFLPALTLLVRLSLMLMGR
						QAILRSRRNY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \≔possible nucleotide insertion)
				sequence		
26120	56488	I A	26267	1	1657	MLIQRRRLAFDRAKHRRAEML
20120	30488		20207		1037	AQRARGEEEAHHHSSPEGAIEV
						DESEVDLDAISAQSLRLVRSILM
						· -
						LIALLSVIVLWSEIHSAFGFLENI
						SLWDVTSTVQGVESLEPITLGA
						VLIAILVFIITTQLVRNLPALLEL
						AILQHLDLTPGTGYAITTITKYL
						LMLIGGLVGFSMIGIEWSKLQW
			•			LVAALGVGLGFGLQEIFANFIS
						GLIILFEKPIRIGDTVTIRDLTGS
			ŀ			VTKINTRCHTHRRQQLLLQQA
						ATSSADVIYLGEAVCSKRRATK
						VGDWLEMAKSLAGSGKQIVLS
						TLALVQASSELGELKRYVENGE
						FLIEASDLGVVNMCAERKLPFV
	ľ					AGHALNCYNAVP\LKILLKQGM
	ŀ		į			MRWCMPVELSRAWLVNLLNQ
						CDELGIRNQFEVEVLSYGHLPL
						AYSARCFTARSEDRPKDECETC
						CIKYPNGRNVLSQENQQVFVLN
						GIQTMSGYVYNLGNELASMQG
	:					LVDVVRLSPQGTDTFAMLDAF
	ŀ					RVNENGAAPLPLTANSDCNGY
						WRRLAGLSLRQIKTCLIFLLCQP
						RGRRPYRTRAMPPILTMPANSP
26121	56489	Α	26268	482	605	
26122	56490	Α	26269	1	298	MWPGMVTHAVRIPLHNDTVTL
						SDNFQPFAGTDAMTITRPLEML
						RDGKCPQPDWISSEGACAGNA
						TDSPHPFELKAGKTITLEDGRQI
	ļ					NGADYLAAPVPGKALAIFGDT
						GPCDAALDLAKGVDVMVHEA
						TLDITMEAKANSRGHSSTRQAA
						TRESELFRYTVKHSLIFASVIGII
						TLLQASTKIYTPGRKEQGEPMT
						PRRTPARF*IKSGQNNHAGRWK
	1	1	ĺ			AD*RRRLLSCSSAR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first)	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26123	56491	A	26270	1	1707	MTRDGLANKALAVARTLADSP
						EIRQGLQKKPQESGIQAIAEAVR
ŀ		1				KRNDLLFIVVTDMQSLRYSHPE
		1				AQRIGQPFKGDDILKALNGEEN
<u> </u>						VAINRGFLAQALRVFTPIYDEN
				:		HKQIGVINDSRWSIIWSVLFGM
		1				LVGLIGTCILVKVLKKILFGLEP
		ł				YEISTLFEQRQAMLQSIKEGVV
						AVDDRGEVTLINDAAQELLNY
						RKSQDDEKLSTLSHSWSQVVD
						VSEVLRDGTPRRDEEITIKDRLL
	}					LINTVPVRSNGVIIGAISTFRDKT
						EVRKLMQRLDGLV/NLC*RTS*
						TIPLRAHSPQSKSAIYHEIAP*NA
						PAFYRRKCHCADIFLPYF*TCR\
						RDRAMSAYLRYIVQKADSSFL
						YDKYQNQSIAAHVMRALAAEQ
		1				SEVSPEQRRAICEAFESANNTH
						GLNLTAHKYPGLRGTLQTAST
		1				DCDTIVEAAALLPAFDQAVEGN
		1			1	RHQDDYGSGLGMAEEKFHYYL
		1				DLFRAVGDGHNSKEDATFGLG
		İ				WRVNGNATMTPTFGTLASPQT
						YGHTGWTGTVTVIDPVNHMTI
<u> </u>			<u> </u>		}	VMLSNKPHSPVADPQKNPNMF
						ESGQLPIATYGWVVDQVYAAL
26124	56492	A	26271	257	817	TSSRCISLRTSVLSLKVEMAPMI
						TPLLRTGTVLISNSRSLIVISSSR
					1	RGVPSRNTSETSTTCDHEWLSV
		1	•			DSFSIVLRLTVIQQFLCGIVDQR
						DLAAIVHGNDAFFDRLQHGLA
						LLKQRGDFVGFQAEKDFFQYL
						NQNAGANQSDQHAK*Y/LTR*C
						SSDCH*SVGSHGLTQGRSPPRQ
						FVYDFHRRWG
26125	56493	Α	26272	1	2700	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	1
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		İ		sequence		
26126	56494	Α	26273	1	1038	MGCLDLGDGRAGSVARYFRRY
						RPPCDAALDLAKGVDVMVHEA
				1		TLDITMEAKANSRGHSSTRQVL
						KKILFGLEPYEISTLFEQRQAML
						QSIKERSRRHRLPKEKKIMTPTI
						ELICGHRSIRHFTDEPISEAQRE
						AIINSARATSSSSFLQCSSIIRITD
		1				KALREELVTLTGGQKHVAQAA
		1				EFWVFCADFNRHLQICPDAQLG
1						LAEQLLLGVVDTAMMAQNALI
		1				AAESLGLGGVYIGALRNNIEAV
						TKLLKLPQHVLPLFGLCLGWPA
						DNPDLKPR\LPASILVHENSYQP
						LDKAALAQYDEQLAEYYLTRG
						SNNRRDTWSDHIRRTIIKESRPFI
						LDYLHKQGWATR
26127	56495	A	26274	1	1338	EBIENKQUWAIK
26128	56496	A	26275	2	375	HSDPEASGPLTRLRAMEQRRVT
		-				DFFARRRTPGSVPSTDRR*TIVR
						MIPCTSSGRRTKAMVILRTSLV
						NPASNE/CATELFNALDVSIQNP
						RMIISP*IQHRTELSGSPLVAVG
		}				RMCSLTPRVIFEH
26129	56497	A	26276	219	767	RFTQGKGPINNPAVIRPLDFPQN
						GSRPLANQ\IFTTSLKVGDYFGK
	1					RHKDVLRAIRNLKCSDDFTQRN
						FAPIDFIDKNGDVQPMYNITRD
						GCMMLVMGFTGKTAAAVKEC
		1				YINAFNWM\AEQLNRRMAMGE
	İ					ELQHRYAIKETRSKLKGTIG\TR
						LMNERKKEKRVLELEHEHIMQ
						VTQPELLIG
26130	56498	A	26277	16	104	HICQSAPL*RGSSGLNGYGQYR
	-					PAGFLDG
26131	56499	Α	26278	3	399	
26132	56500	Α	26279	1112	1831	TGIRNCAPLSLTWKSKTANRKV
		1				RCGHIRYPLADGAKTSDGKDY
						LVVATTRPETLLGDTGRSRLTR
						KIRVTKELIGKYVILPAGTAPGV
						RQGPVWMPGDEVKKVTCKNG
						VVNEIWTRNHADIPLRPRFAVL
						ASGSFFSVGLVAERNGIREPILG
						LDVLQTATRGEWYKGDFFAPQ
						PWQQFGVTTDET/LRPSQAGQT
						IENLFAIGSVLGGFDPIAQGCGG
						GVCAVSALHAAQQIAQRAGGQ
26133	56501	Α	26280	3	790	
26134	56502	Α	26281	334	609	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26135	56503	Α	26282	1	1338	MTRHYGAEATNALLPGKASKH
						QIVGCGVNALSDLDPRRPDKTR
		ĺ				SVASGIGAALLLRLIKTLADDL
				1		QNLTDLSVFNGERYKDAQHVV
:						IRAAGEKNQAFIAGARHDLGGE
						LGVGLVWIPASKVNGIMGPSPV
						WLTFRVSNIAGESAEGLLVTKP
						KNYDQVPANKPIVDAIKAKKQ
						DPSGAFVWTTYAALQSLQAGL
						NQSDDPAEIAKYLKANSVDTV
		l				MGPLTWDEKGDLKGFEFGVFD
1		1				WHANGTATDAKRYCANVKGV
1						NPDTQEPSPSGVKVNDPKVDER
1						LIRQEAGMVFQQFYLFPHLTAL
1]			ENVMFGPLRVRGANKEEAEKL
						ARELLAKVGLAERAHHYPSELS
			!			GGQQQRVAI\ARALAVKPKMM
						LFDDPTSALDPELRHEVLKVMQ
						DLAEEGMTMVIVTHEIGFAEKV
						RSRLIFIDKGRIAEDGNPQVLIK
						NPPSQRLQEFLQHVS
26136	56504	Α	26283	1170	1575	DPPVLVQRDANSTVRFPHASAS
						ADPAGDIPPIF\AQAAGADLVY
		ŀ				VGVEPPKPKAEVILVAEYSPIKT
		l				VADLGCPLHVQKVSRYPPEFTQ
-						VITPVQCYVTIDALGQYAAWT
		ľ				RANMTYRPGSNIIQNLGNDIRL
						RTVQ
26137	56505	Α	26284	3	1351	RTAPETPNQRPATLDSGILGGYI
						APDNLTITFIGGHSLFDERFCLA
						HRCQKAAEDDAFPHDSLDAAS
		l				LLEYAREKLNGLDVEVYHWNL
						QNFAPEDLLYARFDSPALKTFT
						EQLQQADGLIVATPVYKAAYS
						GALKTLLDLLPERALQGKVVLP
						LATGGTVAHLLAVDYALKPVL
						SALKAQEILHGVFADDSQVIDY
						HHRPQFTPNLQTRLDTALETFW
						QALHRRDVQVPDLLSLRAPKP
						KAEVILVAENSPIKTVADLKGH
						K/VAFQKGS/SSHNLLLRA/LRQ
						AGLKFTDIQPTYLTPADARAAF
						QQGNVDAWAIWDPYYSAALL
						QGGVRVLKDGTDLNQTGSFYL
						AARPYAEKNGAFIQGVLATFSE
						ADALTRSQREQSIALLAKTMGL
						PAPVIASYLDHRPPTTIKPVNAE
						VAALQQQTADLFYENRLVPKK
L		<u> </u>		L		VDIRQRIWQPTQLEGKQL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26138	56506	A	26285	364	1937	KLSGRHCTAAMFRFLTFCLCEG
20136	30300	^	20203	304	1937	MPMRNIIKLALAGLLSVSTFAD
	:					AAESSPEALRIGYQKGSIGMVL
						AKSHQLLEKRYPESKISWVEFP
						AGPQMLEALNVGSIDLGSTGDI
						PPIFAQAAGADLVYVGVEPPKP
						KAERILVAENSPIKTRTDLKGH
						KGAFQKGFSSHNLLLRALRQA\
		l				GLKFTDI\QPTYLEPRWRPRAA\
						FQTRGTVDA\WAIWDPYYSAA
						LLQGGVRVLKDGTDLNQTGSF
				1		YLAARPYAEKNGAFIQGVLATF
						SEADALTRSQREQSIALLAKTM
		1				GLPAPVIASYLDHRPPTTIKPVN
						AEVAALQQQTADLFYENRLHY
						~ ~ ~
						SEYCRPMVSVGNWFLDGSHSV
						FSYDALDRLVQQGGFDGRTQR
						YHYDLTGKLTQKQWQYDGHG
						WLTDISHLSEGHRVAVHYGYD
						DKGRLTGECQTVENPETGELL
		İ				WQHETKHAYNEQGLANRVTP
						DSLPPVEWLTYGSGYLAGMKL
1						GGTPLVEYTRDRLHRETVRSFG
		<u> </u>				SMAGSNAAYEMTSGTELIDLC
26139	56507	A	26286	511	1152	SVRFNIVFHFMRLLRFCCVLDH
		1				LICFTSPVNTFLRYNAFTLCNGE
						FGMSHPALTQLRALRYCKEIPA
]					LDPQLLDWLLLEDSMTKRFEQ
1						QGKTVSVTMIREGFVEQNEIPE
						ELPLLPKESRYWLREIL\LCADG
1						EPRLAG\RTVVPVSTLSGPELAL
						QKLGKTPLGRYLFTSSTLTRDFI
						EIGRDAGLWGRRSRLRLSGKPL
						LLTELFLPASPLY
26140	56508	В	26287	184	415	
26141	56509	Α	26288	15	87	
26142	56510	Α	26289	78	157	CKRYGKARDTG*QPRTQKCTC
						CELDE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26143	56511	A	26290	1	1817	MTSAISLGSRCSGRIPSDIIGSNL
						DITAFNWQPDLLTIWHRQLHLH
						LTRLDGGGHFYRQEVHLWRTD
						KSGDKRRPQGDPKTTGITAKVI
						NVRSTKLVGLPHRITATRWKR
						KRSRMLHTNTGKLVFNNRDQK
						RCTRKVMFDKALKLLDEAERL
						GSTSARSTIYQQCKRQGVITPHS
						ADFATTVRLLAHLSQERLGKLQ
						DSIYISLTDHCQFAIKRFQQNVL
:						LPNPLLWDIQRLYPKEFQLGEE
						ALTIIDKRLGVQLPKDEVGFIA
						MHLVSAQMSGNMEDVAGVTQ
						LMREMLQLIKFQFSLNYQEESL
1		İ				SYQRL\VPHLKFLSWRILEHASI
						NDSDESLQQAVKQNYPQAWQ
		l				CAERIAIFIGLQYQQLGLTQPAV
1		1				SKIINDIEDYFGVELVVRKNTG
						VTLTPAGQLLLSRSESITREMK
		l				NMVNEISGEKNPGEGSEKELET
						VYVQAVGAHWEGNQVWLILA
		l				GGALFAAWPRVYAAAFSGFYV
1						AMILVLCSLFFRPLAFDYRGKIA
1						DARWRKMWDAGLVIGSLVPPV
						VFGIAFGNLLLGVPFAFTPQLR
						VEYLGSFWQLLTPFPLLCGLLS
						LGMVILQGGVWLQLKTVGVIH
ł		l				LRSRVRIPCDLHIYAQMA
26144	56512	A	26291	557	808	
26145	56513	Α	26292	8	274	
26146	56514	Α	26293	523	1851	
26147	56515	Α	26294	1	589	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	I .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26148	56516	A	26295	1	1848	MDLSTPERGSPYPRLLPCGDPL
						GETIVAIDQEAKPSTEDLGNKK
						ETKYIKLKVIRWDNSDFNFLYS
				<u> </u>	İ	NYERIRARTTKKEDSATNVPVT
						FEKHGSHAVVYARRSATVLTD
						RNKEAPRVPQGGYMVSFVDIPE
						ALTQGETVAEAMEAAKDALLT
						AFDFYFEDNELIPLPSPLNSHDH
						FIEVPLSVASKVLLLNAFLQSEI
						TQQELARRIGKPKQEITRLFNLH
						HATKIDAVQLAAKALGKELSLE
						CLMDILNLNKHISGQFNAELESI
						RTQVMTLGGMVDKQLSDAITA
						IHNQDSDLAKRVIEGHKNLNM
						MEVAIDEAR/C*AIIAKHQS\TAS
					ľ	D\LRLVMVI/SKTIAEMERIG\DV
						GRNKICRTALEKLSQQHQP*VV
						S\LE\SLDRHTIQMLHDVVKAFA
						RMDIDETAKCQIFVEYVLKPKV
				:		IWLLCFANIFLYVVRIGIDQWST
					,	VYAFQELKLFKAVAIQGFTLFE
					İ	AGALVGTLLWGWLSDLANGR
ŀ						RGLVACIALALIIATLGVYQHA
				:		SNEYIYLASLFALGFLVFGPQLL
						IGVAAVGFVPKKAIGAADGIKG
						TFAYLIGDSFAKLGLGMIADGT
						PVFGLTGWAGTFAALDIAAIGC
						ICLMAIVAVMEERKSAARKKFS
26149	56517	A	26296	395	1428	TSATATSTFALPRGGGYLVVSE
201.5	150517	' '	20290			WVVLRFTDIFLRIFPCDNGRTILI
						RFGIFRMLMIVAIETQQFPVTAI
	Ĭ		·			FRVIGMVVINVVNASEETNRRL
						HHRSLRLIQECVMDSLNLNKHI
						SGQFNAELESIRTQVMTMGGM
						VEQQLSDAITAMHNQDSDLAK
						RVIEGDKNVNMMEVAIDEACV
						RIIAKROPTASDLRLVMVISKTI
						AELERIGDVADKICRTALEKFS
						QQHQPLLVSLESLGRHTIQMLH
		t				DVLDAFPRMDIDEAVRIYREDK
		ļ				KVDH\EYE\GIVRQLMTYMMED
						SRTIPSVLTALFCARSIERIGDRC
						QNICEFIFYYVKGQDFRHVGGD
					1	ELDKLLAGKDSDK
26150	56518	A	26297	667	1002	ELDRELAGROODIC
26151	56519	В	26298	1	1716	
20171	130313	٦	20270	<u> L'</u>	11/10	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26152	56520	Α	26299	1001	2193	LMAATKPAFNPPGKKGDIIFSV
1						LVKLAALIVLLMLGGIIVSLIISS
						WPSIQKFGLAFLWTKEWDAPN
						DIYGALVPIYGTLVTSFIALLIA
						VPVSFGIALFLTELAPGWLKRP
						LGIAIELLAAIPSIVYGMWGLFIF
						APLFAVYFQEPVGNIMSNIPIVG
						ALFSGPAFGIGILAAGVILAIMII
						PYIAAVMRDVFEQTPVMMKES
		1				AYGIGCTTWEVIWRIVLPFTKN
						GVIGGIMLGLGRALGETMAVTF
						IIGNTYQLDSASLYMPGNSITSA
		ı				LANEFAEAESGLHVAALMELG
						LILF\VITFIVLAASKFMIMRRIA
:						LTLSMATMAFGLFWLIWILMST
						ITRGIDGMSLALFTEMTPPPNTE
			l i			GGGLANALAGSGLLILWATVY
						CGPLSDDRGGIRPTI
26153	56521	A	26300	1	1645	MPAFPYTADYFSGLTATTAALA
						ALHKVRETGKGESIDIAMYEV
		İ				MLRMGQYFMMDYFNGGEMCP
						RMSKGKDPYYAGCGLYQCAD
						GLLSLDCVHRRLGAIDPILNECF
						KDIGLAHLLGTPEIPEGTQLIHRI
						ECPYGPLVEEKLDAWLATHTIA
		1				EVKERFAELNIACAKVLTVPEL
						ESNPQYVARESITQWQTMDGR
						TCKGPNIMPKFKNNPGQIWRG MPSHGMDTAAILKNIGYSENDI
						QELRPPNNKRTKMDRGAMDII
						GGQHLRQMWDDLADVYGHKT
						ALICESSGGVVNRYSYLELNQEI
						NRTANLFYTLGIRKGDKVALHL
						DNCPEFIFCWFGLAKIGAIMHE
						AVIALASPDNMNAFELTP*SGK
						LITTFPHLPLAISA*ASPACSSEK
						RWVMALRGHSFQSVRSWAHFS
						IWNRLVTQEPIIRR
	L	<u></u>	<u> </u>	L	l	IMMENIQUIMA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	i e	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26154	56522	A	26301	12	1021	TPGNNVDSIFLAFFLNQFLTLGY
20131	30322	` `	20301	ľ		IMGKTISIKVLFGIYLLLMAAKV
						FAFSCNVDGGII\IGAGTTSVYV
						NLDPVIQPGQNLGVDLAHHISC
						WNGDGGWYDTDHMNLVQGS
						AFAGSLQSYIGSLYWNNVTYPF
					}	PLTTNTNVLDIGDKTPMPLPFK
						LYITPVGAAGGVVIKAGEVIARI
						DMYKIATLGSGNPSNFTWNIIT
						NNNAVMPTGGCTVDSRNVTVD
						LPDFPGSAEIPLGVYCSSEQKLS
						FYLSGATTDSSRQVFANTAPDA
						TKASGVGVTLMQRQLAGINDS
			:			HLLHYLDDEVWDNDYLATPHF
						LLKSAILRSMNDALMTRVTGE
						KNGQVRLEEIER
26155	56523	A	26302	522	714	RNGQVREBEIER
26156	56524	A	26303	1	976	STCSSRSHLHLIQASPILPNYVA
20130	30324	^	20303		1970	TAVAARIIADVQGISDTCVIAQP
						SPPHPGALRTLVFTTDEPETPQP
				ĺ		PGAAGFQLVQKKQVQLHNVLY
						VMTPHAFAQGTVTIYLPGEQQT
						LSVAPLKNVVQLVTQQHLRDR
						LWWPGAFLTDFAAKVKALKD/
		1				YPNHVMAQRASGEAEADDDV AATIKSVRQQLLNLNITGRLPV
						KLDPDFVRVDENSNPPLVGDYT
			1			LYTVQRPGTEQGSFKVKRARA
						RVRQTRAPLFGPKSPAPEHMES
		1				ELEFELIGPSKSTSGNPRGLRSE
		1				RPVLFCLYPEMPTAAARAILIAE
						EQSREVKIALVVLDRLQRE
26157	56525	A	26304	1	1701	LQSREVRIAL V VLDREQRE
26158	56526	A	26305	1839	2038	ARSGCFVRQSCPRGRCSKNRR
20136	30320	^	20303	1039	2038	WRDPYDHYPARPAYCP*R/WC
						M*LSTLATPKKVSPCKPAPAAH
						RWR
26159	56527	A	26306	1	3270	KWK
26160	56528	A	26307	1962	2049	
26161	56529	Α	26308	94	942	
26162	56530	Α	26309	1	4104	
26163	56531	Α	26310	879	1367	TASELGKSCSRDHTPCTASVRA
		1				LYYARLRHAPANDPGEDGWAL
					1	AAKPPALPPRNSLNSQAIFRDKP
						NLPHRSPATYRQTERG*DTRSE
		1				FHA*TDAIPVATRARAGEFCRQ
		1				MFWGEDQADEQPA**ACCHRK
						*PVPK*DLAMLRAPPRMDSPPD
		1				ASRTSDLHN
		4				

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
}	sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26164	56532	Α	26311	1203	1911	SRPAYHPAPREFQRQWRQDPAP
		l				GLAITPGQQLFITIKLWNDDH\K
		l				RPREALLDSLKKLQLDYIDLYL
		1				MHWPVPAIDHYVEAWKGMIEL
		1				QKEGLIKSIGVCNFQIHHLQRLI
		1				DETGVTPVINQIELHPLMQQRQ
		1				LHAWNATHKIQTESWSPLAQG
		1				GKGVFDQKVIRDLADKYGKTP
		ĺ				AQIVIRWHLDSGLVVIPKSVTPS
		1				RIAENFDVWDFRLDKDELGEIA
]						KLDQGKRLGPDPDQFGG
26165	56533	Α	26312	3	793	
26166	56534	Α	26313	181	336	
26167	56535	В	26314	1	374	
26168	56536	Α	26315	591	679	
26169	56537	A	26316	937	1395	YRLAAGSCGIRRRNRHCQRRPG
						RNSKRLIALISAIGMSIFLQNYV
						SLTEGSRDVAPSSVPLTPASLLI
		İ		1		AGSPPH*TISRLSGPLLREIMLK
		İ				QLYHCGKSLTNLPIREILRM*G*
						LTGEEIELARGDFHIRDIWHRA
		<u> </u>				VTNTAHKTGITQAQHRH
26170	56538	Α	26317	627	878	VVEWFEPLICVNGWESKWPVL
						LSE**PETVGTNCDSSN*IPASLN
	-	İ		1		TSYTGLMAFDAIMVAVPTS*TC
		<u> </u>				KIRRRVAGTKCGNPRA
26171	56539	Α	26318	125	3078	IYTVEIQNLGFAFVTGENTTGIN
						SGTISLLQNGKDPAPSPIVLLAT
		j				NGGSATNAGTITGKVTEQHSVF
		l				NKYSTGTSNSFIFNNDVSSITGL
		ł				VAQSNSTIINTDSGIIDLYGRGS
		1				VGMLAIADSTAENQGKITLDSM
						WVDANDTTAMRDIASNSAIDF
		l				GTGVGVGTDRYRGGRKNAPAF
		İ				N\QLGGVITIYNAGAGMAAYG
		1				ASNTVINQGTINLEKNGNYDDS
		ŀ				LAANTLVGMAVYEHGTAINDQ
		<u> </u>				TGVININVGTGQA
26172	56540	A	26319	205	419	A WWW. VOVICE A PROPERTY STATES
26173	56541	Α	26320	1829	2903	AWKVSHCAARPSFSRRWRGEK
						CTAGRRSQQFSARSTLKPMPSP
				1		R*SSMHRR**MPSASCALRLPIP
		}				PAAAQSSHQSKKLRTSDNASPV
L	<u> </u>	<u></u>				AAARPVRPIRWT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26174	56542	Α	26321	402	1781	QRTTGAERYVPHHQPCPPASSL
						SAGPRG\LHPAKVQEGVDIAIEN
						DVIVAIGDALTQRYPDASFKEM
						HGRIVMPGIVCSHNHFYSGLSR
						GIMANIAPCPDFISTLKNLWWR
						LDRALDEESLYYSGLICSLEAIK
						SGCTSVIDHHASPAYIGGSLSTL
		1				RDAFLKVGLRAMTCFETTDRN
						NGIKELQEGVEENIRFARLIDEA
	,					KKATSEPYLVEAHIGAHAPFTV
						PDAGLEMLREAVKATGRGLHI
						HAAEDLYDVSYSHHWYGKDL
			<u> </u>			LARLAQFDLIDSKTLVAHGLYL
						SKDDITLLNQRDAFLVHNARSN
						MNNHVGYNHHLSDIRNLALGT
						DGIGSDMFEEMKFAFFKHRDA
						GGPLWPDSFAKALTNGNELMS
		1				RNFGAKFGLLEAGYKADLTICD
		1				YNSPTPLLADNIAGHIAFGMGS
		1				GSVHSVMVNGVMVYEDRQFN
		<u> </u>				FDCDSIYAQARKAAASMWRRM
26175	56543	A	26322	284	340	WELLIN WAR STORY OF BEACH
26176	56544	A	26323	113	646	WTLVPNWNNTQPYLGLFF*FIR
						DFADFGTTIKQDFRLLGQTSVD
		1				RLLQLSQGQAVKGNQLLPVSL
		ŀ				VKRKTTLAPNTQTASPRALADS
						LMQLARQVSRLESGQRSDSSLR EKKITKKHTKKRTASLILHAMI
						CCRSLNSSKTKNTKCLNSINQR LKILSLQKDLMCGTAGRCKTLT
		ł				EQ
26177	56545	A	26324	1	582	
26178	56546	A	26325	3	947	QTQEWSGSATFTSDGKIRLFYT
20170	30310	``	20323			DYSGKHYGKQSLTTAQVNVSK
						SDDTLKINGVEDHKTIFDGDGK
						TYQNVQQFIDEGNYTSGDNHT
						LRDPHYVEDKGHKYLVFEANT
						GTENGYQGEESLFNKAYYGGG
						TNFFRKESQKLQQSAKKRDAEL
						ANGALGIIELNNDYTLKKVMKP
						LITSNTVTDEIERANVFKMNGK
		1	1			WYLFTDSRGSKMTIDGGATQA
						FAKENNQKAYKETYGVSHITR
						HDMLQIPKQQQNEKYQVPQFD
		1				QSTIKNIESAKGLDVWDSWPLQ
					1	NADGTVAEYNGYHVVFALAGS
						PKDA/G*HINLHVLSK
			<u> </u>		L	1

SEQ ID	~	Met	SEQ ID NO:	Nucleotide	ľ	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	ł .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26179	56547	Α	26326	2	223	RIPIKNIESAKGLDVWDSWPLQ
1						NADRTVAEYNGYHVVFALAGS
1						PKDADDTSIYMFYQKVGDNSID
				}		SWKNAGRVFKDSDKFDANDPI
						LKDQTQEWSGSATFTSDGKIRL
						FYTDYSGKHYGKQSLTTAQVN
						VSKSDDTLKINGVEDHKTIFDG
						DGKTYQNVQQFIDEGNYTSGD
						NHTLRDPHYVEDKGHKYLVFE
						ANTGTENGYQGEESLFNKAYY
1						GGGTNFFRGATQAFAKENNQK
						AYKETYGVSHITRHDMLQIPKQ
					İ	QQNEKYQVPQFDQSTIKNIESA
						KGLDVWDSWPLQNADGTVAE
						YNGYHVVFALAGSPKDA/G*HI
						NLHVLSKGRRQLNRQLEKRGP
26180	56548	Α	26327	***	803	MLEDPRKGLETPSPVSHNLHFQ
						FHLGPLLPGSPMKKWPALVVT
						GSKSPKLESYKHFQKIWDMHG
						EPSKREEGAGLTVNQHIPNGAS
						TCNEGPQRLEALGARIPMAAGF
						SSSKPTLVTPRRAYRADLRLEG
						YWGCQGVPGGPLVAQGGATQ
						AFAKENNQKAYKETYGVSHIT
						RHDMLQIPKQQQNEKYQVPQF
						DQSTIKNIESAKGLDVWDSWPL
						QNADGTVAEYNGYHVVFALA
						GSPKDA/G*HINLHVLSKGRRQ
						LNRQLEKRGPCL
26181	56549	A	26328	2	439	MULA AMETOL CHICATON TANK
26182	56550	Α	26329	[1	1084	MVIAAMETQLSNGPTCNNTAN
		1				GPTTINNNCSSPVDSGNTEDSK
		l				TNLIVNYLPQNMTQEELKSLFG
						SIGEIESCKLVRDKITGGATQAF
		1				AKENNQKAYKETYGVSHITRH DMLQIPKQQQNEKYQCDNLKT
		1				CHTSHGSVMAETAVINHKKRK
		l		•		NSPRIVQSNDLTEAAYSLSRDQ KRMLYLFVDQIRKSDGTLQEH
		1				DGICEIHVAKYAEIFGLTSAEAS
						KDIRQALKSFAGKEVVFYRPEE
]		1
						DAGDEKGYESFPWFIKRGATQ AFAKENNQKAYKETYGVSHIT
						1
						RHDMLQIPKQQQNEKYQVPQF
			1			DQSTIKNIESAKGLDVWDSWPL
						QNADGTPERR**HINLHVLSKG
	1.		l	l	l	RRQLNRQLEKRGPCL

26183 56551 A 26330 34 1949 MGYLNNVAGYREDLLANRAI KHGNFALLTPDGVVKNIPGY NCDATILSTPKLGASFVDYLV LHQNGGNQQGFGVEGIETFRY VISGNITAKAEGKTYALSEGG LYCPPGSLMITEVNAQAEDSQI LYKRRYVPVEGYAPWLVSGN SELERIHYEGMDDVILLDFLPH LGFDMNMHILSFAPGANHGY THVQ\EHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGH RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGO YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC	SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
Sequence	NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
26183 56551 A 26330 34 1949 MGYLNNVAGYREDLLANRAI KHGNFALLTPDGVVKNIIPGY NCDATILSTFKLGASFVDYLV LHQNGGNQQGFQVEGIETFRY VISGNITAKABGKTYALSEGG LYCPPGSLMTFVNAQAEDSQI LYKRRYVPYEGYAPWLVSGN SELERIHYEGMDDVILLDFLPH LGFDMNMHILSFAPGANHGY THVQUEHGGATQAFAKENNHH AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGI RLWGDTDVIGLFDAETDMND VAILENIPPILGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNML PGLAFGTGTIGTLSVPAMLDS; THTRRMSTTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTENEFFVREIDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGG YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIVVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRIGLLYGRRFVPPP*YALINI DSSPWYPFSVPVLASKTRYLW LSPT LSP		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
KHGNFALLTPDGVVKNIIPGY NCDATILSTPKLGASFVDYLV LHQNGGNQQGFQEGIETFR VIGNITAKAEGKTYALSEGG LYCPPGSLMTFVNAQAEDSQI LYKRRYVPVEGYAPWLVSGN SELERIHYEGMDDVILLDFLPF LGFDMNMHILSFAPGANHGY THVQVEHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGI RL WGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENA VNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYL-W LSPT 26185 56553 B 26332 I 3090 26186 56554 A 26333 3 832					sequence		
KHGNFALLTPDGVVKNIIPGY NCDATILSTPKLGASFVDYLV LHQNGGNQQGFQEGIETFR VIGNITAKAEGKTYALSEGG LYCPPGSLMTFVNAQAEDSQI LYKRRYVPVEGYAPWLVSGN SELERIHYEGMDDVILLDFLPF LGFDMNMHILSFAPGANHGY THVQVEHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGI RL WGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENA VNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYL-W LSPT 26185 56553 B 26332 I 3090 26186 56554 A 26333 3 832	26183	56551	ΙΔ	26330	34	1949	MGVI NNVAGVREDI I ANRAIV
NCDATILSTPKLGASFVDYLV LHQNGGNQQGFQVEGIETFR VISGNITAKAEGKTYALSEGG LYCPPGSLMITFVNAQAEDSQI LYCRYPGYAPWLVSGN SELERIHYEGMDDVILLDFLPH LGFDMNMHILSFAPGANHGY THVQ\EHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGH RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVQESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 I 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYL-W LSPT 26185 56553 B 26332 I 3090 26186 56554 A 26333 3 832	20163	130331	^	20330	34	1947	
LHQNGGNQQGFGVEGIETFRY VISGNITAKAEGKTYALSEGG LYCPPGSLMTFVNAQAEDSQI LYKRRYVPVEGYAPWLVSGN SELERIHYEGMDDVILLDFLPP LGFDMNMHILSFAPGANHGY THVQ\EHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGI RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE ICLSDTEFGPMAQILVGATNG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 I 1145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 I 3090 26186 56554 A 26333 3 832			l		İ		
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LYCPPGSLMTFVNAQAEDSQI LYKRRYVPVEGYAPWLVSGN SELERIHYEGMDDVILLDFLPFI LGFDMNMHILSFAPGANHGY THVQVEHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGI RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENA VNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 1145 LRIGLLYGRRFVPPPYVALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832		1	İ				
LYKRRYVPVEGYAPWLVSGN SELERIHYEGMDDVILLDFLPI- LGFDMNMHILSFAPGANHGY THVQEHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPR QQYEKYQDTHDTPYCEPLPGI RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 I 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 I 3090 26186 56554 A 26333 3 832							
SELERIHYEGMDDVILLDFLPH LGFDMNMHILSFAPGANHGY THVQEHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPH QQYEKYQDTHDTPYCEPLPGH RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832							
LGFDMNMHILSFAPGANHGY THVQ\EHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGI RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 115 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832			l				l I
THVQ\EHGGATQAFAKENNHI AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGI RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832							l .
AYKDTYGVSHITRHDMLQIPK QQYEKYQDTHDTPYCEPLPGH RLWGDTDVIGLFDAETDMND VAILENHPLLGAGFAHKIEQLI DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDS: THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 1145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832							
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DKDWEREWMDNFHPMRFGE LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDSS THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832) ·
LWICPSWRDVPDENAVNVML PGLAFGTGTIQTLSVPAMLDS: THTRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNG SIETPESEGATVDESFVVGGPV DFELLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC QLSKSSIYSTKPPSRQVSVMLC QLSKSSIYSTKPPSRQVSVMLC LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT LSP							VAILENHPLLGAGFAHKIEQLE
PGLAFGTGTIQTLSVPAMLDSS THTRRMRSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832							DKDWEREWMDNFHPMRFGER
THTRRMSTLNLYEITRMSTV TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832		1	ŀ	1			LWICPSWRDVPDENAVNVMLD
TSEHSMTYTLVQVDMKEAQK DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832]	1					PGLAFGTGTIQTLSVPAMLDSS
DTASYRTFNEFFVRPLRDEVR DTDPNVLVMPADGVISQLGKI EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC QLSKSSIYSTKPPSRQVSVMLC LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832							THTRRMRSTLNLYEITRMSTVS
DTDPNVLVMPADGVISQLGKI							TSEHSMTYTLVQVDMKEAQKP
EDKILQAKGHNYSLEALLAGN YLMADLFRNGTFVTTYLSPRE YHRVHMPCNGILREMIYVPGI LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832							DTASYRTFNEFFVRPLRDEVRPI
YLMADLFRNGTFVTTYLSPRE							DTDPNVLVMPADGVISQLGKIE
YHRVHMPCNGILREMIYVPGILFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC QLSKSSIYSTKPPSRQVSVMLC DSSPWYPFSVPVLASKTRYLW LSPT 26185 56554 A 26333 3 832 3090 3090							EDKILQAKGHNYSLEALLAGN
LFSVNHLTAQNVPNLFARNER ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC QLSKSSIYSTKPPSRQVSVMLC DSSPWYPFSVPVLASKTRYLW LSPT C6185 56553 B 26332 1 3090 26186 56554 A 26333 3 832							YLMADLFRNGTFVTTYLSPRD
ICLSDTEFGPMAQILVGATNGG SIETPESEGATVDESFVVGGPV DFELLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56554 A 26333 3 832							YHRVHMPCNGILREMIYVPGD
SIETPESEGATVDESFVVGGPV DFELLLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC	į						LFSVNHLTAQNVPNLFARNERV
DFELLCHGTVCVVGKMRDL QLSKSSIYSTKPPSRQVSVMLC 26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832			l				ICLSDTEFGPMAQILVGATNGG
QLSKSSIYSTKPPSRQVSVMLC							SIETPESEGATVDESFVVGGPVG
26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832	1						DFELLLCHGTVCVVGKMRDLIL
26184 56552 A 26331 1 145 LRLGLLYGRRFVPPP*YALLNI DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 1 3090 26186 56554 A 26333 3 832							QLSKSSIYSTKPPSRQVSVMLC
DSSPWYPFSVPVLASKTRYLW LSPT 26185 56553 B 26332 I 3090 26186 56554 A 26333 3 832	26184	56552	A	26331	1	145	LRLGLLYGRRFVPPP*YALLNK
LSPT 26185 56553 B 26332 I 3090 26186 56554 A 26333 3 832							DSSPWYPFSVPVLASKTRYLWL
26186 56554 A 26333 3 832							
	26185	56553	В	26332	1	3090	
26187 56555 A 26334 1	26186	56554	Α	26333	3	832	
	26187	56555	A	26334	1	3258	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
26188	56556	A	26335	184	2324	ENRVRLFVLIVFQDLPTCYVNH
						NFVCTAADTFTTDITPKAGDAR
		1				LIGIAQTVRHLEDPMRAWKSIH
	1					KSCEILDPIHRAPVKENTHPARK
			!			INISDPAAGAVARIRYEGVLSVC
						RASASAYVSRSRTITVACWYVS
						NTGVTGATIGVKRQHRHARLFS
						GDGAPGFGTGKRDIRQLRRLVR
	1					IQIQRTFFAAVLHVPTPWSRAID
						AAALLTVIDVKVLTACACQAC
		ļ				RTLALRVAQVIDRCSNPGDIMS
						SVARRYWFISRWSAKRDCAVS
						YDQDPGQAQRSCRSCLVAVDR
						GLWLSAYCRSLMTQTLLPDDV
						PRILPNASSPSRLRCLQHLGNYR
						LLDLRKLIWLHRSQFSLCGWEK
						RLVKDLTRIQDTGRAKEILGAT
						ATLEFRLVNTNVDQAAAASGR
						VPGDSEVKQTREGQPVVLYKR
						VILTGDHITDSTSSQDEYNQPQ
						VNISLDSAGGNIMSNFTKDNIG
						KPMATLFVEYKDSGK\KDANG
						RAVLVKQEEVIIIANIQSRLGNS
						FRITGINNPNEARQLSLLLRAGA
						LIAPIQIVEERTIGPTLGMQNIEQ
				1		GLEACLAGLLVSILFMIIFYKKF
						GLIATSALIANLILIVGIMSLLPG
	1					ATLSMPGIAGIVLTLAVAVDAN
						VLINERIKEELSNGRTVQQAIDE
						GYRGAFSSIFDANITTLIKVIILY
				İ		AVGTGAIKGFAITTGIGVATSM
						FTAIVGTRAIVNLLYGGKRVKK
26189	56557	A	26336	1	369	

	of first codon for last amino acid *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) ce
sequer	
26190 56558 A 26337 1	
20190 30336 A 20337 1	
	RLHEILQKDRDFTAEDYEKVES
	RIYHFARLSVGGYTADSSLTLK
	VYLQLMKAPKKRGEVNVGT
	VVAFIKGGFPVVKKDYFRPAA
	DGSSALCRFFPTGNVHDQSDPQ
	KVTDGAVVPVQPTDGPGLRCL
	RRARGCGAGRQGREQAQDCG
	AEIQAEAASRASRVQEGSYPRP
	PNGPFSTDLTGLMQFTKLLVLK
	VESQLTRRIRKCHNLREANIREE
	LRFFNCTNVALRTGVQFNRRPD
	SPGYSRGVLSPERHVRTRLYFT
	SESHVHSLLSILRYGALCNRGG
	TLCCRAIHTLHRHTIVLNGVTV
	TLNLVQLTFYGNVSEIIRHQCQ
	LTRHGNHPLPLTAIQGIALFSDN
	QAAYRFRADQRTLRPFGLPVAR
	QPVRRGGFHDIVIVFDFGTARQ
	QQE/LRLQLRVFSSFVLHEKKR
26191 56559 A 26338 2	1415
26192 56560 A 26339 1434	1667 KRTDWRDRVAFRCRSIAESG*R
	QAIAKELELTASAEILLWDDYF
	APGYGVPNDEGMEAVKLLARL
	EGILLDPAVRLR
26193 56561 A 26340 1	1671
26194 56562 A 26341 1067	3947 FCTVPNAVYIGGPGFGARHNAS NSLKDIAELVPFAHRYGAKIFV
	TLNTILHDDELEPAQRLITDLYQ TGVDALIVQDMGILELDIPPIEL
	HASTQCDIRTVEKAKFLSDVGF
	TOIVLARELNLDQIRAIHQATD
	ATIEFFIHGALCVAYSGQCYISH
	AQTGRSANRGDCSQACRLPYT
	LKDDQGRVVSYEKHLLSMKDN
	DQTANLGALIDAGVRSFKIEGR
	YKDMSYVKNITAHYRQMLDAI
	IEERGDLARASSG
26195 56563 A 26342 182	881 HAEPLPYRGLLLKLGESRGCLL
	PASLPFSLQEFFYSGPREELAQK
	TLLVSVWDYDLGTADDFIGGK
	CDPADQDVVHTALRE\TREELG
	LAVPEEHVWGLLRPVYDPQKA
	TVVPVLAGVGPLDPQSLRPNSE
	EVDEVFALPLAHLLQTQNQGY
	THFCRGGHFRYTLPVFLHGPHR
	VWGLTAVITEFALQLLAPGTYQ
	PRLAGLTCSGAEGLARPKQPLA
	SPCQASSTPGLNKGL
26196 56564 A 26343 237	338

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26197	56565	A	26344	279	533	IHLRRILQRGQ*PRQRWRERCC ESGRGTSGPGSSQ*LTGSPQECC TPAGETGPRAHSPQ*SCWCHCC TPQGRQSICTRTSHRTA
26198	56566	A	26345	126	303	LLLSYGVGASHQSLECHHRSNH GSLWMHSKRCAGGKIRVGTPE CQ*SALERPGLPPLC
26199	56567	A	26346	368	746	SLLHTTSRAPEGPSRYPGPGPPS AATKGQRTRRPLCARPP/PGLPD APL/SPAAPTPTLPLPCPRVAQP AHGPPSASALSSWENRPCCRHE LAAKPPEQAARRGHARTPTAG PAPPGRRAALSGSQFP
26200	56568	A	26347	79	159	SFLGVSRRGGFGRVTGQ*WRE GQQINK
26201	56569	Α	26348	1	3369	
26202	56570	A	26349	3	529	MELAKVVKSHPSAKMVLCIAT DDSHSLSCLSLKFGVSLKSCR\T LLENAKKHHVEVVGVSFHIGR GCPDPQAYAQSIADARLVFEM GTELGHKMHVLDLGGGFPGTE GAKVRFEEIASVINSALDLYFPE GCGVDIFAELGRYYVTSAFTVA VSIIAKKEVLLDQPGMEEENCS
26203	56571	Α	26350	146	502	

NO: of peptide sequence hod objection of first codon for peptide sequence codon for last amino acid deletion, \=possible nucleosible nucleosible sequence codon for last amino acid of peptide sequence codon for last amino acid deletion, \=possible nucleosible nucleosible nucleosible nucleosible nucleosible nucleosible nucleosible sequence codon for last amino acid codon for peptides	X=Unknown,
Sequence Sequence	e nucleotide
26204 56572 A 26351 3 2212 MKRSRCRDRPQP QRAAELSQSLPPR LEERTGPAGPEGK SAEIAASARLPPRI ACRCWSLNPHILM DKKHPQVWRGRI LFSRVKVRSSVVI RGLSQRRRRKK KKRKKKKKR RKKKKKKKKR RKKKKKKKKR RKKKKKK	leotide insertion)
QRAAELSQSLPPR LEERTGPAGPEGK SAEIAASARLPPR ACRCWSLNPHILM DKKHPQVWRGRI LFSRVKVRSSVVI RGLSQRRRRKK KKRRKKKKK RKKKKKKKRKKKR RKKKKKKRKKR	
QRAAELSQSLPPR LEERTGPAGPEGK SAEIAASARLPPR ACRCWSLNPHILM DKKHPQVWRGRI LFSRVKVRSSVVI RGLSQRRRRKK KKRRKKKKK RKKKKKKKRKKKR RKKKKKKRKKR	PPPDRREDGV
LEERTGPAGPEGK SAEIAASARLPPRI ACRCWSLNPHILM DKKHPQVWRGRI LFSRVKVRSSVVI RGLSQRRRRKK KKRKKKKKKF RKKKKKKKKF RKKKKKKKRK RKKKKKRKKRK KEEEEERRKKEEF RKRRKKRKKRK AAAAGERLGKW' VAYFLRRRLQQR QGMAGYLSESDF RDLLKELTLGASO FVADLGAIVRKHI RPFYAVKCNSSPO GLGFSCANKAEM SKIICANPCKQISO QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEF DLYPPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	
SAEIAASARLPPRI ACRCWSLNPHILM DKKHPQVWRGRI LFSRVKVRSSVVI RGLSQRRRRRKK KKRKKKKKKF RKKKKKKKKF RKKKKKKKKF RKKKKKKRKRK KEEEEERKKEEE RKKRKKRKKRR AAAAGERLGKW' VAYFLRRRLQQR QGMAGYLSESDF RDLLKELTLGASC FVADLGAIVRKHI RPFYAVKCNSSPC GLGFSCANKAEM SKIICANPCKQISG QLLSFDNEMELAI NFHIGSGCPDQA LVFEMGTELGHK FPGTEGAKVRFEE DLYPPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	•
ACRCWSLNPHILM DKKHPQVWRGRI LFSRVKVRSSVVI RGLSQRRRRRKK KKRKKKKKK RKKKKKKKK RKKKKKKKK RKKKKKK	
DKKHPQVWRGRI LFSRVKVRSSVVI RGLSQRRRRRKK KKRKKKKKK KKRRKKKKKKF RKKKKKKKKR KEEEEERRKEEE RKRKRKKRKRR AAAAGERLGKW VAYFLRRRLQQR QGMAGYLSESDF RDLLKELTLGASO FVADLKELTLGASO FVADLAGIVRKHI RPFYAVKCNSSPO GLGFSCANKAEM SKIICANPCKQINSO QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	•
LFSRVKVRSSVVI RGLSQRRRRRKK KKRKKKKKK KKRRKKKKKKK RKKKKKKKK	
RGLSQRRRRRKK KKRRKKKKKE RKKKKKKKKE RKKKKKKKRK KEEEEERRKKEEE RKRKKKKKRR AAAAGERLGKW VAYFLRRRLQQR QGMAGYLSESDF RDLLKELTLGASO FVADLGAIVRKHI RPFYAVKCNSSPO GLGFSCANKAEM SKIICANPCKQI/SO QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	
KKRRKRKKKK RKKKKRKKKR RKKKKKRKKRK KEEEEERRKKEEE RKRKRKKRKKR AAAAGERLGK WVAYFLRRRLQQR QGMAGYLSESDF RDLLKELTLGASG FVADLGAIVRKHI RPFYAVKCNSSPG GLGFSCANKAEM SKIICANPCKQINSG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	
RKKKKRKNKR KEEEEERRKKEEE RKRKRKKRKKRK AAAAGERLGKW VAYFLRRRLQQR QGMAGYLSESDF RDLLKELTLGASC FVADLGAIVRKHI RPFYAVKCNSSPC GLGFSCANKAEM SKIICANPCKQI\SC QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	
KEEEERRKKEEE RKRKRKKRKKRK AAAAGERLGKW VAYFLRRRLQQR QGMAGYLSESDF RDLLKELTLGASG FVADLGAIVRKHI RPFYAVKCNSSPG GLGFSCANKAEM SKIICANPCKQI\SG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	
RKRKRKKRKRR AAAAGERLGKWV VAYFLRRRLQQR QGMAGYLSESDF RDLLKELTLGASG FVADLGAIVRKHI RPFYAVKCNSSPG GLGFSCANKAEM SKIICANPCKQI\SG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKH EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	
AAAAGERLGKWV VAYFLRRRLQQRI QGMAGYLSESDF RDLLKELTLGASG FVADLGAIVRKHI RPFYAVKCNSSPG GLGFSCANKAEM SKIICANPCKQI\SG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKH EEENGSTSKTIVY NSVLFDNICPTPIL	
VAYFLRRLQQR QGMAGYLSESDF RDLLKELTLGASG FVADLGAIVRKHI RPFYAVKCNSSPG GLGFSCANKAEM SKIICANPCKQI\SG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	
QGMAGYLSESDF RDLLKELTLGASG FVADLGAIVRKHI RPFYAVKCNSSPG GLGFSCANKAEM SKIICANPCKQI\SG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	
RDLLKELTLGASG FVADLGAIVRKHI RPFYAVKCNSSPG GLGFSCANKAEM SKIICANPCKQI\SG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	•
FVADLGAIVRKHI RPFYAVKCNSSPC GLGFSCANKAEM SKIICANPCKQI\SC QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	
RPFYAVKCNSSPC GLGFSCANKAEM SKIICANPCKQI\SC QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	-
GLGFSCANKAEM SKIICANPCKQI\SG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	
SKIICANPCKQI\SG QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRLI	•
QLLSFDNEMELAI NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	-
NFHIGSGCPDPQA LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	•
LVFEMGTELGHK FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	
FPGTEGAKVRFEE DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	•
DLYFPEGCGVDIF TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	
TSAFTVAVSIIAKI EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	
EEENGSTSKTIVY NSVLFDNICPTPIL TTIGEAFERLHRL	
NSVLFDNICPTPIL TTIGEAFERLHRL	•
TTIGEAFERLHRL	
	-
I I I I I I I I I I I I I I I I I I I	
EELEADTARTLTI	
QQLRKVQEGAQII	
HTFLAGVASLSER	
26205 56573 A 26352 1 860 MKKEDAFLKAFY	
KGSLTRTPCCCTN	
MRVQIFQLENKVI	
VDLYGQIGFDAA	-
AEPLVKKAPPELR	-
SDNLKYLFDNKD	~
KKEHSFRKNNGC	
DFRKLGCEVLGIS	-
ASGLSEDYAVLK'	
RFISDGKGVL/SQI	
SVDEALRLVQAFO	-
CPAGWKPGTDTI	KLNVGDSKE

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
110.	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26206	56574	A	26353	70	745	ERGSTRVIVRASSLCPRSFQSWP
1						PVTRASESQPLTSRPQRWSDGA
	ļ					FKEVKLSDYKGKYVVLFFYPL
l						DFTFVCPTEIIAFSNRAEDFRKL
						GCEVLGVSVDSQFTHLAW\ITT
					1	PRKEG\GLGPL\NIPLLADVT\RR\
						LSEDYGVLETDEG\IAYRGL\FII
						DG\KGVLRQITV\NDLPVGRS\V
						DE\ALRLVQAF\QYT\DEHGEVC
						PAGWKPG\SDTIKPN\VDDSKE\
						YFSKHN
26207	56575	A	26354	1	689	MAAEDELLLPRLPMLLETGKQ
						LLDEVELAAETTGYQIVQEKRA
						REHFINYLTQCHYYHIAKFELL
	İ					KTKNNSAENHTANSSMAYPSL
						VAMASQRQAKIERYKQKKELD
						HRLSAMKSAVESGQADDEHER
						PPVKSFILTRNTAQAKLFGASYP
						SLATMTVSDWYEQHRKYGALP
						DQGIATATPEKFRKAAQQQKY
						QEVKEGEDDE/ALYRVREWDN
						WKDTHPGGYGNRQNMG
26208	56576	Α	26355	1	810	NYLTQCHCYHVAEFELPKTMN
						NSAENHTANSSMAYPSLVAMA
						SQRQAKIQRYKQKKELEHRLSA
						MKSAVESGQADDERVREYYLL
						HLQRWIDISLEEIESIDQEIKILR
						ERDSSREASTSNSSRQERPPVKP
						FILTRNMAQAKVFGAGYPSLPT
						MTVSDWYEQHRKYGALPDQGI
	İ					AKAASSSSSSSSSSSSSSSSSS
						SSSSSSSSSSSSSSS/PSSQEFR
						KAAQQQEEQEEKEEEDDEQTL
						HRAREWDDWKDTHPRGYGNR
		<u></u>				QNMG
26209	56577	Α	26356	223	359	RKQQDEPCGHLQSPGKPFLTLS
						CRDPWGGLPV*LEKDHRKKKS
26210	56578	A	26357	1	3855	ODDDVIEW DOOD TO THE TOTAL OF T
26211	56579	Α	26358	1005	1293	SDRRYEWDPCPR*LNGALLCLL
						LLEHPEGCPWHSVWSTGHSLEP
1						MHFRFPSSQDLQLLLPLPGKLG
						YRARIRNHGHSCFLQRRKTVYQ
0.6010	56500	<u> </u>	0.60.56	5.0	0.70	GDGPLREP
26212	56580	Α	26359	763	978	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26213	56581	I A	26360	11	1217	I MQRRLKRRNAGLPCCEVPGYY
20213	30301	ľ`	20300	1	1.2.17	REDASSPLLPKYKTNFSQCLVH
					!	FFDELRHHLVKTRHVLFIPLNH
						DIMQAFTLHARVIVGKVPGIFS
ĺ						RHPHAVLHLGHSQIGLLMEYPD
		ŀ				ELLWECKEDALALIRRDAPMLT
						DFTHNLLNAPLLDKQAEWCEV
						FDRGRTTSLLLFEHVHAESRDR
						GQAMVDLLAEYEKVGLQLDCR
						ELPDYLPLYLEYLSVLPDDQAK
						EGLLNVAPILALLGGRLKQREA
						PWDALLDALV\QLGGSSLSSDN
						VKKQVNSEERDDTRQALDAV
						WEEEQVKFIEDNATACDSSPLN
						QYQRRFSQDVAPQYVDISAGE
						GQSSFQLVSYWEKDVQTCLEFL
						PSGGFVVSLASGVKLQTFTETD
						NLVKDITFFGKISTRSLKTYLKD
						VTEKREQSCVNLELK
26214	56582	A	26361	1	783	VIERREQSCVILLER
26215	56583	A	26362	2	1646	PGSTISFRRVTQREKKQPEAELC
20213	30303	^	20302		1040	QGSTSNLFQFIHPSLLSAQTVEL
		1				GLSKFVPKKMIITQTSH\CYMTS
						LGILFLINILPGTTGQGESRRQEP
						GDFVKQDIGGLSPKHAPDIPDD
						STDNITIFTRILDRLLDGYDNRL
						RPGLGDAVTEVKTDIYVTSFGP
						VSDTDMEYTIDVFFRQTWHDE
						RLKFDGPMKILPLNNLLASKIW
						TPDTFFHNGKKSVAHNMTTPN
						KLLRLVDNGTLLYTMRLTIHAE
						CPMHLEDFPMDVHACPLKFGS
						YAYTTAEVVYSWTLGKNKSVE
						VAQDGSRLNQYDLLGHVVGTE
						IIRSSTGEYVVMTTHFHLKRKIG
						YFVIQTYLPCIMTVILSQVSFWL
						NRESVPARTVFGVTTVLTMTTL
		1				SISARNSLPKVAYATAMDWFIA
1]	VCYAFVFSALIEFATVNYFTKR
		1		1		SWAWEGKKVPEALEMKKKTP
				1		AAPAKKTSTTFNIVGTT\YPINL
						AKDTEFSTISKGAAPSASSTPTII
						ASPKATYVQDSPTETKTYNSVS
						KVDKISRIIFPVLFAIFNLVYWA
						TYVNRESAIKGMIRKQ
26216	56584	A	26363	217	559	MKKALQVAMFSLFTVIGFNAQ
						ANEHPHETMSEAQPQINSATGV
						VKGI\DL\ESKKITIHHDP\IAAVN
						WPEMTMRFTITPQTKMSEIKTG
						DKVAFNFVQQGTLSLLQVIKVR
						•
L						KPAQ

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	I .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
·				sequence		
26217	56585	Α	26364	72	157	ERRKF**SQSS\QKKNKERLQNA
	-					VIYLEL
26218	56586	Α	26365	3	620	VSGGGWEPSGTLTAFKTASAIT
	İ					TEMASRS\QGIQQLLQAEKRAA
	1					EKVADARKRKARRLKQAKEEA
	ł					QME\VEQYRREREHEFQSKQQA
		1				AMGFQGNLYAEVEQATRRQV
		1				QGMQSSQQRNRERVLAQLLGM
		1				VCDVRPQRPSDLQKEEMTTFSP
	1					SLIIPARACRFLVRAQQSSGHLH
	l	1				YRAKDPVGTRSLRHTRSSRIHG
						GVPTEKTCVAKT
26219	56587	A	26366	28	187	TGTESGQYHCKRRKMGPEPIIK
						SLWARSDEPVFWG/LFGAGGM
		:				WSAIIAPVMIR
26220	56588	A	26367	1	870	MAVWPTGALALTPSPAGDAGA
20220	20000	1	20307			CSTAGGPCQGARGPRGSGPPA
						WGPDAVLEPLRGQRKPYVRPM
		1				TSTWWKKLPFYRFYMLREGTA
						VPAVWFSIELIFGLFALKNGPEA
<u> </u>	1					WAGFVDFLQNPVIVIINLITLAA
						ALLHTKTWFELAPKAANIIVKD
	1					EKMGPEPIIKSLWAEPEMINPNP
						KRSDEPVFWGLFGAGGMWSAI
		1				IAPVMILLVGILLPLGLFPGDAL
						SYERVLAFAQSFI\GRVFLFLMI
						VLPLWCGLHRMHHAMHDLKI
		Ì		ļ		HVPAGKWV\FYGLAAILTVVTL
						IGVCTI
26221	56589	A	26368	741	894	IGVEII
26222	56590	A	26369	504	558	
26223	56591	A	26370	897	1097	RKWSOSTRLPWETGPSSETSPS
		-				GPIVSPTRSHLASPRRPPPTPP*S
						SPRRLLGAIPPGIGVPPLNE
26224	56592	A	26371	200	657	GPRRLSFVTGHKAYRGLGIVSG
		-	20011			PTVPLVCAVCCSYWDPGVPRV
						VRLVVRLWPLCRCGGRSGDAS
						VAAAPLVCGGGI*DWDHCPFV
						CGPSLCALRPSCGCGSGMACRV
						VLLLRCPLAMFAFTSFFSVTEV
						GKFSPFPLPEFFFSGFALDLSLP
26225	56593	A	26372	196	404	
26226	56594	A	26373	1	3162	
26227	56595	C	26374	287	349	
26228	56596	В	26375	366	1637	
26229	56597	A	26376	365	604	VLAVSYPSLCLLL*KPIGPEDAI
						YALSSDFTCGSPTAAGRKQIRG
						EVCPRERCSVETCLSPNFHSLVS
1						SFPFSLLQGFK
L		<u> </u>	L		<u> </u>	or i i obby or iz

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ł	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26230	56598	Α	26377	1	1404	TLVRCFPPLKLIFSIFKKKAASL
						GSSQSSRTYAGGTASATKVSAS
						SGATSKSSSMNPTETKAIPVSQ
						QMEGPHLPNKKKHKKQAVKTE
						PEKKSQSTKLSVVHEKKSQEGK
						PKEHTEPKSLPKQASDTGSNDA
						HNKKAVSRSAEQQPSEKSTEPK
						TKPQDMISAGGESVAGITAISG
1						KPGDKKKEKKSLTPAVPVESKP
ł						DKPSGKSGMDAALDDLIDTLG
		ĺ				GPEETEEENTTYTGPEVSDPMS
						STYIEELGKREVTIPPKYRELLA
						KKEGITGPPADSSKPIGPDDAID
						ALSSDFTCGSPTAAGKK\TEKEE
			:			STEVLKAQSAGTVRSAAPPQEK
						KRKVEKDTMSDQALEALSASL
						GTRQAEPELDLRSIKEVDEAKA
				:		KEEKLEKCGEDDETIPSEYRLK
						PATDKDGKPLLPEPEEKPKPRS
						ESELIDELSEDFDRSECKEKPSK
						PTEKTEESKAAAPGSCVGGCVS
26231	56599	Α	26378	1	688	ITAISGKPGDKKKEKKSLTPAVP
		l				\VES\KPDKPSGKSGMDA\ALDD
		1		ĺ		LIDTLGGPEETEEENTTYTGPEV
						SD\PMSSTY\IEELGKR\EVTIPPK
		1				\YRELLAKPIGPDDAIDALSSDF
	1					TCGSPTAAGKKTEKEESTEVLK
						AQSAGTVRSAAPPQEKKRKVE
		l		•		KDTMSDQALEALSASLGTRQA
	1					EPELDLRSIKEVDEGSLPDFQQQ
		ĺ				SLSLGLPWPKMGQFLSSTFLEG
						SPATQRK
26232	56600	Α	26379	199	384	VYKECR*GFSHESPPSKPQS/HIE
				-		*KFCMCGENGQGLRKKSSSKN
						SFFGTSFTWVGRENVKHI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26233	56601	Α	26380	166	2172	TYILRNLYKEVMLENYRNLLSL
20233	20001	()	20300	1.00		GKAVFFPFLH*FSRDLLIT*YVP
						QSQQFLSQHVLQIFLGLCAENH
						FHPGNSSPGHWKQQGQQYSHV
						SCWFENAEGQERGGGSKPWSA
1						RTEERETSRAFPSPLQRQSASPR
						KGNMVVETEPSSAQRPNPVQL
						DKGLKELETLRFGAINCREYEP
						DHNLESNFITNPRTLLGKKPYIC
						SDCGRSFKDRSTLIRHHRIHSME
						KPYVCSECGRGFSQKSNLSRHQ
						RTHSEEKPYLCRECGQSFRSKSI
		1				LNRHQWTHSEEKPYVCSECGR
		1				GFSEKSSFIRHQRTHSGEKPYVC
		1				LECGRSFCDKSTLRKHQRIHSG
		ļ				EKPYVCRECGRGFSQNSDLIKH
		l				QRTHLDEKPYVCRECGRGFCD
				}		KSTLIIHERTHSGEKPYVCGECG
j						RGFSRKSLLLVHQRTHSGEKHY
						VCRECRRGFSQKSNLIRHQRTH
	l					SNEKPYICRECGRGFCDKSTLIV
						HERTHSGEKPYVCSECGRGFSR
1						KSLLLVHQRTHSGEKPQMTFSG
						VTPQLLERTVLLLAEMHSRDAL
Ì						RSGTHSQPQGAACTTGAMHLC
İ						RGTFWPQPLTQRGQLQKVIPDP
						EIPIELKDHWVADTLQVSFFLCP
ł	1					VLPSLPSESSIFCLVVCSINYAV
1						APQSGLMREKDVHVWECGPPP
						FARTAPITPTSDQNWRPLREKY
26234	56602	Α	26381	434	946	NTFCLTAMKILCMWFSRWHSR
20234	30002	1	20301	134		WVGMQGPSC*PQRTLWMATLS
1						STGRSCVPAACTPAPCGRISAA
ŀ	1					GRLRCSQLLPHAPAPAACCSCP
	1					SVHISFQPL*QLRTSLWTVQMK
	1					SQVTQTQVGSHSSTSQARALQG
						HQQVQKPGSRIRTGGVKPQLEG
						PGRWLKIRLEGHSWTCRQ
26235	56603	A	26382	3	2119	I GRADRIGE COLOR
20233	120002	112	20302		2117	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
İ				sequence		
26236	56604	A	26383	3	2237	NRRKFSVSIGFYTVMDAQYKII
20230		l' `	20505	ľ		TKTAHLITKESPQEEGKEMFAT
						MSKLKEQLTKVRK*FNALLYES
						QQLLIPLEELEKQMTSFYDSLG
		1				KINEIITVLEREAQSSALFKQKH
						QVRTILFKWCNSSQKMTLCLVL
						GSMISMLSTAKITIAGYKSEVEV
						SVSHHCI*NCKKTLTLIEKGSQS
						VQKFVTLSNVLKHFDQTRLQR
				İ		QIADIHVAFQVICSPC*DWKKH
		ł				VETNSRLMKKFEESRAELEKVL
						RIAQEGLEEKGDPEELLRRHTV
		ļ				SPPFRDQRVLNAFLKACDELTD
						ILPEQEQQGLQEAVRKLHKQW
						KVSQDRTAYHLLHLKIDVEKN
						RFLASVEECRTELDRETKLMPQ
						EGSEKIIKEHRVRLPHHSPHHLC
						EKRLQLIEELCVKLPVRDPVRD
						TPGTCHVTLKELRAAIDSTYRK
						LMEDPDKWKDYTSR*PQNGLW
						ISTNETQLKGIKGEAIDTANHGE
						VKRAVEVSSGSLSKRGETLSWL
						KSRLKVLTEVSSENEAQKQGDE
						LAKLSSSFKALVTLLSEVQHLL
						THFGDCVQYKEIVKNSLEELIS
						GSKEVQEQAEKILDTENLFEAQ
		1				QLLLHHQVKMPLSSAKKRDVQ
İ						QQIAQAQQGEGGLPDRGHEEL
						RKLESTLDGLERSRERQERRIQ
						VGAGS*ERFETNKETVVRYLFQ
	1	l				TGSSHERFLSFSSLESLSSELEQT
						KVYYGSLESIAVQAENLVKEAS
26237	56605	A	26384	1	390	GTSLFDEEGAKIVKDLMSKAEK
						NGVKITLPVDFVTADDFDENAK
						TGQATVASGIPAGWMGLDCG/P
						ESSKKYAEAVTRAKQIVWNGP
						VGVFEWEAFARGTKALMDEV
						VKATSRGCITIIGKRSYTKLIPI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO	: Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26238	56606	A	26385	1125	2228	NVMSHLGRPDGVPMPDKYSLE
						PVAVELKSLLGK*VPGSGAGRL
						CGGGSCQARCYAGSVILLENLR
		1				FHVEEEGKGKDASGNKVGPVIL
						TLLGVRA*VCKRLWLNVNDAF
						GTAHRAHRYQEPCRLPH*EQYS
						YLLE*PKYFAKALESPERPFLAI
						LGGYEELFKIML*VLFAW**AIT
						WIGGGMAFTFLKVLNNMEVGN
						KCQVDVK*LSMIIAGCINEKNG
						VKITLPVDFVTADKFDENAKTG
				İ		QATVASGIPAGWMVSHLSGLV
						V*VNRNSVVSFIHFVWNGPVG
						VFEWEAFARGTKALMDEVVK
		1				ATSRGCITIIGKRSYTKLIPI*AG
		1				RILIRGRCTGGGASLELLEGEGL
						LFFGLFGIRVDCAVRGG
26239	56607	A	26386	2	482	TRQAWHEGPRGVPHSASLRSA
20237	,	-		_		RRQSAPSLTESPTSVPSCISKMA
		1				LSNKLTLDKLD\VKGKRVVMR
						VDFNVPMKNNQITNNQRIKAA
						VPSI\KFCL\DNGAKSVVLM\SHL
						G\RPDG\VPMP*QVTPLEPVA/V
						VELKSLLGQGMFCS*RDCVSPE
						VEKACANPPG
26240	56608	A	26387	3	378	
26241	56609	Α	26388	311	578	LGIRGQTLGFLSRARCGGSRRS
			i.			LEMQNNAGEFVDL*VPRKCSA
						SNRIIGAKDHASIQMNVAEADK
						VTGRFNGQFKTYAISYFLNLFL
					_	нн
26242	56610	A	26389	3	333	DAWDLCRVTSCFLSLSRAVWW
						QQAQPSLEMQNDAGEFVDLYV
				1		PRKCSASNRIIGAKDHASIQMN
						VAEVDKVTGRFNGQFKTYAIC
						GAI\RRMGESHDSFLRMAKADG
		-				IVSK
26243	56611	A	26390	23	389	LAASFLSRARCGGSRRTQALEM
						QNDAG\EFV\DLY\VPRKN\SAS
						NRIIGAKDHASIQMN\VAEVDK
						VTGRFNGQFKTYAICG\AI\RRM
						GESDDSIL\RLAKADGIV\SKNFL
						TGEESQDVGIFCHK
26244	56612	A	26391	206	354	
26245	56613	A	26392	1227	1430	GSSSPRDPQEEDLKLLKFAFSR
						GPPLSLVHPPPLLSYPSARR*PQ
	ļ					TPPRPPPRHPSLHPLHPPSAQP
26246	56614	С	26393	17	319	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26247	56615	 	26394	<u> </u> 1	645	MIHEQNENIKKNTKTIKKNQTEI
26247	56615	Α	20394	J	043	
ł					}	LELKNTVTEWKNLLEVFNNSFR
						QNEESVNLQTSYLKSLSRGEKR
	1					KKKCEEMIRDLGQYQPGPYMH
						DGYSRRESGPNVPRRAQVDGG
<u> </u>						DARKGTHRRKRVLERGLWLKR
1		1				EDKKAQGYKGR*KGPRV*GTD
		1				PQEEDLQRLSAETWLVL*PEPR
1						P*KAPAKKGEKVP*GRKGKAD
1		İ				AGKEGNNPAENGDVKTDQAQ
						KAEGAGDAK
26248	56616	В	26395	1	663	
26249	56617	Α	26396	265	735	VMWLRYDTLSETHMHQLLGL
						NLLFLLSQD*VAEFHMELEWLP
				·		ATDTQTNAYIKRPVSLEPYLME
1						GGYNKVFLAKGNIPAKSYTFIHI
		1			•	LLDTIRDEMAGCIEKAYEKILFT
						KATWILFLNTPKQMMDNTKK*
						GWVLGPNNYYSFASQQQKLED
						TTIPS
26250	56618	Α	26397	215	386	
26251	56619	Α	26398	3	515	QLPESAYMHQLLGLNLLFLLSQ
ļ						NRVAEFHTELERLPAKDIQTNV
		Ì				YIKHPVSLEQYLMEGSYNKVFL
						AKGNIPAESYTFFIDILLDTIRDE
		1				IAGCIEKAYEKILFTEATRILFFN
						TPKKMTDYAKKRGWVLGPNN
						YYSFASQQQKPEDTTIPSTELAK
						QVIEYARQ\LEMIV
26252	56620	Α	26399	423	4482	KLVWILFDFICLAFL*FFSTYMY
						SCE*ILVKLTLYFSFHVYLLIYC
		1				ECENLTGTLDLVFI*KCKSLLIW
						IA*TVYKKIHMEGEVKG
26253	56621	Α	26400	173	174	AVSLLKHSNNDLCSS/GFPTSRT
						ADPTSCGSH\WPWGPQSLKQ*P
						ELYIGPF*PRLELKQLGCRAPSP
26254	56622	Α	26401	135	699	RDLVPCAPAAPAMAKRGQDTV
						WAMASEGASPNPCQLPQGVEP
						AGQCRRKMWG*SPHTEPPLGT
ł						A*WESLELPRDLLNGFDQNAD
		ı				NDMDNEIQAEVVSDGDEELVG
						NQSKGTWCPVPQLLQLWLKGA
						KIQFGPWLQRVQAPILASFHKV
						LSLQGSAEGKCGVEAPTQSPH
						WALPSGAVRRGPPSSRPQNGRS
					[TNCLHCEPGKAADTQCQPVKA
		1				ARREVVPCKAKGAELPKTMGT
						DLLHQCDLGVRHGVKGDHFGA
					[LRFDCPTGFWTYMGPVAPLVW
1					1	PIFPIWNSCIYPMPVPPIVSRR
L	.i	<u> </u>		1		HITTOCHTMI VIETVOKK

SEQ ID NO:	SEQ ID NO: of peptide sequence	ŀ	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26255	56623	Α	26402	27	264	RLVEWL*PRDLLNGFDQNADN DMDNEIQAEVVSDGDEELVGN QSKGTWCPVPQLLQLWLKGAK IQFGPWLQRVQAPILASFHKVL SLQ
26256	56624	A	26403	624	955	VPSLGSFHVVLVLSVHRRQELR FGNLHLDFRRCMEMPGFPGRSL LQR*SPHGEPLLGQCRREMWG QSPHTESPLGH*LMEL*HPPSPR MIDPPTACAVPLEKLQALNASH
26257	56625	A	26404	851	1387	PKIVELLKYSGDQLERKLKKDK ALMGHFQDGLSYSVFKTITDQV LMGVDPRGESEVKAQGFKAAL VIDVTAKLTAIDNHPMNRVLGF GTKYLKENFSPWIQQHGGWEK ILGISHEEVD*NIRFVIRNTLCLL WSCARWPSDGPTGDYNVQGR WSIDVFKTIIPVTGEASGEVSFV
26258	56626	A	26405	I	229	LRRLGITHVLNASHSRWRGTPE AYEGLGIRYLGVEAHDSPAFD MSIHFQTAADFIHQNKRAISAL HLCRKSGIRQA*MSIHFQTAAD FIHQNKRAISALHLCRKSGIRQA
26259	56627	A	26406	2	594	SVLGLTLPAPRFKTLRRRWVQG QKVLRKAPFGKKPRGSLTFWR ASTRVRDMANNRRELRRLGIT HVLNASHSRWRGTPEAYEGLGI RYLGVEAHDSPAFDMSIHFQTA ADFIHRALSQPGGKILVHCAVG VSRSATLVLA*PHAVPPPLPFVE AIKKVKDHRGIIPNRGFLRQLL GLGPQLAAGSGSMRGGGEKLR
26260	56628	Α	26407	605	1231	NCSNSGVWRISHKKERSIPDSK RRRSRGNTKSSSPRPTTRSLEKL LTSGSPRIWPVRMS*LHDKARR ASFSSSSSAIKKAFSSASRSSNES VSSLSNSSLEGQSKSMSISSSST GVGSRLALGLYTSSEMVKGSSF ILSSSSLGGSSYSRAAFTGELEIK GAEMFSSLGNGTPVLRAVTLEP SLSRRTNTLLLQWFPMCNWRL RRVWI
26261	56629	Α	26408	771	1121	FSPKLLPRREGRKPCEAPARTQ TPRSKSSTPPSQV**SVDSDPQP KGKQDRSRGGPLQERAQRESG PNLLAATVVPRPRAERHPAISTE GPTGPPEGSAPSATSSVAAAGP APHSR

	SEQ ID NO: of peptide sequence		SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
26262	56630	Α	26409	3777	4343	DQEEPFSGNSSIIQSLFTIKLNPQ
					,	SSLQEVCSLDTHNSPVRVFKNS
			!			CSAKFHFKFVWNVILLLQLSSE
						ELILSFVIPGVGHCWSSYCYILQ
						PRIFPLWSFYIVIYVEDSSICVSS
						LFPSWR*RP*IIGSIK*CLSSQMG
						WNFQSW/NLPR/CVVLVLWSIK
						KGL/HIWCMPDFPAFRKESLLN
						FRWLGHLLA
26263	56631	Α	26410	473	667	PCSDWGWRSPWNLQLEETWAL
						*CCSHSHKVSQEGTWMKLETII
						LSKLLQGQKTKHPMFSLTGGN
26264	56632	Α	26411	1416	2108	QRANIQNLQRTQTNLQEKRNPI
						NKWVKDMNRHFSKEDIYAAN
						RHMKKCSSSLAIREMQIKTTMR
						YHLTPVRMVIIRKSGNDRCWR
			}			GCGEIGTLLHCWWDCKLVQPL
					,	WKTVWRFLRDLQLEIPFDPATP
						LLGIYPKDYKSCCYKDTCTRM
						FIAALFTIAKTWNPTPKCPS\MI
						DWIKKMWHIYT\MEYYAAIKK
	! :	ŀ				DEFMSFVGTWMNLETIILSKLL
		<u> </u>				QRQKTKHRMFSLIGGN
26265	56633	A	26412	1	278	FRCSSYYYFKYFFCFFLFSLLLF
		İ				*IFFLFLSLLFASLLFLASPLCVC
						YFFFIVVAQFLNSLFHFFSLFVL
						CFSGLEVSIDISSSVEILSSAMSIT
26266	56634	A	26413	181	742	LMGLSKAFLIT PLLKSGCISFLLLRLLVKLYRFL
20200	30034	^	20413	101	1/42	VRRNNSTFNQVVLKRLFMSRT
						NRPPLSLSWMIQNIKLPDRENR
						KAVAVGTITDDVRVQEVPKLK
						VCALRMTSQARSGILGAGGKIL
						TFDQLAPDAPKGCGTVLLSGPR
		ĺ				KG*EVYRHFGKAPGTPYSHTKP
		ļ				YIRSKGRKFERTRGRLASRGYK
						NYRSYPLIKDCL
26267	56635	Α	26414	368	675	SLSTLLSSRDCPLATISKQLRVL
						ARGCVVNNCFCKHLLNTCSLA
						GTVPG*GASSGRQKFKLLAKFK
]						VLARLCSSGGSRGEPFSCLFLFL
						GATGILRLMASSS
26268	56636	Α	26415	40	355	LLGNPSPVVKGRPCRHDGSEI/A
						PRVYFRGCS*SSHSWVSHFLSA
						PSHPRMLPTSRHRPPLRPLT*ER
						RGKRRDD*PLHHP*P/CWSTCSP
						STSARATPTPPSGSGW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26269	56637	A	26416	347	725	EAKRRRPLSTLMEKRCFQPLWT RPSRKKPRGRTWRPPALNPTRI
						AGPPSPPAVSPGFGPIPP*SISCFP KGPGFSMGFLRLRCFSAVQKVL
						APGSPA*PCLSCGPFRTALGDL ARTPEKLCWLERS
26270	56638	A	26417	525	708	IVAELIQHHQLPCSHPLSGGKIK DQQVVFLSLSP*SSHNKTLY*AP KTNQRPQDYPEGCNA
26271	56639	С	26418	-	1050	RINGRIGOTTEGENA
26271	56640	A	26419	934	1708	PQRGVWVLSVILHFPWLGSGPL
20272	30040	A	20419	934	1708	PNSAGD*AARYSWNQILKPDC* WKLSSAAGISFQRS*VNFHYGE FCPKIPSGMYESKLGSHTDKTP
						HFLPAQKTRSTPSPATAPLPGAT SPRPPRGRRRRRRCPEQQPPPPL QAGPTAAARHRQDPLPRFSPLC
						FHSHPRASGAGSRPAPARVSPW TRRPAAPVSSGRGRLAPKRSLS
						PRPPRPGQGGGRVPARRELPLA PRGLCVRLVYSLCSSLCGSLPSF SLGSLVFSSSDQG
26273	56641	A	26420	630	734	TAARSGYPGRAGTLTGLHPMQ VCRCRR*PYSRGT
26274	56642	C	26421	4	90	
26275	56643	A	26422	216	305	ICWKYFCAG*CGKYFTLGPRSH SYRRSDY
26276	56644	A	26423	859	1248	CVISVFRASRKSKHNVIAVVFS YCSVSVGQRPAVP/QHQVLLQT QGISGYPGRAGTLTGLHPMQV CRCRR*PYSRGT**/REPS*LREG GSAPPKSVCWPVGACIKRLSSM
						SSSFSSFPFIKHAHACCRVLS
26277	56645	A	26424	132	548	SSGFSWGFFSGYQRCRESR/CD YPPPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEVWDHGPTR
						IVGLIISLGPRSHSYRRSDNQTG TTVPLVSSV
26278	56646	A	26425	382	697	YAVKQAKTTFEDMTGRRASLL LHKGYLEFELFLQTAAYQSGSP APQGTWSGTGSVCHCCSLAE*T PFRTTGACCGLMARTGHARAA SICPPDAVAPLSPSPNAWF
26279	56647	A	26426	167	412	SYVKYFPHQPAQKYFQQIHCAI GLHNAGYPGRAGTLTGLHPMQ VCRCRR*PYTILSLQEQTDVVSL N

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26280	56648	A	26427	3794	4021	RGLCAPLPPLTPCFSPPLRRAA SHLAPPTPLPTPQTPTRTRALPS SPGLGRGA*RTVLPSAPPEVPLA WGCRRA
26281	56649	A	26428	65	564	PHPDSGPQ*LQ*PHPDSGPR*LQ *PHPDSGPR*LQ*LQ*PHPDSGP Q*LQ*PHPDSGPQ*LQ*PHPDSG PR*LQ*PHPDSGPR*LQ*PHPDS GPR*LQ*PHPDSGPR*LQ*LQ*P HPDSGPQ*SDSGPRGHR*LQ*L Q*PHPDSGPQ*LQ*PHPDSGPR* LQ*PHPDSGPR*LQ*PHPDSGPQ *LQ*PHPDSGPQ
26282	56650	A	26429	184	438	DPAVDLCDLSSRRLLFS*RYVL VMLFSISLVSFVFISVHVICNYPF ALFFVCASFCGGAGGLVEFVL MIVGDASAALLCMPRCEC
26283	56651	Α	26430	524	1995	
26284	56652	A	26431	601	1058	LPSSGGRCRSPKTR*SACLVSGS PRTPAMIRSGAGQPLARSPPTPT PPFCRPLTRAPQASSMTWTGTS TTTWTLCAMRTDCTGLPSTSPT WCFCTRSSSWPAATSGSNSRAP ARSWSTLCLSC*SASTRPGPRGP CRRQWWRRATPSRPSAR
26285	56653	Α	26432	1	371	
26286	56654	Α	26433	71	335	
26287	56655	Α	26434	2	416	
26288	56656	A	26435	60	370	
26289	56657	A	26436	466	1454	PCVFQIGPRRIHTVRVRGGNKK YRALRLDVGNFSWGSECE*GPL GVGGKTHLNGFKIHRARPALIF LNSAA*EIGAGKDCGLPNITRN VG*GVVEDELMPHGL*RLRVPF ISP*GPHGAEEPGGVCQGHLSSS LLDAKFLL*AGCTRKTRIIDVV YNASNNELVRTKTLVKNCIVLI DSTPYRQWYESHYALALGRKK GAKLVRVTSL*GLWGGQPDSS LLVMKTLSSSATEGREMRAF*A EEGQHWGVQGSRKLPGPAFLP* AHIFVSPFQTPEEEEILNKKRSK KIQKKYDERKKNAKISSLLEEQ FQQGKLLGEKADELEVGSRRD

SEQ ID	_		SEQ ID NO:		1 8 1	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
26290	56658	A	26437	2	787	SQWLKLPSPLPHAGISRY\NWD
						QAP*KTGGPRESPYHKKREVM
						KLGRPSCPN/NPKIGPPAGIQHSP
		İ				VCRGGYQEIPVPLRLDRGEFLP
						GGSECCTS*NKGSSIVVLQCHL
ł						NNGAGFVPKTPGWKEFCIVASS
						DQQQPYRPVVTSSHLCACPLGP
						QRKGAQAGLLEERRDF*TKKRS
						\KKLRKEI*LKRKKNCQNSAVL
					•	PGREQFPARGKLSCRA/SRFQGP
		1				GQLWAEQDGFCA*EGQKSLEF
						LSLGKSKARKGQIKSFVLSSPM
26291	56659	A	26438	62	872	ANWTEPDDTKTMWRLSVPLDR
						SPQTQNCTGEPLMPTGRQELPQ
						RGPEPMEAPAPARPQSRRVPAA
						GPVARQPHMRPPHSKQGEKQK
						MPGSRWPGQRGRGRWGSPLES
						A**TRKIFTGIPILPLLPGTPGRP
						APEEGMQSADKNRVKRRGGTQ
						RNSALALEFCELLFVSSKWFCA LPSTLRLKALSAAVALLAGDPE
						FGVRNVWVWVAGGVRCKRVA
						HRTTEAGAFFPDWFVWVFAAT
						KRGDGETSGCEHSEPVSGSSGG
						SPPRGQYLPGM
26292	56660	В	26439	1	606	
26293	56661	В	26440	48	381	
26294	56662	Α	26441	16	209	
26295	56663	В	26442	466	1275	
26296	56664	Α	26443	2	252	
26297	56665	A	26444	95	266	CTI DODGILI CD CDI TA DDI (CCDD
26298	56666	A	26445	119	343	CTLRQESKLSRGDLTAPPVSSPR GHRSSKKGGNT*LGSMQL*AES
						CRAEPPRPALLCPGRSVSACQW
						GPEGPFF
26299	56667	A	26446	1	383	NTGLGRGKAMTPSMSCRISML
20299	30007	^	20440	1	363	LQRPGGVLVGWDPDAAHPVGT
		ŀ				*RHSVAQHN*MPW*GAEGMGQ
		İ				PC*WHGMGTSDGPGLSDSERPE
		İ				LS/HADSEGRVSKAKQSELAGP
						GQKR*GQKPPKGYRFQERTQR
26300	56668	В	26447	430	540	
26301	56669	A	26448	111	591	PGAPSSHSGPRLLAWEPIVLAP
					1	VASLGLGEAEDCSFLGRKAGV
						GPRHPR/ARRVHGSGSRETCRG
						*QEPRPMLREPVCSAFLRTVKK
						LSGRVFPPLAVKQVLSAAPAVP
1						ALLRTAPKTPWDGPESAESQPP
						SLGPAVVLDISDRRKQETIKAT
				<u> </u>		GGPGRLRR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26302	56670	A	26449	11041	1410	QEERGKVEE*ELEGRRREEKRR
20302	30070		20117	1041		GRGRRGSGLEEGRRRRRRGGG
						DETKDKR*RKRGGHRKEKKEE
						RRRRRGGGAAKKEEEEDRLP
						TRAFSCVEQQSASKSPLVELHP
						GPIPQGPPLAAAGAC
26303	56671	A	26450	288	424	KRPAEGAPNP*GRPGIRPQA*K
		-				RPAEGAPNPRGPRRKEGRSGAK
						GSLDTGDGGEAWWAGSPHPS
						WP
26304	56672	A	26451	111	540	LPLALSNPKQEVVSGRGGQVDS
						QAGLTMTGRAVCCLQLCLNAS
					ļ	GAGDAEAMSAGPPGPGPARAD
		İ				TEQLPSPSLPQVS*HWRGSASTS
						ATRTWPLRRRCSSMARSTCRAS
			1			ASASAGPWPWPGAPVPWRHSA
		İ				EPSCSQLPGPSA
26305	56673	В	26452	57	558	
26306	56674	Α	26453	804	1524	ARETSHGDFLHFPLIWLFSLKG
		1			İ	NVPAARINIMNWNQGLISHVGE
				Ì		GNVNRKHDVIGFNFPWNCLFN
					1	VSDLVTMIGSPRQRNHFGLVM
				·		VLTGIHTFHRHVGHCRCGPWS
						NQASHQKGDDLEHEQNPTNNA
						QLLGAHVFYNCPRPFLRPPFFFS
						P*NKCFRGELFAPSSHHSPSFLA
						SFLGAAKLQRCWSAARMGPGR
						KAPARIPPAQPARVPPMPGAVI
						VAAPPPVDAPIVRICVHVCLHH
26307	56675	Α	26454	2	330	SCSRSGTALGVPVLAGPVRSAL
						TYLPAHSAGQRHQHDAGPTRG
						LGAI*DLPPVVTPGEQPSPCRGQ
						DQVPIVAAGE/PRCAPSLGSPPG
						LE/PVSLSSMSSPPRPPSCPLSG
26308	56676	В	26455	1	969	
26309	56677	Α	26456	43	568	RSRLVFPLYFHASQGPGTASRE
						VPGGWAWGPVAQRINGICLLH
						STGPEAPSTMPPPTRLCGGPCGP
						ALPFSSQLAARGNPRSLPAAQL
						RALLSKISPPVVTPREQPSPCRG
						QDQGADCGKQVNKMCSQAWG
						SPPGLELCPCHQ*AGPPRPPSCP
		<u> </u>				LSG*FVLRTGAPGAAPPSGTV
26310	56678	Α	26457	1	456	HEDAASSFQADVSLGNDAAVP
					1	LSGRGGINTYIPLIIPGFPYPTAA
						TTAAAFRGAHLRGRGRTVYGA
						VRAVPPTAIPAY\PGVDMQPTD
	1					MHSLLLQPQPPLLQPLQPLTVT
						VMAGCTQPTPTMPLPLPLAME
L		1		<u> </u>	<u> </u>	LALWRVYTEVATADLPPTEVT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26311	56679	A	26458	609	1031	VCKSYPGHQGSSCLPDGQIQLW LHGYGQEFCGQETHPFLDG*RG AESL*GHNSGHDQWCLGDGCC WGWLLTYERHEQLPAELEAPG GWGKDGDSRGTESTC*EAGAG AGPAHPAPPAPAAEGEPDLFQL
2 62 12	7.6600	<u> </u>	25150	<u> </u>	200	PGQGCSRIPCG
26312	56680	A	26459	1	393	OTEGO A OTEGO OGO TOGGENIO
26313	56681	A	26460	357	843	QTEGGAQTDGQQSQTQSSENSE SKSTPEDNKICG*KPDHK*TFLF YQEISISI*RCACFPPFSRCMQGF GFVTFEKCNFMFPNVVHFFPAL FSPCYDMH*SSLSSNSLKCLPSI VVTVHLLLNAS*NFCHILGLPL VPGFPYPTAATTAAAFRGAHLR VFV
26314	56682	A	26461	3	1172	GRAHGEAAADGGGGMQNEPL TPGYHGFPARDSQGNQEPTTTP DAMVQPFTTIPFPPPP*NGIPTEY GVPHTQDYAGQTG\EHNLTLY GSTQAHGEQS\SNSPSTQNGSLT QTEGGAQT\DGQQSQTQSSENS ESKSYPRNGLHVSYYFLSGFRD P\DFRQMFG\QFGKILDVGIIFN* RGSKVNNATARVMTNKKMVT PYANGWKLSPVVGAVYGPELY AASS\FQADVSLGNDAAVPLSG RGGINTYIPLIIPGFPYPTAATTA AAFRGAHLRGRGRTVYGAVRA VPPTAIPAYPGV/DLPGTDFTVL TSMVDMQPTDMHSLLLQPQPP LLQPLQPLTVTVMAGCTQPTPT MPLPLPLAMELALWRVYTEVA
26315	56683	A	26462	1196	1459	TADLPPTEVTVKPLQMGQPPSS KQCQRRCLETEVWKLSKLQIST KASNRQDRSTFSAPPRKSQLM W*TSLLSYFQKLPQSPQPSATT ALISQQPSTLNPQPWPGSCPGG
26316	56684	A	26463	2234	2702	MLFIAAMAPPSLSSDAAMTTGI SSCLPSTACRRAFGTKSIG*GPTI PESSRWQQKGGVSGDGRSSCR RAVAPLEPVPRAPEAA\ARPRPP SHGRDPPPGPDPPPLRTPASAM DKSAGTSCRLSPLKALGSARAE QTMGRPAAERSYPLLRAQYSSR
26317	56685	A	26464	70	398	MLFIAAMAPPSLSSDAAMTTGI SSCLPSTACRRAFGTKSIG*GPTI PESSRWQQKGGVSGDGRSSCR RAVAPLEPVPRAPEAA\ARPRPP SHGRDPPPGPDPPPLRTPAS

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26318	56686	В	26465	18	123	
26319	56687	A	26466	19	347	
26320	56688	Α	26467	3	746	SRKLLSKSVP*LNP*SR
26321	56689	A	26468	1705	2031	CDAPGDPQPGLRDISWLGTTDR SASPQRLAAAALTAGNGRRCSS GPRRRPPP*PLARPRQRRQPPER QPVVWPPAFPARWAEHTCPLA PWQPRSPTTPSQPAAVTARAS
26322	56690	Α	26469	1	420	
26323	56691	Α	26470	65	330	RDCEARCARGPFWSWLSPRRK GKRQKSQLISQRLERHFLSGKN RQKRPSKMAGPDGAAPLEPGA VAAPMGPKSSRGSPGRAGKAA ETS*SPGRAGKAAETS
26324	56692	Α	26471	327	981	ASYQKFFQLLPDCNLAPSPHPQ VPATPSTSWGHLSKPPGAFRKR HSSSRCPKAGHQWGGGQRNTP TAAHFRRLSAGSLQLCPQLRVS PLTTGSLPPRSREPPRTPAPPSPY PNCRPLPKSTRTPSVGWSGPPSC GTRLQSHPQEAPAG*GSVRRPF LGP*RMPS*ALL*KHTGGL*GPP HPPMPTMCQPKQASKLQLLNC PQPSPSQGAGATMGNVG
26325	56693	A	26472	336	923	LKNIFLSLPRSINIRFATLLDTPG VENLVIACLQKHS*PYF*GS*NI CLSFQDGTLYHKMHAVCLKCL *KPSLLSLL*DIEYIRSHYNIEDFI YFSHHQREEHGHMHHFALNPIF RHYTKFFLKVYL*SCTQTSVLS LSDILSPKI*IAVFQFQNPYAHSL TSALHYLVPVRPRLLPGLDDQC PGHNTFPVVSIN
26326	56694	A	26473	97	298	DNLTLLPRLECGGMIMAHCSLN LTFSSDPAASAS*VAGTTGT*H HAWIFVFLCNWLRNRGVTVKK RS

SEQ ID	SEQ ID NO:			Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	hod	in USSN 09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	joequenee		0,7,0,10,10	sequence		, ,
		<u> </u>				
26327	56695	A	26474	1958	3269	KFTMSILKIHARELFDSRGNPTV
						EVDLFTSEGLFRAAVPSGASTGI
						YEVLELQDNDKTRYMGKGVSK
İ		1				PVEPINKTIAPVLVSKKLNVTEQ
						EKIDKLMIEMDGTENKSKFGAN
						AILGVSLAACKASAVEKGVPLY
						HHIADLSGNSKVILPVPVFNVIN
						GSSHAVTKLAMQEFMVLPVGA
						ANFREAMPIGAEVYHSLKNVIK
		}				EKYGKDATGVGDGGAFAPNIL
						ENKEGLELLKTAIGKAGYTDK
						VIVSMDVEASEFFRSGKYDLEF
						KFLDDPTRYISPDCLADLYKSFI
						KNYPVVSTEDPFDQDDWGAW
				İ		QKFTASAGIQVVEDDLRVTNPK
						RTASAVNEKKCNCLLLKVNQIR
						SVTESLQACKLAQANGWCVM
ĺ		1				VPHHSGETENTFITDLVVGL*PG
						QLKTGAPC*SERLAKYNQLLRI
						EEELGSKAKFAGRNFRNPPAK
26328	56696	Α	26475	2	684	HSGSSLLHFPILLINRKGFSPTG
ļ						MISLMCNRIVLSTHAKLQSCTP
						SNLPSQLPIGLSMSTPTKYRKLS
						FPGKTSQNITVPDSIVSPTFKETL
Ì	1					EFISKGGSSTCIVSPGPA*SLSNA
1						VSSSSMSSSLSNATNTPQSSSH*
						KSCFPWYTPSVKP*PRPSSSNST
1		١.				PKNIPETVLSANRGPLKRTTPG
						NFSSPDLSCTFTGQPPSIWRPLL
						KLVSGFKQAEPLLTIGNCQK
26329	56697	Α	26476	1284	2339	APPSARGACAASRRAAVPALPT
						PPSVCSGSHMSTYWPAAPR**T
	1					PGSSTAASPSPAASRAPRAASPV
		-				LTASPPLPAASPSPAASHAPPAA
1						SPVLTASPPLPAASPSPAASPAP
						PAASPVLTASPPLPAASPALAAS
1						PVHTASPPVHVASPPVHTASPP
						VHVASPPVHTASPHVHVASPPV
						HTASPHVHVASPPVHTASPPVH
						VASPPVHVASPPVHIASPPVHT
						ASPHVHVASPPVHTASPPVHVA
						SPPVHTASPHVHVASPPVHTAS
						PPVHTASPPVHVASPPVHVAYP
		1				PVHVASPPVHVASPPVHVASPP
						VSCSGDSTSDCFPPQPGAVFPHS
						LAPSLGGWSHLVAALP
			L	<u> </u>	<u> </u>	2.11 3233 11 3112 11 11 121

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26330	56698	A	26477	131	544	TGRPLPRPLKTQEIPSGCGVMG RATPGTSGLGDSVRRVRGAIPA PRSSLGRGFTCV*LTTGAQLAPS LVPAAPRLPAALMDIQPEPLAS AAPAATGPAQVTAATPLTTASA TPLTTETACSLGSSAASPLAPRA HCV
26331	56699	A	26478	1440	1877	PFQNLFQRNERTSCLCCLCMGA TWASLRALCCSPSP*HGWISW WWSTPTPFANGSVTSCSALTRS RWRPTWSEASGLWHAPAALL WKLRPLTPCFRSPISLSDLDLTS HHQQGAPTMHTCLGVGSSSWE LQAIFVLSYWFSPLHC
26332	56700	A	26479	56	345	ITWHLGLMMLSRSLGL*SGISFI NFPM\K*EMIPY*KLS*IQNLFQF PKVRPKGSQFGQVKH
26333	56701	Α	26480	392	634	
26334	56702	A	26481	416	601	FLITDPRIWKASSDPSAKLFTFP SGFLM*AGTWMKLETIVLSKLT QEQKTKHCMFSLISGS
26335	56703	С	26482	34	279	
26336	56704	Α	26483	173	307	
26337	56705	A	26484	196	527	SAVAAACSRPEEDAMELVLVF LCSLLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLFS VGILLILSRRCKCSFNQKPSGPR R*GSPGGRTSSPPMQQKPQKAE
26338	56706	A	26485	597	797	PSENELKALGYTSSAWKRFSEQ QWGLSLGSSAPSWRLPW*GDW ELPGEPGGDSSHRPFPGPIPRAP
26339	56707	Α	26486	3	184	
26340	56708	A	26487	256	635	GCVAPQIREQHAQSTENAAKPT RRIHSRQSEKPGRWRHGWRAG GWRRSKRAPARHRPRCPAVCP RDGEDCSREAAGA*GLSGSSAC PTSSTGASCCFCVPGQLNSVGF AVLGSKVLWTPGESPFCQ
26341	56709	Α	26488	1	378	
26342	56710	Α	26489	1	571	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
26343	56711	A	26490	1105	849	 RRQDSGQSPAWPAGALLLTLLT
		1				HCAVPGSWAQSVLTQAPSASG
		1				TPGQRVTISCSGSSSNIGNNPVN
						WYQQLPGTAPKLLIYRNNQRPS
		1				GVPDRFSGSKSGTSASLAISGLQ
						SEDEAQYYCAAWDDSLNGSYV
						FGTGTKVTVLGQPKANPTVTLF
						PPSSEELQANKATLVCLISDFYP
		1				GAVTVAWKADGSPVKAG\VET
		1				NKPSKQSNNKYAASSYLSLTPE
		Ì				QWKSHRSYSCQVTHEGSTVEK
						TVAPTECS
26344	56712	A	26491	129	1191	RSRPQCLGPQGRRVTISCTGSSS
						DIGAGYDVHWYQQLPGTAPKL
						LIFRNSNRPSGVPDRFSGSKSGT
		l				SASLGHHWGSRVEDEADYYLP
		Ī				VPIDSSLSGSTVLQARGELRQEP
		ł				TSSSARRSMKKGRDLGEAQLQ
						LRVEKTGLRTISSMAWSPLFLT
	İ					LITHCAGSWAQSVLTQPPSVSE
						APRQRVTISCSGSSSNIGNNAVN
						WYQQLPGKAPKLLIYYDDLLPS
			į			GVSDRFSGSKSGTSASLAISGLQ
						SEDEADYYCAAWDDSLNGYVF
			İ			GAGTKVTVLGQPKAAPSATLF
						WPSFEDASDDEAEL*CAIRDYY
		ŀ				PKAVMVA*KTNITPLKQGKDTP
		<u> </u>				SPSLLTPSSDEVKSYKNLLPGFP
26345	56713	Α	26492	283	840	TLPAGFTDVISIHKTGENFCLIC
						GINGRFAVHCITLEEAKYKLCK
		ŀ				VRKIWFHDAHTIHYLDSFVKVN
		-	Ì			DTV*TGKITDFIKFDTGNLGRIG
		İ	Ì			VITNRKKHRGSFDVVHVKDAN
		Į.			ľ	GNRFAPWLSNIFVTGKCNKPWI
						SLPRGKGIRLTIAFHSDKWFCSD
						ISVQNLCKRFSQGDTGIKNSEA
06046	5.651.4	ļ. –	26402	1,	0.40	RRCSNLQV
26346	56714	Α	26493	1	843	MARGPKKHLKRVAAPKHWML
						DKLTGVFAPRPSTGPHKWRECL
						PFIIF\LRNRLKYALTGDEVKKIC
		ļ				MQRFIKIDGQVR\TDITYPAGFM
		1				DVISIDKTGENFRLI*LTPKGSAF
						AV\HRITPEEGQVQSCAK**RYI
		1				VGTKRNPFI*VTHDAR\TIR\YPR
		1				NPLIQGEMDTPFQIEFKKTWPR
		1				LT*FPSKVPNTG*PCVMVTWRC
		1				LTLGRI\GVIT\NRERHP\GSFNV
		1				VHVKD\ANVNRFA\TRLSNIFVI
		1				GKGN\KPWISLPRGKGIRLTIAE
		<u> </u>		L		ERDKRLAAKQSSG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26347	56715	Α	26494	375	1327	QPYFPMETVMTLEGGQKPVME
						SYTLHYLPCLLCLPWRNPESSE
						WQRQLLDFPLASAPGSGLTQH
						MAAPKSGQNLEAKPKGQASLV
						LSSRKICGVLSGACAACPGGPA
						R*VDPAIPFPLAGEAGLEGRPRP
						QRCAAKWQSRDLIPGLPGSTGL
						PFPPY/PPCSPGALLSQSPPQAAG
						SLLARTPHAQGCPPPRLRPARIL
						PWPASSARRYTPQPSRKGTQRT
						PLFSLNLLETTTASYSLDFLLTA
						PEGFSPLFTASQEHDQNQQEHD
						FLLQDEGLRSPVKTRARLPLGL
						HGDKVEKAGPWSLGARESNLC
						SATSQRSAVAAGVPRAQPLPPK
						GKGWLDPPTWQGRRDTQRTLR
					1	SIHHRFYGYSARGWPGPLALLQ
· .						GFVRSLELPCAGSDQNRGQRLK
						GNPGAAFAIPKTLDFSKAGKED
					ļ	KGGNGVCTTPSQAFDPLPRSSQ
						SPLGNMAVSGSSSSGSWKSSGT
						QEKKSLNQKRKVDEAEKKEEK
						EKKKEPEPNFQLLDNPARVMP
						AQLKVLTMPETCRYQPFKPLSI
						GGIIILKDTSEDIEELVEPVAAH
						GPKIEEEEQEPEPPEPFEYIDD
26348	56716	В	26495	1919	2074	
26349	56717	Α	26496	179	431	PPTSLIRVSCTSTSTSLCTSWLCS
						SLSWLYSWAGPFFSGKMTASC
						RGSGQINREIVLMLLLRS*VFVV
	- 4-10				100	ISPLEGGSETSPFMDL
26350	56718	Α	26497	37	199	DGLPGLALGLDAQASWSASVV
						TGHRPPAPPGLALGGCHGPAAP
2 (2 51	7.4740	<u> </u>	26400			P*SGPAGSPCH
26351	56719	Α	26498	3	224	TGHRPPAPPGLALGGCHGPAAP
						P*SGPAGSPCH*TAPRGAGTPLP
	-					GSRRTGTSPWPHPPGLPHIPDVT
06250	5.6720	<u> </u>	26400	151	1402	GGHRH
26352	56720	Α	26499	151	403	MPRHRRSASVVTGHRPPAPPGL
						ALGGCHGPAAPP*SGPAGSPCH
						*TAPRGAGTPLPGSRRTGTSPW
				l	L	PHPPGLPHIPDVTGGHRH

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26353	56721	Α	26500	1	465	VSPKLLPSYASRPYLVPNALSSP
						SVPPALSASSAPPRPATRRRPPP
						RGLSASWPLRRRSRQDAGAGS
						RRLRERQNRGRRRSDLAPTLGA
						GLRRDRPGRQPRPGKALAPFAV
						PRPRTNFRGRS*KSGSQRTRTPP
						RREICRTHSRDRPRKLVRGRGT
			ŀ			ANGARALPGRGWRPGRSRRSP APSVGARSERRRPRFWRSLRRR
						EPAPASCRLRLLSGHEADRPRG
						GGLRRVAGRGGAEEAESAGGT
						LGDERALGTR
26354	56722	Α	26501	1	1344	
26355	56723	Α	26502	548	689	LGKFAPGLTASKAEATAAELCL
						KYPLEICTFL*GCVCVCVCVCV CVL
26356	56724	Α	26503	154	476	TLA*AAAASTSCSPRPPPPSPAS
						TTTRWRAPWRTR*EPPESLCTG
		1				MRSWPSGMTACTQTPSTAPPSP
		1				HPPSLSDSSALCSSASVRRMWI
0.62.57	5.670.5	ļ	26504	1020	1420	MKRLKPSMMHVLCMTVDL
26357	56725	Α	26504	920	1420	TLA*AAAASTSCSPRPPPPSPAS TTTRWRAPWRTR*EPPESLCTG
	-					MRSWPSGMTACTQTPSTAPPSP
1		ŀ				HPPSLSDSSALCSSASVRRMWI
						MKRLKPSMMHVLCMTVDL*LI
		1				PTSTPTT*PSELLAPSPNSPIDTT
						QMSGLTATSVPKKLAFSWQQL
						CYISLIQPLSL
26358	56726	Α	26505	1118	1403	AGWDPSFLISFSGLSNAISSSSSS
ļ		1				LSSQ*ESNASA*YSSATSGSSGIS
						WYPRSDVASSTIDSSSWRSMEG
i				1		IG*DSGRFSKVGSSDSSSLPCHL
26359	56727	С	26506	29	379	SS
26360	56728	A	26507	3	948	GVSLCCPGWSAVVGSWLTAAS
20300	30720	 '`	20307		7.0	TFRAQAILSSSWAYREPPVRVG
						RRPQPPLLLTRAQGRVISSSFRH
						LHDFVWRTAGKESTSGANETG
:		1				PLPERGRRPGGRGPGSRSPRSH
						AVQREGAAGSVPAAGRDGGRA
						GHDVPHEGQRAEAAAGEAGGE
						FPLLLSDRRGRARRSPAAGALQ
						SRPGRARHLLHQLH*GP*EEVS
1		1				L*VQQRGAVSGVDGGSASGQL
		1				RVHAEKAHLLQERNPEG*RAK
		1				DPLGTVSALSEEARFQLRWLAG
						VSAGHGGQRAAGRDWPCPAM
						NRLAMPGSVLFWFLVFGSGFH
			<u> </u>	<u> </u>	<u> </u>	CVAQARVQWCHSSL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26361	56729	A	26508	31	202	ILITYIIKLINQADFSTP*FMSHLI
						VSSRILCTEKWNFHFPPHF*D*Q
						QTFCTLQFL
26362	56730	Α	26509	471	1716	FKRGQYGQLLRPRFHHGQILYA
						RRQGADAAGDSDFCTEWPAAL
	ŀ					DSDEKCEKHFPIEIDSTDYV\HH
						GPSVRNPRARVVVLRWLRITLH
		1				ESAAVEGLAVFPPARRHREPEY
		1				SIPSPSQAFTPAVLATRVTGQLG
				1		GHTQIQNPTVAPTILGNTPTFHL
		ļ				TCFRIFSLPRHLFPKDKWRTLG
						APFLRTLLLVGTESSVHLSGIDP
						DLLVFEQSPTYLNTRSSSNRWD
						RLRILKAMNLDKQTTTINGMLP
						STEAPSSTTHQDLVVNTNSTSY
						SKELTTDFWARFTSLNESITTKI
						NKVSPSTDFISNPDNKTISPFFEP
	1					IDTKLSHMPVPPGLNSSKQLLN
						KTKGYNSRNHTSANEDEVSVT
	İ	ļ.				SKTWLVSVALCTSVIFLGCCIVI
						LASGCCGKQQGQYKPGQRKSG
						SLQIKNRNHMKENSS
26363	56731	Α	26510	410	867	LLTLSRTTPLMSLGFPGIPKMIN
						RPRQSSPIKLQNSSSLSNLLFFQ
						EDSSTLDSGLERSQGLDSTGGG
						EDICRVWTAS*SFICLSDPQKVQ
						IQSAPNRKAWCLVILVVVSHSS
						TPFSWQKVMKWIKKISFRVFAA
L						GQGLLGGYSNPRYSFSF
26364	56732	A	26511	135	756	VITILTPMLADRTRRIERPPKKK
						GTTSLGQRKWLLTQDWPSVYP
						VA\HPFKPSAVP\LPVPNGLSSK
						KRACPWQ*EGN\LELLKI\PNFS
						GF*LPVGN*KSTCEALKDF/CAL
						SGPAALGQWTRKC*GR/PFSI*I*
						QH*LWFHQDHPVRNPRARVSS
						LKSKAFSV*I*HDHAKKTLITLV
						GERYCKTPDVLTIKQNRWPLRS
	1					QITIMPVYL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hođ	in USSN	location of first	L .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26365	56733	A	26512	161	2150	YLDAEKMGQKASQQLALKDSK
20303	30733		20512	1.01	2130	EVPVVCEVVSEAIVHAAQKLKE
ļ						YLGFEYPPSKLCPAANTLNEIFL
[IHFITFCQEKGVDEWLTTTKMT
		1				KHQAFLFGADWIWTFWGSNKQ
						IKLQLAVQTLQMSSPPPVESKP
		1				
						CDLSNPESRVEESSWKKSRFDK
	1					LEEFCNLIGEDCLGLFIIFGMPG
						KPKDIRGVVLDSVKSQMVRSH
						LPGGKAVAQFVLETEDCVFIKE
		l				LLRNCLSKKDGLREGGASPGSL
				1		RLAAPGPPLTLNAACPLRLAVL
						AAMAAAALPAWLSLQSRARTL
						RAFSTAVYSATPVPTPSLRVDD
		1				LHLTEIVGMLDSVLTPEDSSGK
	1					YRFISGEVLCRITGCFTGVRVEA
					İ	KDLFGGCCSNPNEVMVTWIKVI
]	VEKEVWLYLRYILKALPPRTEK
					}	MAVDQDWPSVYPVAAPFKPSA
						VPLPVRMGYPVKKGVPMAKEG
						NLELLKIPNFLHLTPVAIKKHCE
						ALKDFCTEWPAALDSDEKCEK
						HFPIEIDSTDYVSSGPSVRNPRA
						RVVVLRVKLSSLNLDDHAKKK
						LIKLVGERYCKTTDVLTIKTDR
		Ì				CPLRRQNYDYAVYLLTVLYHE
						SWEYWKEWGKK*D*SRHGKSI
						YGENSSSERKYPGKRFSR*KLL
						RKNMGN*LKKSSLGTKEIEEYK
						KSVVSLKNEEENENSISQYKES
26366	56734	Α	26513	3	1186	PASTMSIRVTQKSYKVSTSGPW
						FFSSCSYLSGPSAHISSLSFSRAG
						SSSFQGGLGRGYGGASGMEVIT
						AVMVNQSLLSPFIDKVQFLEQQ
						NKMLENKWSLLQQQKMAQSN
						LDNMFESYINNLRWQLETLGR
				İ		KKLKLEAELGNMQGLVEDFKN
						KYEDEINKYTEMENEFVLIKKD
						VDEAYMNKVELEYRLEGPTDEI
						NFLRKLYEQEIRELQSQILDMS
			İ		}	VVLSMDNSHSLDMDSIIAEVKV
				1		QYEEIANRSWAEAERMYQN*Y
1					}	AKLSQLEAALQRAKQDMALQL
						HEYQELMNFKLAQDIVITTYRK
						LLESEGSWLESGMQSMSIHMK
						TTSGYAGSLSSAYGGLTSPSLS
1						
						YSLGSSFGSGAGSSSFSHTSSTR
26265	56705	-	26514	261	1215	AAVVKKIEAQNGKLVSKSSDV
26367	56735	В	26514	361	1215	L

NO:	EQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NEKPTEEVKTENNHIN QDGSVVQFKIKGTPILS	io:			in USSN	location of first codon for peptide		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
ERGGGANNRGGGRLLO	:6368	56736	A	26515	230	561	VRTRHLFCEAAAEETPVFTMA NEKPTEEVKTENNNHINLKVAC QDGSVVQFKIKRQTPLSKLMK AYCEPRGLSVKQIRFRFGGQPIS GTQRNLS*KKESVDAASFIVVL
26371 56739 B 26518 258 1081	.6369	56737	А	26516	1242	1415	NSPSDSSLVWAWRRPQSRSWS ERGGGANNRGGGRLLGNSVFG RK*LPHRRVSRVPNTK
26372 56740	6370	56738	В	26517	1	585	
HRNTPAQTGKPPKRAW	6371	56739	В	26518	258	1081	
26374 56742	:6372	56740	A	26519	42	275	TFAWSEEGTSPPSIQSSWDPRCP HRNTPAQTGKPPKRAWPRHPV HH*EPHGDQQDDGPAVSPP*SY SQYPWPEGLDV
26375 56743 A 26522 I 879 DCQDKVPRRKEPSMCSG KSWVSLQTYWKPRATQ LPLTEERMVVLGASRVG SRFLNGRFEDQYTPTIEL VYNIRGDMYQLDILDTS PAMRLSILTGEAHWCI RARAWVRSVLGT*QILE KNKTKEAAELPMVICGI GELCRQVPTTEAELLVS AYFEVSAKKNTNVDEM SMAKLPHEMSPALHRK GDAFHPRPFCMRRVKEI MVSPFARRPSVNSDLKY LREGQARERDKCTIQ 26376 56744 A 26523 2 478 26377 56745 A 26524 120 1167 GHVGHMCTGQHMASA NVLRKEVDRACFGEKA S*EELWAIWGQGREVCI GAIISTRHCNSQNGVRV WALEAAPV*VQDRSSPC LPSPCALTMGTGIMPLY WKPRQRPGTSGGTVSSE AGSGCWLCQPGLREVA ITYTSKHSVEVQVNVMS GTSGSDSVDWSSKGRGILLRAEDAPGPGFKVLEV RCPFYFSLGGRWQRSGF	26373	56741	Α	26520	646	1905	
26375 56743 A 26522 I 879 DCQDKVPRRKEPSMCSG KSWVSLQTYWKPRATQ LPLTEERMVVLGASRVG SRFLNGRFEDQYTPTIEL VYNIRGDMYQLDILDTS PAMRLSILTGEAHWCI RARAWVRSVLGT*QILE KNKTKEAAELPMVICGI GELCRQVPTTEAELLVS AYFEVSAKKNTNVDEM SMAKLPHEMSPALHRK GDAFHPRPFCMRVKEI MVSPFARRPSVNSDLKY LREGQARERDKCTIQ 26376 56744 A 26523 2 478 26377 56745 A 26524 120 1167 GHVGHMCTGQHMASA NVLRKEVDRACFGEKA S*EELWAIWGQGREVCI GAIISTRHCNSQNGVRV WALEAAPV*VQDRSSPC LPSPCALTMGTGIMPLY WKPRQRPGTSGGTVSSE AGSGCWLCQPGLREVA ITYTSKHSVEVQVNVMS GTSGSDSVDWSSKGRGI LLRAEDAPGPGFKVLEV RCPFYFSLGGRWQRSGF	1	1	A	26521	6510	7361	
26377 56745 A 26524 120 1167 GHVGHMCTGQHMASA NVLRKEVDRACFGEKA S*EELWAIWGQGREVCI GAIISTRHCNSQNGVRV WALEAAPV*VQDRSSPO LPSPCALTMGTGIMPLY WKPRQRPGTSGGTVSSE AGSGCWLCQPGLREVA ITYTSKHSVEVQVNVMS GTSGSDSVDWSSKGRGY LLRAEDAPGPGPKVLEV RCPFYFSLGGRWQRSGF							DCQDKVPRRKEPSMCSGLLRV KSWVSLQTYWKPRATQGVYV LPLTEERMVVLGASRVGKSSIV SRFLNGRFEDQYTPTIEDFHRK VYNIRGDMYQLDILDTSGNHPF PAMRRLSILTGEAHWCLGWGG RARAWVRSVLGT*QILEVKSCL KNKTKEAAELPMVICGNKNDH GELCRQVPTTEAELLVSGDENC AYFEVSAKKNTNVDEMFYVLF SMAKLPHEMSPALHRKISVQY GDAFHPRPFCMRRVKEMDAYG MVSPFARRPSVNSDLKYIKAKV LREGQARERDKCTIQ
QQQVPLLTGDA*EAGAI HGGKKEAPWPLHSCPLA			_				GHVGHMCTGQHMASAYVGRV NVLRKEVDRACFGEKAKQ*VG S*EELWAIWGQGREVCLGIEEA GAIISTRHCNSQNGVRVWAPYL WALEAAPV*VQDRSSPGSQACS LPSPCALTMGTGIMPLYQEAK WKPRQRPGTSGGTVSSEPHC*D AGSGCWLCQPGLREVAHVSAE ITYTSKHSVEVQVNVMSENILT GTSGSDSVDWSSKGRGYTAAS LLRAEDAPGPGPKVLEVPPVVV RCPFYFSLGGRWQRSGHLT*LE TKWRNGDIVQPVLNPGKSRGH QQQVPLLTGDA*EAGALHGFV HGGKKEAPWPLHSCPLAHCCFS
26378 56746 A 26525 225 438	26378	56746	Δ	26525	225	438	GRYNRPGAVAHACNPSTLGDG
26379 56747 A 26526 216 364							

SEQ ID NO: of peptide sequence No: of pe	GOLTAISASWV GGSNPEGTG* LGDRARIHLH SRAQTRRVW YGRL*CCSPST KAIAREIERYS FSSYCLIFSHG THWAAPFRPP KTSAGEPEIPP HHHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
26380 56748 A 26527 2 397 SCCSDWSAMA*SQAMLLPRRPE*LSERRLCHYA/HSIKKGRQEGSKEMHATMETEQKQNNTRRRTSMRKNIKGI 26381 56749 A 26528 312 1061 QQTLYSFGVSFYCSSSSICRRARLYGRKRDCTGQRIPLHHHHHYSHIHHHHGLQRSSKICGSRRLGRAALFQGAESLLGKQS*RGRGS*EKWPRAAAGAAGLAHGPEK*SGLRGEGNRHPLLQRSPAESSILEGRPASFR	GQLTAISASWV GGSNPEGTG* LGDRARIHLH SRAQTRRVW YGRL*CCSPST KAIAREIERYS FSSYCLIFSHG THWAAPFRPP KTSAGEPEIPP HHHRHRHHH NFLLWPE*ILF TLLRSFSHPAK KHLASTQCGP
QAMLLPRRPE*L SERRLCHYA/HSI KKGRQEGSKEM HATMETEQKQN NTRRRTSMRKNI KGI 26381 56749 A 26528 312 1061 QQTLYSFGVSFY CSSSSICRRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	GGSNPEGTG* LGDRARIHLH SRAQTRRVW YGRL*CCSPST KAIAREIERYS FSSYCLIFSHG HWAAPFRPP KTSAGEPEIPP HHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
QAMLLPRRPE*L SERRLCHYA/HSI KKGRQEGSKEM HATMETEQKQN NTRRRTSMRKNI KGI 26381 56749 A 26528 312 1061 QQTLYSFGVSFY CSSSSICRRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	GGSNPEGTG* LGDRARIHLH SRAQTRRVW YGRL*CCSPST KAIAREIERYS FSSYCLIFSHG HWAAPFRPP KTSAGEPEIPP HHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
SERRLCHYA/HSI KKGRQEGSKEM HATMETEQKQN NTRRRTSMRKNI KGI 26381 56749 A 26528 312 1061 QQTLYSFGVSFY CSSSSICRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	GDRARIHLH SRAQTRRVW YGRL*CCSPST KAIAREIERYS FSSYCLIFSHG HWAAPFRPP KTSAGEPEIPP HHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
KKGRQEGSKEM HATMETEQKQN NTRRTSMRKNI KGI 26381 56749 A 26528 312 1061 QQTLYSFGVSFY CSSSSICRRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	SRAQTRRVW YGRL*CCSPST KAIAREIERYS FSSYCLIFSHG HWAAPFRPP KTSAGEPEIPP HHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
HATMETEQKQN NTRRRTSMRKNI KGI 26381 56749 A 26528 312 1061 QQTLYSFGVSFY CSSSSICRRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	YGRL*CCSPST KAIAREIERYS FSSYCLIFSHG THWAAPFRPP KTSAGEPEIPP HHHRHRHHH NFLLWPE*ILF TLLRSFSHPAK KHLASTQCGP
NTRRRTSMRKNIKGI 26381 56749 A 26528 312 1061 QQTLYSFGVSFY CSSSSICRRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	FSSYCLIFSHG THWAAPFRPP KTSAGEPEIPP HHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
KGI 26381 56749 A 26528 312 1061 QQTLYSFGVSFY CSSSSICRRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	FSSYCLIFSHG HWAAPFRPP KTSAGEPEIPP HHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
26381 56749 A 26528 312 1061 QQTLYSFGVSFY CSSSSICRRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	HWAAPFRPP KTSAGEPEIPP HHHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
CSSSSICRRARLY GRKRRDCTGQRI PLHHHHHHYSHI HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	HWAAPFRPP KTSAGEPEIPP HHHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
GRKRRDCTGQRI PLHHHHHHYSHI HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	KTSAGEPEIPP HHHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
PLHHHHHHYSHI HHHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	HHRHRHHH NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
HHHHGLQRSSKI CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	NFLLWPE*ILF LLRSFSHPAK KHLASTQCGP
CGSRRLGRAALF QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	LLRSFSHPAK KHLASTQCGP
QGAESLLGKQS* RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	KHLASTQCGP
RGRGS*EKWPRA AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	
AAGAAGLAHGP EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	
EK*SGLRGEGNR HPLLQRSPAESSI LEGRPASFR	\QLGRKQPSES
HPLLQRSPAESSI LEGRPASFR	QDSLVLERAG
LEGRPASFR	PFGGSSSLGG
	'AGTGVRTSH
account of the second of the s	
26382 56750 A 26529 161 453 SSSLPCSPSSCPH	TSFFLDARQEP
RTCRVVGLKEL*	QKQGLPHCR*
QEREKSCSPSGSI	'DLGAPQPRA
VTPSLGLCSSWH	LQASRRHCTP
RCPQWKR	
26383 56751 A 26530 301 630 RWKPKIRGSEGS	AS*PQGR*LLP
SGRRG\ATGSAE	
DGPVPYSQGSSS	LIMPRPNSVA
ATSSTKLEDLSY	LDGQRNAPLR
TSIRLPWHNTAG	GRAQEVKA
26384 56752 A 26531 1 1394	
26385 56753 A 26532 240 1150 LLLHVPSPSPAST	GPPSCGPCWP
PRSAPAAGRGSS	SGCLAGEDPA
TTHKSAGTGECF	(RGPVGHCGQ
AHTGPSYPSGPP.	ASCGPAASAV
TRGQSCRSLTFR	7
QLPRGQGETGRT	GLGHYLTLLS
CSSRWPLPKSGD	GSPSRWEYRD
S*ERPGRRTAPRO	CSRSTGLGD
GLKKFPSSY*GP	'KCAPSGCGG
QAPWSAGGSTCI	PDART*MPR
ARARSWAHTGR	PCFPRLLSIQA
TP*RTGGRTCGF	CLAS**GSRRG
RPSSAESLPIPAPI	PGCGQH**PER
SARLSWGGGMR	GPR
26386 56754 A 26533 1463 1627	

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26387	56755	A	26534	1	1758	MHKYVRYSTVHNSEDMESTQ
						MSINDRLDKENIIHIHRGILCSH
						KKKQDHVLCKNIGEAGNHYPQ
'						QRNTGTEKQIQCVLTYKWKLN
						NKNTWTQSEEQYAVGPVGGRI
		1	ļ			GRLTNNRHTQDSESWVRGVTA
						FWSRGANNALDIPAFIIKFSEGR
			ŀ			GSLHTHDGPPGPTSSLKLSFSHS
						FDSTGLCRPHDLVLGLIIPTMVN
						ITSQLDWLEDAQMAGEALFLE
						GKLTTRKDIYTENPSLHHHHQR
						PKVDKTTKMGKKQNRKTGNS
		1				KTQSASPPPKERSSSPATEQSW
						MENDFDELREEGFRRSNYSELR
						EDIQTKGKEVENFEKNLEECITR
						ITNTEKCLKELMELKTKARELR
		ŀ				EECRSLRSRCDQLEERVSAMED
		ł				EMNEMKREGKFRDKRIKRNEQ
						SLQEIWDYVKRPNLRLIGVPES
				İ		DVENGTKLENTLQDIIQENFPN
						LARQANVQIQEIQRTPQRYSSR
						RATPRHIIVRFTKVEMKEKMLR
						AAREKGRVTLKGKPIRLTADLS
						AETLQARR/DVGANIQHS*RKE
				1		FSTQNFISSQTKLHK*RRNKILY
		İ				RQANAERFCHHQACPKRAPEG
		İ				SAKHGKEQPVPAAAKSCQNV
26388	56756	A	26535	620	886	INGVILSKPPLPPISTTPIAGALLL
						PLTKEQRGDF*KPSRNMRTSCW
						KTPESRANFLKFRPRSHCLTRM
						GSSCLLPSKTCLSSSSTFHH
26389	56757	A	26536	237	415	RCLQRPSAGTAGHPPSAGRPPL
						AAGLAG*RARHRSDLPGSAASS
						QESWCLRAALPEAPA
26390	56758	Α	26537	373	691	
26391	56759	Α	26538	2	233	
26392	56760	Α	26539	5	68	ALQWEEKHEL*EQSLHRKPGG
26393	56761	Α	26540	184	434	GGRRGCTVGEAAVTQSLSLCS
						HEGRAIRHQRDSASIVLLDQ*Y
						TRHPVLDKLLAWI*ALAEDKAT
						LGSAIAAEWKITPAFSFP
26394	56762	Α	26541	466	683	GRPHSLPHPHADSSELTTDCS*
						WRWIFKHKTDHIRHQRVHTGQ
						KPFKC*Q*GKAFRHSFDVTKHQ
						RTDAVGLHQTCCLGGVLLWGA
						HWRGHPSYSLWSAHCCQHGGE
						GASGGGLSLHLDRLSLDAAGRP
						QPVLPPTGQNILVGPLPQISLCS
						RSLCVLRLDGLSQLSPGEEGSH
						SQKWTSQEVKLFRSRHQSTSDV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26395	56763	Α	26542	194	558	GCDRPSRPRPGAPRPPAATASC
						PPRSCWPLVPSPHCP*PCRKRRY
						PGERRTSPAPPVPPGPGRPAG*T
						PPCELRPSSTHVALLGLALPGSE
					1	GTGLRTSVRARDRLHRRTRERA
						AAGTAPGP
26396	56764	Α	26543	1	248	MVAIHNADDAKCWGDVEQLE
						LSFTAALPVLPHPSLPGERPLQE
		l				AVAFLCWLLVDVLLKATVSKV
						GGGSALASVARVMKAQAFSPL
						LRILHKASTSSFRARKDSAHTPS
	1					CLLTPSGPERAGPLTQDSCQPSP
						HDSFRAPALLEPSSALSTAVASL
		1				RRREERLEPEQRVGELGSLGER
						QHEPSDNHDFQPKSKQEQLQK
		1			i	TLQPSGGPHCSSLLLMVFWWK
						QWRKTEPLKAERTGYKEKEIST
						KCSSSPSGQLSQSSAAGPAWPE
			,			DARPEATWSATLLSFDPRCKND
						SIEEPCSVHISCTAYSDPLKIHNS
				}		YRECGLCPEVNLEVADPSSSSR
						ELWFRAGAQGAGAMQGVTEL
ł						RPPEFVKSRKPQVGSGHMGNC
						LSKGKRFLGHCQYKQGLPQRH
					į	QLQAEERESGMRHTTGGAYAV
						LTTGVSPWWIWIWERRWPCAF
			•			PGKNEEPAGKVPFPSELVLTLQ
						RC**CQMLGGCGAIGALIHCCS
			ŀ			ACAASPFSPWRKAPPRGCCFSL
						LASGRCAPEGNCLKGGRRQRT
			:			CQCGSGYESTGF
26397	56765	Α	26544	423	621	LPSRGAGLGTCSPPCLSLPSPPW
						APVRPEPPR*SPPPAPQRPVPSTT
						QGLNCAGAGHGTGRQLHR
26398	56766	Α	26545	1162	2027	MTPEPEWSLS*VGNYKRTVKRI
						DDGHRLCSDLMNCLHERARGV
						SRADPTMAGAE*PAASLPCTGP
						QYGTVEKAWMAFMSEAERVS
1						ELHLEVKASLMNDDFEKIKNW
						QKEAFHKQMMGGFKETKEAE
						DGFRKAQKPWAKKLKE
26399	56767	Α	26546	1	504	

SEQ ID NO:	of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26400	56768	A	26547		1215	QTMYFLTPILVAILCILVVWIFK NADRSMEKKKGEPRTRAEARP WVDEDLKDSSDLHQAGAGGN AVEGVDQSKVNGRATGFASKL DIGKRREGELETGSYPPKTHA YALKKSGPWNPGTWQHRKIVR GLQFYTVFFPHSSVLAFLAPVID PSVASSSSLRSSTTDNELAELSE FADADEWQESEENVEHIPFSHN HYPEKEMVKRSQEFYELLNKR RSVRFISNEQVPMEVIDNVIRVT GTAPSGAHTEPWTFVVVKDPD VKHKIRKIIEEEEEINYMKRMG HRWVTDLKLHRTNWIKEYLDT APILILIFKQVHGFAANGKKKV HYYNEISVSIACGILLAVF*NAG LVTVTTTPLNCGPRLRVLLGRP AHEKLLMLLPVGYPSKEATVP DLKRKPLDQIMV
26401	56769	A	26548	3	263	RPGEMACKYPLRCSGARVERL AKKKAHACLLWTATIKVITNSV KLRRSS*GNRLKPSILC*DMKA LRQYPMPLRAWLLPMVVWVM
26402	56770	A	26549	82	318	SGEAGKEEGTRMVRIRPEPKRS LLWTATIKVITNSVKLRRSS*GN RLKPSILC*DMKALRQYPMPLR AWLLPMVVRVMV
26403	56771	Α	26550	91	714	SESLVLVWCGRVSCVLFCVCD VCVLVGGSGVAVRCFGGRGCG PRRVGRRWSCWCGWCGAVLIR RVCLAVMFGLALCVHPLLYPR TLLLRGQKVDRFKTNLSSGESL VTLVIFPAHGLARSRFLNLDVL FGVHFIAVEFWHAVGLIVNKQ VKGKILAKRINALIEHIKHSKSQ DSFLHCANEQRQT*QCAGPCM GPEPRQACLNTCIRS
26404	56772	A	26551	29	363	FAKMTNTKGKRRGTRYMFSRP FRKHGVVPLATYMRIYKKGDI VDIKGMGTVQKGMPHKCYHG KTGRVYNVTQHAVGIVVNKQV KGKILAKRINVRIEHI\KHSKSR DSFLKR

SEQ ID	1 -		SEQ ID NO:	1		Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		07/340,217	sequence	or peptide sequence	deteron, -possible nucleotide insertion)
26405	56773	A	26552	186	512	FHLSKHRAPPYPVTAPPRTSWG
						SLVKQVNESNGSRLLRTSLVHE
		İ			1	DLEGVSVVSGMNCDSALARYII
						ILETLIIYLISPRCWIIDSSGACSG
		1				LAMYLPLLGDDGVLLCTPNFM
						AWRSNRTQFMMRSSSHMVDAS
						PRGRHMSPREEAFGYSSRASHM
						LLSLLAPPWPQLMGRGLGCQQ
		1				QERPQECVPLGMTRSPYSEIHF
						GSSRALGSSPGSCAHEVLGPSIL
						TVNPFIPGSSVHVWPSNGNETN
						KLPHTRAGSCGSATCSVKRWG
		1				PQKPRPLPKPPLVPQALLLVRG
]			PAAAREEAVQPPKEEVTQRPGG
						HSSPGVFAHLKGPRSVVEIRME
						YGEE*PPGRCVTSSFGGWTASS
	ł					LAAAGPLTSRRAWGTSGGFGR
		1				GRGFWGPQRLTEQVAEPQDPA
]		LVCGSLLVSLPLLGQTCTEDPGI
						KGFTVRMLGPKTSWAQDPGED
		<u> </u>				PRAREEPKWISL
26406	56774	Α	26553	1	382	FRTSCRQLSAAPPPARSPLRPPG
		1				GG/EPAPGRTSRGHRPQM*SGT
		1				PAPRPPARSTVSPASPLPKPRAG
						RCGSRPRSACSTFRPC*SLASVS
	1	1				SAKTQGWKMWQPATERLQHF
				}		QTMLKSKLNVLTLKKEPLPAVI
						FHEPEAIELCTTTPLMKTRTHSG
26407	56775	A	26554	797	1213	CKV AWLKFLLGTRRFLRFSKYSFSID
20407	30773	l ^A	20334	191	11213	SARSLVPGRWPAPGRTSRGHRP
						QM*SGTPAPRPPARSTVSPASPL
						PKPRAGRCGSRPRSACR*GAPG
		1				SRGPAFPRRTPSVTRWALGLPW
						LQGLRTAFCWQILSRVTAATLP
						DKIH
26408	56776	A	26555	1002	1655	KEFCIYNRNPNACSYGVAVGV
20406	30770	^	20333	1002	1033	LAFLTCLLYLALDVYFPQISSVK
						DRKKAVLSDIGVSGEPHPAGTP
						CTESTEGCPGHRRRKDNPLNEG
		1				TDAARAAIAFSFFSIFTWVSTAT
						AHQPTLVPFPH*APGWVVFPAS
						AQP*ASPACRGRQPCITPGSEVA
		1				GAPSTLGGQGRHYMDPSQDSS
[1					MPYAPYVEPTGPDPAGMGGTY
		1]			QQPANTFDTEPQGYQSQGY
<u> </u>	L	1	L	L	<u> </u>	2217H111111120123Q01

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26409	56777	A	26556	262	628	QHFQTPWPWPLCAAAGTSAGT SHSGSSSGAFSSWPCWTAAEPA ARKRGRPAGSWSSPATGAPGR CRHRILSRGAGGSAGFVCSGLR GIGPLGI*LSGTFPGLTAGPETPA TERAPGASQHFR
26410	56778	A	26557	1098	1599	RIRKSHHCINTVTLGRGNSLGK DFVRESPGGDRLNVGQTHKHR GLGRFAQPHGTSAGTSHCGSSS GAFSSWPCWTAAEPAARKRGR PAGSWSSPATGAPGRCRHRILS RGAGGSAGFVCSGLAESGL*ES SSPGRSQG*PQGQRHPQPNGLP APPSTSVSVLVRISR
26411	56779	A	26558	440	698	IKLWAATFIKVCRLSFSCGMSIL *RCTGSKSCCCCCRRPLWAGPT SCAGGCGCCWGPGPPAELGPD TPAAEEAAEACCWDAAIFLA
26412	56780	A	26559	448	576	
26413	56781	A	26560	513	782	EIWWWAWTKWCGCWVVSCF HLCGRHC*GTCWSSETWR*MC GTSGTAPPCECWREGKDDCGR DRPMETHGCCSSFSISSPRAGKD ATTGT
26414	56782	A	26561	798	1505	FLRATSPSGHHFSYHLWIWISLR SFLCNECSESCCLLNSSMWQAP GLSHYSLLLIWLWLVFQTLNPR HLLHLLPSPLNVVDRLCSCQHH HHQ*CHHLHHHHLH*NHSHHRH HHHQ*RLPLHYHLHQHHHHHQ NHCQQHHHRYHQHHYQHHDH HYRHHHPWLAGARALCDSND AGCPGSTGDGWRPYSADSDSL DALSFPRPLPFPDCQSLRGLASA VIQGYNWLVLTENHILFHLF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26415	56783	Α	26562	I	1073	MHATNSSSVPQEIQVEALCPLL
						TQPQKSPSITSAMLCQLKKPQPS
					ĺ	RSKEREADPISCGPECQGNWDL
						CVEAATGLYGDGHLRDSSRTR
						VLMTTGTYRDLQGLEGRAGHV
						AELHVLPVWAIQDRGYVLWC
						WTASLHPRDVAREQGFPNDCT
					ŀ	WALGCTLTAESTHTHSAALAR
						QAYSQLSKKPTLLNEPEHITEK
						KFINLARFEALNSRTWLGVLY
						WIAQIQDVPVTVESTTGQRAAR
						ISPREADRTLVKGQVQGIRQTVI
						MSVPGRKEGDKLKEVSDGREA
						ANQAGMKWGKECKSSSGTEN
						AMSGKEVGILQEEKGDWSHGV
						VRGWQEKWMTYNFWACGRG
						KNATCRLEMTRTSENDLKHNQ
	•					EGLWHGRERAMLGDTHTLAW
						REEEMEQKQALRIHSLYGKTSG
						QRALGSWWVERFMGMRSGSSS
						DCNGLVTEG*TLQSACIPEPTCS
				1		H*GSPAP*LHP*GAEKQSSTTEH
						SPCPGLPRQAERGAQPRVPPCP
						QDPADPCKFQWS
26416	56784	A	26563	1	387	MESTEIGPHIYEQFTLTKMTRKF
						NKEQLVLISLALLDSGHTSNSL
		1				AWPSCLIVSGVGSCRWVCGLT
		}				D/CQE*SLRPSQSAGVCRRSTPD
						PVCLGVTRGGCRTEKIAACSFL
						WKLRPRGAPARCQPELSCM
26417	56785	A	26564	47	472	LLRLHFWQEERLKPSRKKITKK
			1			HTKKRTASLILHAMICCRSLNSS
						KTKNTKCLNSINQRLKILSLQK
						GDPLESTCRH*CCHVHRRTKAP
		l				GQRRVGRQHVVSAGNHRHPHK
						GDPLESTCRHATVTGQGLLEFA
						GGPLQTLFA
26418	56786	A	26565	329	615	TKTEIGTRSINELRQQLFATTNT
1						FFFPSIFGESNTTSTSLTLKNSAI
1						WCPTGTKLPEGRTGSNLCCSAA
						SAGDTQANRVWSGPSAN/C*QT
		L		<u> </u>		CRRRSC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
26419	56787	Α	26566	525	716	PTCLLTPPSKGRQTPYATGELR
						LASDGCPSGTKLPEEGAGSNTQ
	1					ANRVWSGPSANSSRPAEEGPDC
						CRTTCCRTTCWKPTTVTTCSST
						PCCQPACCVSSCCQPCCRPTCC
						VTSCCQPSCCSTPCCQPTCCGSS
						CCGQTSCGSSCGQSSSCAPVYC
						VSSCCQPSCC*SGPSSAGLLEFA
						EGPLQTLFAWVLLPAPSSGSFV
						PDGHPSDASRSSPVA
26420	56788	Α	26567	3	390	EGPCCKGWCC/RSPDTML/CPT
				1		VFITCRPGDSLRCLHHQGPRFQ
						AQN\CQPFGQTSS*LQEFFPIPQ
						WCLECRRALAGIWQVPLWDEA
						SLPEEGAGSNLCCSAASTGDTQ
						ANRVWNGPPANSSRPAGEEAD
26421	56789	A	26568	658	1005	NSKYWTPSGPPPRLASGAIYGN
						SLSV*AAGAPYRNAGPLQPGCF
						PPS*SLPNGGIHPGPGPGSGPHL
						GPDG*MVGSQVQHDNELYFC/
						APAGSYPLWVKALPQPPSQPFL
						KPVASM
26422	56790	A	26569	1149	1715	VLQLNLPGPVASWCSRDVGPPL
						ARPIPPPAPHTPLSSAGPSAAAP
					,	GPARQLPHPRGDSRTARLLPGQ
						GSS*SWR*GAWQSGCQSYRKP
						GLSV*AAGAPYRNAGPLQPGCF
		1				PPS*SLPNGGIHPGPGPGSGPHL
		1				GPDG*MVGVGPSGAGAAPEPA
						PGLWDPPGHCSQASTPPGACKE
						RETLPTALPRLS
26423	56791	A	26570	32	335	LWSLFDHHVQRAVCDSRAKYR
						EGRRPRAVKVYTINLESQYLLI
						QGVPAVGVMKELVERFALYGA
						IEQYNALDEYPARRLY*SLSY*I
						YELTKCKDSQEKNG
26424	56792	Α	26571	407	842	TEPLITINRLQRRRRSAPVAAAG
						PAGTLARRAPAVTAERAAGPG
						PASVHRRPGWRRAQSGPAAAQ
						ALRPPPPR*PRDSASPLSRKELL
						KLLGTKHYGRLTATEAQAPQG
						QHKLLCRETGELVPHWAGSHY
						RGISNPINNIQDHIL
26425	56793	A	26572	409	614	GLPPPAVGDRQRCLPVRH*RPS
		Ī -				QTIRAEQEPRSAAPRKRRPKEG
						CRRSRGSSPLADNLGDLGSGGQ
i			1			GG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26426	56794	A	26573	3	266	GNHCRRQYRDAQ*WP*EAGRY
20420	30134	<u> </u> ^	20373]	200	SSCAGSARLGKAKG\RGPQGV
	i					MGNE/MRSRRAQEFKKYLHSK
		l				TSR*KSHTGPEAELTSPGAKKE
						GCSQ
26427	56795	A	26574	36	384	GWYCSSRSDVCSGGNSSAHSQ
20427	30793	<u> </u> ^	20374	30	304	LPHQPLPRLRPGGSCHPRESSSP
				·		SKQRGGPVGDRQRCLPVRH*RP
						SQTIRAEQEPRSAAPRKRRAKE
	İ					GTRRSRGSSPHPEKLGDLGSGG
						OEVRP
26428	56796	A	26575	101	334	CSTSKEKWQCGLRAECSPVFPA
20420	30790	A	20373	101	334	TEVPEYSC*GRKPSHLSCHRAP
						TLEEAANRKWPCTQYDAIQNA
		ŀ				CYYNDSLVLRLS
26429	56797	A	26576	435	761	QGTNTWVPHWVLRLGLLHTSP
20429	30797	^	20370	433	701	PEGIAELPRSLPSLTEHQACQLD
						CVLVAIGTAILVAQTATTSPPIC
		l				GEADAHPASTPLPPSWPPQGRQ
						LSC*NPPLGPWPSGRVQTP
26430	56798	A	26577	38	236	RLLPLENCCLSSASGTCAHQAP
20430	30/90	A	20377	36	230	LLLCSCPNC*SCCCCHHCCCPC
						GCCCWHCHRPSTKGNSATFTA
26431	56799	A	26578	1316	1548	FFSITGLSSVAGGQFVNLYLKR
20431	130799	A	20376	1310	1346	LNSNFIYLSGYVIVYINIYVFIYC
						I*KFVLHVTLRTDCCKTIVKKH
						VFRLFLKAM
26432	56800	A	26579	1	272	RPVNSRLDDFVAACAAMAKIK
20432	150000		20317	1	212	ARDLRGKKKEELLKQLDDLKV
						ELSQLRVAKVTGGAASKLSKM
]				*VRRPDHSPRGWGARVHRDRR
		ł				RISKLA
26433	56801	A	26580	1	363	
26434	56802	A	26581	286	867	IYALSLGAGGAAASAGLCSNEP
20131	30002	`	20301	200	007	RFKARDLRGK\KKEELL\KQLD\
						DLKGGSCPQLTRSPKVTERCGP
						PKLSKIR\VVRKSIC/RVFSPVIYP
						DFRKENLQGNSYKG\KKYKPLG
						PCGP*GRTRAMRPPGSNKARRE
						NLEGPKEAGSGKGAAFTRCGK
						*RGSRALRGRLCQLKHKENLKT
		1				KKQQRKERLYPLRKYAVKA
26435	56803	A	26582	164	346	LHPGRRPGLTHLGVPSPGPGPT
20433	20003		20302	107	1570	EKLAPGKPSSAACAPSPPALD*
					1	HIAFGVDALCPTFGLN
L		<u> </u>	L		<u></u>	HIALOADALCLILOFIA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		•
26436	56804	A	26583	316	723	LVGGWGGLWGGLHGPLYGQA QGASPLLPPPPPAHRPPPHRHST EHGVEHPLVT*TAPLSPCPLGFR LGQLALHRGASTKGLLTGGVW GLHSWPIGDGRATIHEAVVRAS PWPSRLGTIHGVRGGRDVQEG AELPAV
26437	56805	A	26584	177	418	RNPVVAQGLLCACRMFKVGNR TPSSSAEWPSSFAPPKKGPLPKA TSEPLFPHPKRR/PLASVPSHREC RPPLGASKTAPRD
26438	56806	C	26585	149	277	
26439	56807	Α	26586	1037	1455	EESYGLLSVPSVTGSLLLQDLH KLGCHQFGHSKKRRVSGIWMA VLPFPFRCQPHLLLLENPRAN GPARQPTNHQPP*KAGTQLPNS VAPVQSQTGFPPTPARKARAPT WPGAARPPGTASNKSPARSPCS SPSFSILP
26440	56808	Α	26587	175	450	
26441	56809	A	26588	77	337	RDHEPTRRKKVRTHPNVRRNK LRTRRL*EL*HSLRGSAASFLKE GRPWRSGGGAQRR*KYWRKG KYSGKMQSWSRVYCSLAKVRA
26442	56810	A	26589	1043	1555	ALRQGPEGARAPNMDSSVSRC QVPGPQVCRAVPTEILASPAVE RAPAAALSSTTIWMPMSLCPW RPVLAACTSMTVRGRSTMYLP TTTGNAGCTWPKASLATRWLS SPMGRQARSLMLGAQVTLSWD RSMPWRRGGRSSGRNLSTI*WR LDWSLRRTWRSGRAWMSGIST
26443	56811	A	26591	313	462	VCFTPEPARPRIRQTRPDRRNSE HIRT/RRRKKLRTHLNIRRNKL WTRHL
26444	56812	A	26592	630	777	KERRGREKKKEEEKRRRGRRG GRRRKRRRRRGRGRGRGR* KERRGREKKKEEEKRRGRRG GRRRKRRRRRGRGRGRGRGRR RGSRRFL
26445	56813	A	26593	284	461	HSPGGSAASFLKSVRRRTHQFR TH*FHIHKNRTFTSR*SH*RMRQ WDQREVKVLFL
26446	56814	A	26594	573	968	AQRFCHSQWRCSSSRAVLEENP APLDTTPLSGRSKSSGRGCLVS LGL**PPSTRRSSHL*QPSSP*AS TFLQVRMTAPSGL*PQRPA*KL RSSPLLLTKNPFPEAAAF*SRGP PVSLKDTASLQAAFLGWP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26447	56815	A	26595	.3	699	RGRSRANSPQLLLEGGADPTVG DIGHLSVGVGPVHNAVGACQP DQTTPKHLADNPGPWTLDALT YQPHAANSCHKRGIAAS*SLMII MVIIFLVLLFWENEVNDEAVMS TLEHLHVDYPQNDVPVPARYC NHMIIQRVIREPDHTCKKEHVFI HERPRKINGICISPKKVACQNLS AIFCFQSETKFKMTVCQLIEGTR YPACRYHYSPTEGFVLVTCDDL RPDSFLGYVK
26448	56816	Α	26596	2	483	
26449	56817	A	26597	2	1041	WPQDGSCTWLAVAMGCWLAT QQGSLTRVPVATSGIQGCQAAP SPMWAAWTHGWASCYFRAAL QLPLPPGSTGNGSMSTSTAYSA SSPGFM/YTKAQGERSDHKENV FYVQHQKYVGGATQAFAKEN NQKAYKETYGVSHITRHDMLQ IPKQQQNEKYQVPQFDQSTIKNI ESAKGLDVWDSWPLQNADGT VAEYNGYHVVFALAGSPKDAD DTSIYMFYQKVGDNSIDSWKN AGRVFKDSDKFDANDPILKDQT QEWSGSATFTSDGKIRLFYTDY SGKHYGKQSLTTAQHLQQYLT YKRSFSIVVDAIIALPPLKRAAW PKSRHPPQVGLMEVQHLFPIPN NFEEHV
26450	56818	A	26598	116	338	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26451	56819	A	26599	971	2485	I FISSCFVRACGTLNPGVTMFYVI
20431	30017	`	20077		2.00	LGKFCDFAEPWFPHVMQEQLR
						VVGKGLWGFVRVSLSGFRIHGP
						HQKTASLAQVHKAVLHDGRTV
						AVKVQHPKVRAQSSKDILLME
						VRALPFSFLCPQSTFMWLVDEA
						KKNLPLELDFLNEGRNAEKVSQ
						MLRHFDFLKVGGTMQCRVWW
						SGGLMEFVDGGQVNDRDYME
						RNKIDVNEVRSRAQGCCAGER
						GVNGFVHCDPHPGNVLVRKHP
						GTGKAEIVLLDHGLYQVEEAFV
						TQPWGLWGQSLIWTDMKRVK
						EYSQRLGAGDLYPLFACMLTA
						RSWDSVNRGISQAPVTATEVG
		1				GPSRPCLFLNAEISHLLNHVPRQ
		1				MLLILKTNDLLRGIEAALGTRA
	ļ	1				SASSFLNMSRCCIRALAE*VWA
						PPSPPLLAP*ISFSEAFNLWQINL
						HELILRVKGLKLADRVLALICW
						LFPAPLCTVHVTILLLLWNPLRT
						LWPLSQGPQAELWHSSLFFSKK
						TQQPTFPFLVCAIGLDVPTTSVK
26452	56820	A	26600	831	1205	RKEGQGPSVHPLGSGCFPPGHA
20432	30020		20000	1851	1203	FWEALEANTWVPCVRL*RTPV
		ŀ				SAELLGLAPGGRWRAVNRDRG
		İ				RVAAASSLGEPCYSSPADASFP
						RSDSGGLDRQGGSCRYPKELFG
1						SHPQRARCTEGSLQVL
26453	56821	A	26601	377	962	LFSIFITQDPKLRELLDVGNIGR
20,03	00021		2000.			LEQRMITVVLKACV**LCSI*AN
•						ASVIYIFQEWTNDHLLVL*SMC
						HLNLSPLLCSLHSIYRNREGGS
						WGRKKTIC*LRCFISQNDSIPQE
		ļ				DFTPEMQILE*NLV*KILIAWFFI
						VFSGAKSKPYLTVDQMMDFIN
						LKORDPRLNEILYPPLKOEQVO
						VLIEKYEPNNSLARK
26454	56822	A	26602	1	810	MDAKKRKLYKYASTDSPAFAI
						TFIIMPYMENQAAKLAFERLSL
						NELVFSSEALTHSETFLPQPDNR
						HQNMSSTIHTAPIDTALGGNPA
						FLYLFLODFOPTODNSLASVTP
						SAGVSARLAPPPTPGPFTDVVV
						LDVLDEVGQGGEVESAAPESA
						GIGEEGGGDACHGATSRAP*Q
						ASPPPPSSPIPADSGAADSTSPP
					1	WPTSSSTSRTTTSVNGPGVGGG
						ARRAETPAEGVTDASELSCVG
	<u> </u>	<u> </u>	L	J	<u> </u>	ATTION I DAGE BOOVO

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
: :				sequence		
26455	56823	Α	26603	28	457	GGIPDSTARLSILTPRHHLQRSC
						SCNGTATRFSGQSYVRYRAPAA
						RNWHIHFYLKTLQPQAILLFTN
						ETASVSLKGFEGCLDAVVVNEE
į						ALDLLAPG/NDGGRLAGDTSPH
						PVLPPQ*LLQPEHMPQWWEVL
						MDPRGRLCLQMS
26456	56824	В	26604	205	1722	
26457	56825	A	26605	11	374	VSPSRSGIPGSTHASGQL*TGDR
	-					S/GPMGPPITAT\Q*DGDSDAYH
						GLATLHALLPALPGAAGF/PSGT
	1					SEPCPSSPC\GQHHHAGQLGHD
						LPVHCSEDPRPQPPPLGGPLEDL
						PSLLWHSDFFI
26458	56826	A	26606	69	551	QSGRSPQHVFPSVRGSGARSRG
						WILVHPSQYHHNPQRIYSACGR
						SGEHISPGYPCS\DGHDAYDQQ
						ADGTHHDACIFH\PRGSPRSP\G
						QCCLLTGGSRSGT\SGASATPG
						GRRGG\PAQGGE\PASRNSSVEE
						LTARVLAPAPAPALASAQPTLP
						GFSISPSTK
26459	56827	Α	26607	476	1016	CLWLLSCLYCSLGDCCLWWAV
						SVLCQVSAPRQALCFAPGENGD
						GGQQGLRGAPPGPGPRGPAPQP
						GPGYPGARQRGSPQQP*LSSEP
						GPYLRLSRSGGR*GPGRCCSRSP
						PGR*PVQAGDEDGQDAGSHI*T
						QPRVSEEGGTDEDQWSLPQEVP
						SASVPYQPLSHCQTVPASLQPH
						CLFS
26460	56828	Α	26609	247	342	RSIMPWLPKGSGWEVSSIPP*RC
		1				LHQLWSTSRNMAL/HVRVLQT
						EQAVKEYNALVAQGVRVGGV
						FHSTC*WSLKRRINH
26461	56829	Α	26610	129	272	NDTVSGLGRLESPTLMRQRNV
						CSHCYPGSAK*GYMIYKDALPR
						RTSL
26462	56830	A	26611	133	453	QVDPNTVLRNAVHTNTYLQGL
				1		THPSANHKSLYTLLNNFLHICR
			1			LHTRRMHGKTGRVYGITQRAV
				1		GIVVNK*VTGQILAKRIVPIEHI
						KHTKSQ*SFL*ELRPSPVAS
26463	56831	Α	26612	352	543	VPSINCGVPQGNMALMCRVLQ
						TEQAVKEYNALVAQGVRVGG
						VFHST\SDGSLKRRINH*VPKKK
	<u></u>		<u> </u>	1	1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26464	56832	A	26613	576	927	FAERTRTHH*PKPRWKGALGC RARTAVTSRGCLAPSRRRRRLP GRRAASQPGPNADPKACRPWN PRGSQVHAKRNALCFSRASDAP PRPDASPGQIFPGRRRKECQTC KTRVRLGCL
26465	56833	A	26614	67	415	ALARKLPTNFQWVKKIDASPGS PIPLNAP*PSPSVQTTPTTGHPG RALSTVSEVPGAGARLTYRVPF TRCKRSLILPSPVWVSRIPSTAK SPILISSPGGAHAASVSALTLVS GYE
26466	56834	A	26615	87	347	GIRY*LCHGFYHAYLGFRRRTS SPLQVSRPPPPRGTQSEP*AQSP RSPELELGLHTASHSRAANAAS SFHLRFGFPGFHPRPSPLF
26467	56835	A	26616	3	175	GFVTSSFFLGCLSFPDAYDLVFL LARE*HWKH*TQSILTLIAQCVF PEQPKRLCWVS
26468	56836	A	26617	539	788	EKEVPTLLDCCAALGQ*KCKMI QLLWKMV*SFSTKLNILLPNNP AVVLLGIHLKELKTYVLTETCT LMFIAGSQRNLRDYFRP
26469	56837	A	26618	843	1136	VKEQVYRRIAASRSVRRCSYQS RPGLLPTAGHHPQFHLYSDCHG NDIYSVYYQCEHGHAASSSETG VPRFPCPWWSETAQ*TGCASHP GPSAQRSAL
26470	56838	A	26619	2073	2329	LVQTSRPPDPSWA*SATVTRPE QASWARNLSRFPLLGMATVSG RGLPSGPGPRAMSPAGEPAPGA AEPAPPGSAAIPHRRPLLGQ
26471	56839	A	26620	723	1023	ITLLGLSLIPLISRLPWTQSWGPL SFLSTPTSLLISSTPLILNTINSLM TLRFLPPGGAFP*TPEPCIPPTQH PHLDVSLTGISNLPRPQSCFHCL HLS
26472	56840	A	26621	99	288	CLCQNKLGEGRDDNFTSWQSS AC*TFCFLLAVDSAETTAAES*C CCCCCCSAAGGWRRLVH
26473	56841	A	26622	130	450	RQLKLTAGCAKSPWLFWLKSY HSLYLAAACLLGLTYTRLGRSQ SSPPIHSHEFPPATSL*QQLHGQ PA*WLYDGPATP/SIAPPAHLLP PPWRGGTPSPWLPPSPLQE
26474	56842	С	26623	1	672	
26475	56843	A	26624	408	581	LIKDESAPRTPQTVLASAQFCLL CR*ARCCRGGSCCCCCCCCCC WWWCCCCYFGND
26476	56844	С	26625	66	264	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	1	in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26477	56845	A	26626	70	551	AAEDVWVYPSELYWPGPHGHC ETPRAGVFVVTSHEEGPGAGTA SSSSKGPSWARWGLEVSPLRWP
						SGQVGGAGSAESGQPLGSGFTF KAMGNLGESRARQAQLIHDRN
						TASHTAAAARTQAPPTPDKVQ
						MTWTREKLIAEKYRSRDTSLSG FKDLFSMKP*VSPLRWPSGQVG
						GAGSAESGQPLGSGFTFKAMG
						NLGESRARQAQLIHDRNTASHT AAAARTQAPPTPDKVQMTWTR
						EKLIAEKYRSRDTSLSGFKDLFS
26478	56846	A	26627	479	961	MKP PQSSLQGNLQMPWGSCLDSST
20478	30840	A	20027	4/9	901	HYRPSLVGVDFQLPSFWLVICG
						TCKHCHRMLHSVALFWVPLHC
						GWSIPRPRCPHPHHPPPLRGPSC
						HPPSPPWACPPRTGVQSATCPF
						A*RPTWSFTCDPTTKRSMRGLT
						HILRSGEKRPLPALCARSTSGSA TTSPGT
26479	56847	Α	26628	1	223	MGAVQKAYNLQKKRRRRRGR
						RGRIRGRRGRGRRRRK
						KKKKEEEEEEEEEEEEEEE
						EEEEEEEEE*EVEEEEEEEEEE EEERRRRKKKKKKKKKKKK
						KKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
26480	56848	A	26629	1	341	
26481	56849	A	26630	78	354	ENDSFYNDL*ATQRRRRRRKK
						KKKGEERRRKEKKGEERRRRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
						RGRGRGRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
26482	56850	A	26631	1	327	- Articological Control of the Contr
26483	56851	Α	26632	41	246	
26484	56852	A	26633	1	170	RKRRKRKKRKKKKKKKKE
						KEKEKEK\RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
25405	56050	-	26624		202	RRRRRRRRNTNNETGE
26485	56853	A	26634	1	282	MCIESEREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
						KKEEEEEERRRKKKRKKEEEE
						EEEEERR/MRKKKKKKKKKKK
						KKKKRQSL
26486	56854	A	26635	1	396	
26487	56855	Α	26636	1	255	MLWLPQPALGTRAAETLACSR
		1				RRRRQLYNCCLYLRRRKKEEE
						KEKEEEKGKEKEKEKKEE\KRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
L	<u></u>			<u> </u>		RRRRN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26488	56856	A	26637	1	290	MKKKKEGRRRKKEEEGEEGE E/DRRRRRRRRRRRRRRRR RRRRRRRRRRRRRRRRRR
						RRRRRRRRRRRRRRRRRTTT TTTTTTT
26489	56857	Α	26638	2	423	
26490	56858	A	26639	3	167	QQKEDEEKEKEEEKEEEDEEEE /ERRRRERRRRRRRRRRR RRRRETQEAETI
26491	56859	A	26640	1	325	MEKNEKEQEEEEKKEKNSKKK EEEEEEEGGGEE/ERRRRRRR RRRRRRRRRRRRRRRRR
26492	56860	Α	26641	1	618	
26493	56861	A	26642	1	291	
26494	56862	Α	26643	3	155	YRHLPKKKEEKEEEEKEEEEE EEEEEEE/ERRRRRRRRRRR KYEKKCL
26495	56863	Α	26644	1	1410	
26496	56864	À	26645	578	842	TQEAELAVSRDHATALQPGQQ SKTPSEEEERRKKEKEEERRRR KKKKEEEEG/MKKEEEGRRRR RRRRRRRRRRRRRRRRRR KKKEEEEE
26497	56865	Α	26646	215	471	
26498	56866	Α	26647	432	761	
26499	56867	Α	26648	1	357	
26500	56868	Α	26649	2	281	
26501	56869	A	26650	533	758	EQKKKKKEKKKKEKEKEEE EEEEE\ERRRRRKRRTRRRRR RRSRRRRRRRRRRRRRRRRR RRRRNTEK
26502	56870	Α	26651	264	429	HRAAPATSDTQE*HRSNAFGEE EEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEE
26503	56871	Α	26652	1	279	
26504	56872	A	26653	1	795	
26505	56873	Α	26654	1	642	MKKCKTSVIGIATFYLSIPHIYT PPNQTSSFMACAIAIEVQLTSAE PASIGFPVQKSPCGHLQLNGYK SSSKQGFPTPLLKQESWNSSVKI TTCNVGDKKNINDRRSANMMH VNNFPFRRHSWICLDRVQSETL PQEKKEEEEERRRRKKKEEE ERRRRKKKKKEEEEEEEEEE

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26506	56874	A	26655		1167	MAPRPQAARLPSCGTRSQGAA RPPPLGTAAAYRPLSSRLLTGPP PASSSWLAIHFRIRVGSSGQGN QRIKYLGIQLTRDVKDLFKENY KRLLNEIKEDTNKWKNIPCSWV GRISIVKMAILPKVQAILMLVLF LHLFCKYNIVGMENAGNGHD WSLDRHLMQASANQQATQLAI SRPSNQSKAQDFLRLLRKEKQT ALDTFAPLKEQAQKWNEDGIR SSVIPGIQHQSLLLAVLTFNSSK TSLGDRARPVSKKKKEESRKK KKKKKKKKKKKKKKKK RKRNKNKKKKKKKKKKKK
26507	56875	A	26656	342	616	RILHKSFRKLLCKGSFCSTRSPT REIRSKKKEEEEEEEEEEEE/ERR RRRRRRRRRRRRRRRKKRKK RKRKKKTKTKTKKKKKKKK
26508	56876	Α	26657	1	705	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26509	56877	A	26658	<u> </u> 1	2267	<u> </u> MKVELMGFAEGLAVRVREQEE
		į				VRLNWKVELLWTDLRDVPKG
						ANSFRVSGSSGVEVFMVYNRT
						RVKEPIGKARWPLDTDADMVV
		i				SVGTASKELKDFKVRVSYFGEQ
						EDQALGRSVLYLTGVDISLEVD
		1				TGRTGKVKRSQGDKKTWRWG
		Ī				PEGYGAILLVNCDRDNHRSAEP
						DLTHSWLMSLADLQDMSPMLL
		1				SCNGPDKLFDSHKLVLNVPFSD
						SKRVRVFCARGPEDVCEAYRH
						VLGQNKVSYEVPRLHGDEERFF
						VEGLSFPDAGFTGLISFHVTLLD
						DSNEDFSASPIFTDTVVFRVAP
ŀ						WIMTPSTLPPLEVYVCRVRNNT
	İ				CFVDAVAELARKAGCKLTICPQ	
						AENRNDR WIQDEMELGYVQAP
		1				HKTLPVVFDSPRNGELQDFPYK
						RILGPDFGYVTREPRDRSVSGL
						DSFGNLEVSPPVVANGKEYPLG
						RILIGGNLPGSSGRRVTQVVRD
						FLHAQKVQPPVELFVDWLAVG
						HVDEFLSFVPAPDGKGFRMLLA
						SPGACFKLFQEKQKCGHGRAL
		ł				LFQGVVDDEQVKTISINQVLSN
						KDLINYNKFVQSCIDWNREVLK
						RELGLAECDIIDIPQLFKTERKK
						ATAFFPDLVNMLVLGKHLGIPK
						PFGPIINGCCCLEEKVRSLLEPL
						GLHCTFIDDFTPYHMLHGEAYS
						LECRQHWGKNLYFRVGLKKK
						KKKKKKEKEEGQEEEEEEEE
26510	56878	A	26659	1	990	
26511	56879	Α	26660	1	235.	MTAKCVCGWGVGEREREKER
						EEEEEEEEEEEE/ERRRRRRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
25512	1.5000	1	0.5561		1101	RRRRRRRRRRKI
26512	56880	A	26661 26662	1 249	1101 806	
26513	56881	A	26663	348	684	LRCENPISSHVGHVGVSLAHTR
26514	56882	A	20003	39	004	GLFSRLILADREDISENWCSLVC
						CVCVCVCVCVWWLCISLFPGD
						MMTLLMKKDTLTEEET\QFYIS
						ETVLAIDSIHQLGFIHRDIKPDN
						LLLDSKGHVKLSDFGLCTGLKK
						AHRTEFYRNLNHSLPSDFTFQN
						MNSKRKAETWKRNRRQLAFST
						VGTPDYIAPEVFMQTGYNKLC
						DWWSLGVIMYEMLIGKLHG
L			L		<u> </u>	DW MOLO VIM I EMILIOKUNG

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26515	56883	A	26664	3	276	IKSIDDTSNFDEFPESDILKPTVL SSAP*AVHWRQGSESTLTSISFP VATSNHPETDYKNKDWVFINY TYKRFEGLTARGAIPSYMKAA K
26516	56884	Α	26665	95	405	
26517	56885	A	26666	3	349	GPGGWLSLSPLVL*ALES*KEEE EEEEEEEEEEEEEEEEEEE/ ERRRRRRRRRRRRR
26518	56886	A	26667	1	370	MHVAWSCPTAQSSQATVDSGK TLAETESPIGLSSKVGGKNIRAG EWDELKYDRFPGQKPKKKKRK RKEEEEEEEEEEEEEKKKKKK KKKKKKKRRRRRGRRRMQ QSHPNPTSAILAPWA
26519	56887	Α.	26668	1	430	MTFFPFDKRETDILLILNFSMEH CTRGQDPLGYQTTKKGFKDTE TPEKESLESKAECLGRRRKKN KEEKEEKEKKEKEKEKEKEK KRKKKKKKKKKK
26520	56888	Α	26669	1	708	
26521	56889	Α	26670	1	1233	
26522	56890	A	26671	1	366	MSYVAAVMFFCSVLGKFQMNL EEEVEKRRKKKDKKKEKEEE EEK/DERRRRRRRRRRRRRR RRRRRRRRRRRREEEEEGEE EEEEEEKKKKRRTLYCM*IA CKLKYLWTVSGHILCPNTN
26523	56891	A	26672	1	667	MSKEGNNRHWDRLEGGGWRR VRVEKRLFRDYPSSHPRGAEAF TSPDSIGRCTLRFPGLQMGLHQ PALIAILRSGADLSHLEGPMLEA GASACAPAVSPGDQALQQHPG EGRKVPGKRRRKEEEEEEEEE KRKKKKKKEEEEEEEEEEEE KKKRRRRRRRR
26524	56892	A	26673	365	670	
26525	56893	A	26674	29	370	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26526	56894	A	26675	<u> </u> 	1364	 MEMIWPSKGMPFTSTSYSNKES
20320	3007.	`	20075			SLLSVVQTSSYSHTHTRGSSEE
						VESLNRPITGSEIVAIINSLPTKK
						SPGPDGFTAEFYQRYKEELRIK
						YLGIQLTRDVKDLFKENYKPPL
						NEIKEDTKKWKNIPCSWVGRIN
						IVKMAILPKIIVEDALQIYYDMV
		1				LVCVGVGVSCRIVISSLEVLESR
		İ				RGQRIFFLVQAEQVLWAFKEVS
						SNCNDKSTLRGSVVKLQCTSGT
						SAFDIFQVGSRVLGEHRLPSVH
		1				SATYMSLTYFELAGLLEKSSQL
	1					VGSTGVEDIVAIMIPEPKGKEIV
	Ì					SLLERNITVTMYITIGTRNLQKY
						ERWKKKRTKGLEYQEFGFDDV
				1		KFRSLLDIEAEMPDLHRLPRNM
						HASSPSKRTARGRNKNKSSRLT
	}					MFGVEIQEEEEEEEEKKKR
						RKEEEEEEEEEE/ERRRRRRRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
	ļ	<u> </u>				RRRRRRRRRRRRRKH
26527	56895	В	26676	1	499	
26528	56896	Α	26677	1	1684	
26529	56897	A	26678	2	297	
26530	56898	Α	26679	68	319	IQHITS*TKKKRKRKKEEEEEEE
1						EEEERRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
						RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
						RRSHTSIPKESTLLQSQSVGLG
26531	56899	Α	26680	1	1617	
26532	56900	Α	26681	92	338	LEKEEEEEEEEEEEEEE
						EEEEEEEEEEEEEEEE
						EEEEEEEEEEEEEN*NVERY
						KKEGQW*KQRRQEKGLILPDG
26533	56901	Α	26682	1	548	MVDQRHLVLTSSTKKNQNNNF
						QVFVIENVGREPQTDKIASPGA
		1				GQSCTASVTADLLSRDLHFTKV
				İ		PSWSSDGPPYYPPACHLMSEPY
		1				FWGSCCYDTPIKTKTTNEEEEG
						EGEEEEEEEEEEEEEEEEEE
		1				EEEEEEGEGEE/ERRRRRRRR
		1				RRRRRRRRRRRRRGRRGRRR
		1				RKPRGGR
26534	56902	Α	26683	1	1215	
26535	56903	Α	26684	1	571	
26536	56904	A	26685	1022	1365	TSLLPPSSSIPSRLPSVVLSVRILS
		1				LWILACLAPWRWDLLRKASCL
		1				PAFSLLLSGANGSFSLGFQALL
		1				GRKEEEKEEEE*EKEKEKKK
						KKKKKKKKKKKKKKKKK
						KKKKKKKNF
26537	56905	A	26686	24	355	

I	_			Nucleotide	I THE COMMENT OF THE CO	Amino acid sequence (X=Unknown,
	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
ŀ	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26538	56906	A	26687	120	594	
26539	56907	Α	26688	117	487	
26540	56908	Α	26689	2	2482	
26541	56909	Α	26690	2	654	KGDVGEWLSAGKGESSAMFAS
1		l				EQEISKDEQGTPVLGSFYWEVD
1		ŀ				SPRKESSQAWAPGQEWIKLERD
1		İ		1		TTEEKMFEQLKPIEPVQKTLPW
		ĺ		1		VGEVAATLQEAMKRDCWREA
						RVKKKPVTFEDVAVNFTQEEW
						DCLDASQRVLYQDVMSETFKN
						LTSVAWVRKKEEEEEEEEEE
						EEEEEEEEEEEEEEE
						EEEEEEEEEE\KRKRKRKRERK
						KKKKKKKERTTWLWGNPLT
26542	56910	Α	26691	789	1072	
26543	56911	Α	26692	1246	2367	
26544	56912	Α	26693	579	1214	
26545	56913	Α	26694	119	1870	SCSRNRLLPPVSESLTRPLPSLA
						RWLPPPGLRQPSSRDYWPKGRL
						RLSAVPSPASPWALVSCLLPPSS
						SQEKAGKILKKRVEKQQPEEKV
						GKGLEESLCPCSSMSNHTKERV
						TMTKVTLENFYSNLIAQHEERE
						MR*RILFEKIEEEGLKDEEVINIG
		Ì		,		NVFLRKETEFLRLKRTRLGLED
				•		FESLKVIGRGAFGEVKITATCQ
						VGHVYAMKILRKADMLEKEQ
						VKHSCSSAFILVEADSLWVVK
						MFYSFQDKLNLYLIMEFLPGGN
						YLTMKGHKDTLTEEETQFYIAE
]						TVLAIDSIHQLGFIHRDIKPDNL
						LLDSKVLGGHWHELPFQEPRLR
						GFLSQCCDTPFRALRFLASPSFQ
						VPLHSPRPDLCTGLKKAHRTEF
						YRNLNHSLPSDFSKW*QLR*PK
1						AETWKRNRRQLVSNICGF*KN
						AENVSLGQVRWLTPVIPYIAPE
						VFMQTGYNKLCDWWSLGVIM
						YEMLIGKLHGFRGLPQETYKK
						VMNWKETLTFPPEVPISEKAKD
						LILRY*RTSLHLQIKSIDDTSNFD
				1		EFPESDILKPTGNTTSIVSCDYK
						NKDWVFINYTYKRFEGLTARG
26546	56914	Α	26695	271	446	YLVHILDALPRDPTALRRRQRC
						LGS*RKHQTRLRSGRPSSGPGG
						TDISVTAVSAPAQK
26547	56915	Α	26696	1	171	WGVIWRENGRCFSGLLRAGLG
						AAWEPRVGEIKILVS*LGTC*IK
						LICQSWVGANPRA

SEQ ID	SEQ ID NO:	Met	-	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26548	56916	A	26697	1	179	MWKGPKGLDMYGKSSVSPKTS
						DILGRD/NSPAGLEGANSGVAN
						CLWRGPCGRKLWEASRN
26549	56917	Α	26698	2	140	DN*KGVHKRILSKLAPELGSFK
						GFRSLAVNTHNSYGGKGNRPL KIR
26550	56918	Α	26699	3	601	
26551	56919	Α	26700	232	1809	
26552	56920	Α	26701	1	851	MQQEDPEESTKSPNPTTNKKQE
						KKLSLFGGLFTWTRVKFGAVT
						QIGGPPLGDQSPVLLLLQRLFSK
		İ				GYRVSPSKAQISSPSVTYLNSVS
						LIKTLLKTTLLPKEAGVIHCKG
						HQKASDPIALGNTSADKGLFRP
						PPFPSHQARGFAPAQDWQIDFT
						QH/RP/GVRKQKYLLV*VDTFT
						G*VKAFPTRSEKATAVISSLLSD
		ı				IIPRFGLPTSIQSNSRLAFISQISQ
						AFFQALSIQ*NLYIPYSPQSSGK
		İ			İ	VEQTNGLLKTHLTKLSLQLKK
ļ						DWTVLLPLALLRIRACP
26553	56921	A	26702	434	867	RLILPNRLGSPLLVWVDTFTG*
20000	130,21	-	20702			VEVFPTGSEKVTAVISSLLSDIIL
ļ		1				RFGLPTSI*SDSRPATKSSFSLISP
		1		İ		TLGSHDAPNPTRSSPEKHRPLSL
		1				HTIPQNFRCPDTLPLFRFIFFAFF
				1		SNTLHIMGKMAAEGPKSTLYC
						QFTEK
26554	56922	A	26703	96	415	Q. I.E.L.
26555	56923	В	26704	1	933	
26556	56924	Α	26705	1422	1774	DCPPSPIAFPQCTHQHHHHQYH
ļ						YHHRHHHRHHHYQR*K*NPGL
						PLFVYCYFQNH*ACHCSWGNS
		1				EHMTIASESQAVPLQPPQDSQG
						FFEDLELHYFFGDPSETRPGKQP
						KVSVQQIL
26557	56925	A	26706	355	1014	RHLRPQERAPAPSGSVPSRPGCS
						QAPGGLLRVGRGGMLLPGCAA
						VADLQEEVPGFSWDAWAVKG
						EQRQGGGGVVKH*DAIPGQRV
						SDPGPPEPLASAPGQLSPSTPEY
						RRPPGESRRHRRPDLAQDQRGA
1						AVLLLAGARGLSPLPRIPALGA
						ASFPPTLQFFLQLPSSGASTTSA
						GFFLLVLHQPLWLLLLDFLFDN
		1]	LLLLRHSLFIPHGFLKCVSIPAF
26550	56026	Ι.	26709	05	1208	
26558	56926	A	26708	95	298	GSTQVLWAAWGGAGWTPRWP
		1				VFATWPWVQDMWPQQAWPLP
						QGVDIP*ACPPPPLRT*WL*ENR
06550	T COOT	 	0.000	110	105	KAGS
26559	56927	Α	26709	110	195	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26560	56928	Α	26710	241	957	KSPQIGLQGSWGAVGVGMRDP
						KERATEASKPDLLAQRQGEGHI
						FILFFSDYIPIFSSYLSLQRSSRGP
		l				SFFGPFSSPHNIPCEGRQNSETPP
	1					WPSLGKRSKKSSLYPLPKAPQP
						KSRAPSPISNNLKNFPQPSEKKD
		1				GPQPLWPQKWPLAPLFSRSPS*
		1		;		DDSGPCTEYCRRARRFKSFEDM
						AHIGPPKKVLYKIALGKFWELA
						DAKKKRKKGTSETETCLLSRAT
						ELLPKGKRHCRGIL
26561	56929	Α	26711	496	708	GMLFRGSGACRRGGRTGGSGH
				ŀ		A*PEPPVLPPLLHAPEPLNSMPH
		1				GLPAPPASPCHFPNLDSCVHSHS
						DTPLSVLPLPHLKSPLSSSDFCS
]				YEVKKDAILSPMLSWWAGHRS
						AAGED
26562	56930	Α	26712	302	561	TFLLQLAAVWSADRVREALRP
						ALWDWRSAVPHPSPQGPTG*R
						GVGVHPAAASRGGESSHPTAF
				ļ		DRSPPPPKPLRI*PEPSARSGLP
26563	56931	Α	26713	1	411	LLVFQVHQCLHCKLL*/PSYVPL
						GYTEAFLATQNIGRVSLWAKH
		1				GHPDPFPLARADFRAQESPSPN
		1				DPSWLL*YFER*WSQATTKG*N
l						RCC*RCD*LQAPSRRPEAVHTN
						DPR*REVREEHMVLQVLTR
26564	56932	С	26714	361	642	
26565	56933	Α	26715	1805	2260	
26566	56934	A	26716	472	1667	AIHLLSLQTEFLVAERSSAAGRT
						TPATRAAFLAASCGPLHSCPTL
						LCSQLCCFSRSRSRVSGPKASLG
						IKEIASVDRVNTRRPACSTSSWL
		1				HNSGFTLSLANRDGGKRIRSET
				1		AKKGMSGDRSMKSWEVRRGY
		1				RWSSRAVRRPRACSSDGGTHF
						ALPMAARGSSGPSPGSPANSVR
						QSLKSESSISAIWVAEQAAGNV
						PRTSAQFGTGSESANTAARLIE
		ĺ				KLLRAELDKPEIRDERIVGWWT
						TFGRPQLGSRVGFCACSLAARM
1						SSTSQNLEAAFGGKFCFLWALL
						LGLDDTFESRISDTGSAGLMLV
						EFFAPW*VHSESANTAARLIEK
						LLTAELDKPEIRDERIVGWWTT
						FGRPQLGSRVGFCACSLAARMS
	1					STSQNLEAAFGGKFCFLWALLL
		<u> </u>	<u> </u>	<u> </u>	<u> </u>	GL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26567	56935	A	26717	2	237	SVRQTTATSPAHKNSKRLIRSC QGF/HPEPPPTGACYKCPQPRIP HEPCPI/S/SQDPTENWTVQLTW QPLPEPLELWPKAV
26568	56936	A	26718	1	313	MESAQKEAVEIFGQPHAASSSG DVKPLLFIDFYKCSGEKVVCME HALRACYMCRKSGHWAKECP QPGIPPKLCPIC\GDPTGNQTVQ LTWQPLPEPLELWPKAL
26569	56937	Α	26719	377	583	
26570	56938	A	26720	1221	1394	VASFYSLLQPPYPSTSFSFQSWR HTSISPFS*FQFLSFSGIFWQPLP EPLELWPKAL
26571	56939	Α	26721	160	234	
26572	56940	A	26722	163	414	
26573	56941	A	26723	212	399	YSLKDCWPLSLSLNHFLLSILAS PFNLSLLLISVPFLFW*RTETRFI WQPLSEPLELWPKAL
26574	56942	Α	26724	809	874	
26575	56943	Α	26725	49	220	
26576	56944	A	26726	71	375	LRSGDLPWEI/NPLSSCSLLREK DPPTTSGPQT\TSPRNISPILNPEL ATSARNLATRPRNACSPGFLLS RVPSVRDPTGNRTFQLT\WQPL PEPLELWPKAL
26577	56945	A	26727	1	1011	CSEYEDSSPAPVPATDLSSTLSS SVPQPQDTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSHAEH EHAGLGVQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGDSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKKNGEKRTRL QKRKKGMPPHPAYEDLNIAAIT LPANVVLHQPSGFRTSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQT\TSPRNISPISNPRQRRQV LSMDPKLRHRSRTGKAAFPWC LIIAGTPL
26578	56946	Α	26728	150	211	
26579	56947	Α	26729	445	549	
26580	56948	A	26730	193	249	
26581	56949	A	26731	372	564	LRSADLPWEINPLSSCSLLHEKD PPTSSGPQT\TSPRNISPILN/PEK KETRFIRGPKTPAPVMD
26582	56950	С	26732	185	640	
26583	56951	Α	26733	1662	1774	
26584	56952	Α	26734	233	527	

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26585	56953	A	26735	380	731	LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQT\TSPRNISPILNQEL ATSTRNLATRPRNACSPGFLLS CVPSVRDPTGNQTVQLTWQPL PEPLELWPKALCLTDSFPDLLG LTAED
26586	56954	Α	26736	2	182	
26587	56955	Α	26737	2	89	
26588	56956	Α	26738	2	89	
26589	56957	A	26739	161	460	KMKEFMKKSSRTKDTRQQEQV LEPLFTIAKTWNQPKCPSTID*I KKMWYIYTMEYYAAIKRNKIV FFAGTWMQLEAIILSKLIQEQKT KHHMFSLIRGR
26590	56958	A	26740	2	418	WYQHLLLMRASGSFQSWWKV KGEPAYHMANRP**SLISLRTK AKTGA*LFDYFVPHFIRKN*SLF TIAKAWNHPKCTSVTDWIKKM WYIYTMEYYAVTRRNKIVSFA ET*MELEVIIVSKLTQEQKTKHC MFSLTSGS
26591	56959	A	26741	902	1065	
26592	56960	A	26742	326	484	WYSWDCQLVTPWRPRIIPGPLG TWMELEAIILSKLTQEQKTKHH MFSL*SGS
26593	56961	Λ	26743	527	825	QPLWGQLH*EVPSCWRFSA*IC YSSGLTVMLSSWLDLIRPPWTL R*PREWRQCMGENHIGRGLGF* RPWTWMELEAIILSKPTREQKT KHYMFSLISGS
26594	56962	A	26744	398	557	HYWLGTVVHTCNPSTLGS*GR QIT*AQELETSLGNKNVGCSELI LLSTLGNRV
26595	56963	A	26745	3	359	HRPGIPGTTISSWMDAWGRLEA RYMSYLHSRRGDHA*DKLQRD NRFASQTHSHWAKSSCHCRFES RPFFLPSPSWSYNRSWGGESAE RTWMKQRGTCLSHSPLDLLHP GLCQHKVGAR
26596	56964	C	26746	127	216	
26597	56965	Α	26747	135	197	
26598	56966	A	26748	84	202	VLIHIRRDIMIPETVD*WEY**P* RLVPGQVQWVKPAIP
26599	56967	A	26749	483	669	
26600	56968	A	26750	1	274	EIRNKIHVSENSQIKTVKEKPSIS SSVSRLKGVNKVRASFPEDRKD YTGSKAPKGS*GYTIN*LK*NN KRKKKQNKKLMPKTEQGQKN SIR

SEQ ID	SEQ ID NO:	1	SEQ ID NO:	I	· ·	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26601	56969	A	26751	63	398	TPLRQPCSIRNVQQEPVGRFSGT GLPLSVARSSPWEAWPQCKWR FQNAGD*DIRQPDRGQGPRPAE PEKREPYLRSQQGAFLGSHSSGI QSQLLGLGESCSYGATGKPVHP
26602	56970	A	26752	3	231	SVHEEEKMALPLGQSHCGLLY LYY**RCFKCYSFYCILFIKNAFI Y*NI*IYINTHTHTHTHTHIYIYI YNCLYI
26603	56971	A	26753	4266	4944	TDEIGASRLSRVESLAPEVKQN TTASGCELMHTEMQALRADW KQWEDSVFQTQSCLENLVSQM ALSEQEFSGQVAQLEQALEQFS ALLKTWAQQLTLLEGKNTDEEI VECWHKGQVSWLPV*KAEPRT EDLKSQLNELCRFSRDLSTYSG KVSGLIKEYNW*A*TLLKGCQN KEQILQQRFRKAFRDFQQWLV NAKITTAKCFDIPQNISEVSTSL QKIQVRVLSI
26604	56972	Α	26754	3	556	
26605	56973	A	26755	143	724	GWIPSDNSICVQEDCRIPQIEDA EIHNKTYRHGEKLIITCHEGFKI RYPDLHNMVSLCRDDGTWNN LPICQGCLRPLASSNGYVNIYEL QTSFPVGTVISYRCFPGFKLDGS AYLECLQNLIW\RPAHPGALLW KEEDLNIFSLSFISHTSGWQLLC FIFALC*SPLPPQHLPVPQLAPPH LCSKCCSPAIKDV
26606	56974	A	26756	.3	1393	CLRPLASSNGYVNISELQTSFPV GTVISYRCFPGFKLDGSAYLEC LQNLIWSSSPPRCLALEVKIPVS GAVRVTITLPVTLGHPNVVTQR WKAGASDKGELVVLKLLFSPT AQVCPLPPMVSHGDFVCHPRPC ERYNHGTVVEFYCDPGYSLTSD YKYITCQYGEWFPSYQVYCIKS EQTWPSTHETLLTTWKIVAFTA TSVLLVLLLVILARMFQTKFKA HFPPRGPPRSSSSDPDFVVVDG VPVMLPSYDEAVSGGLSALGP GYMASVGQGCPLPVDDHSPPA YPGSGDTDTGPGES*TCDSVSG SSELLQRLYSPPRCQESTHPASD NPDIIASTAEEVASTNPGIDIAD VDSSNIKLPDWQTKYRVASPAR STCEDRSGAPVGTHESLFFSIPS SARQDWAPLDSQLESPQCRLPT LQRDFLVDPQAERPVPLDPELT EIWCPNKNRIERHMEHSGIEA

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	1	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26607	56975	Α	26758	1	500	
26608	56976	В	26759	19	148	
26609	56977	A	26760	184	539	LPAKEEEGHSKKSGPLLGPRRA LPGTALGARGAEQGDPEADH* GADTTKRCPGLGPAPVPRKGIP AEGPRRGSRAGLGMWGPGLGA HRTAAPSPAEAPSPCQHPSSHSC PVACFEPVF
26610	56978	Α	26761	1	441	DENRELLG\ELDGIDVLLQQLSV FKRHNPSTAEEQEMMENLFDSL CSCLMLSSNRERFLKGEGLQLM NLMLREKKISRSSAL\KVL\DHA MIGPEGTDNCH*VCLTFLALR\T IFPLFMKSPRKIKKVGTTEKEHE EQCCSILASLLRN
26611	56979	Α	26762	1	2403	
26612	56980	Α	26763	17	751	AKMPFDANKLYCSEVLAILFFS PLENRELLGELDGIDVLVFA*Q VFKRHNPSTAEEQEMMENLFD SLCSCLMLSSNRERFLKGEGLQ LTLL*LSHSSDSCEMPTWRGGS MEQGGRMGLGLVSVGLEHALL LTYGLYQRLPPQPQNAQPSFVH REKKISRSSALKVLDHAMIGPE GTDNCHKFVDILGLRTIFPLFM KSPRKIKKVGTTLPPLPAAATPT NRPSAMNGRVRMEAEQSSAHC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	B	*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26613	56981	A	26764	1	1914	MAEGERGADVPH/GPRGLAGR
						RGVGGAARGRAG/PGGT/EGGG
						GPESLSGGSGVGDSGGGCAPGP
						SAPPARRRVPLAMGPRNLLIDW
						IWIMDTTLGLGTEGGGHSPPVL
		1				PLCASVSLLGGLTFGYELAVISG
						ALLPLQLDFGLSCLEQEFLVGS
						LLLGALLASLVGGFLIDCYGRK
						QAILGSNLVLLAGSLTLGLAGS
						LAWLVLGRAVVGFAISLSSMA
						CCIYVSELVGPRQRGVLVSLYE
1						AGITVGILLSYALNYALAGTPW
						GWRHMFGWATAPAVLQSLSLL
						FLPAGTDETATHKDLIPLQGGE
						APKLGPGRPRYSFLDLFRARDN
						MRGRTTVGLGLVLFQQLTGQP
						NVLCYASTIFSSVGFHGGSSAV
						LASVGLGAVKVAATLTAMGLV
						DRAGRRALLLAGCALMALSVS
1						ł control of the cont
1						GIGLVSFAVPMDSGPSCLAVPN
						ATGQTGLPGDSGLLQDSSLPPIP
						RTNEDQREPILSTAKKTKPHPRS
						GDPSAPPRLALSSALPGPPLPAR
						GHALLRWTALLCLMVFVSAFS
						FGFGPVTWLVLSEIYPVEIRGRA
						FAFCNSFNWAANLFISLSFLDLI
						GTIGLSWTFLLYGLTAVLGLGFI
						YLFVPETKGQSLAEIDQQFQKR
						RFTLSFGHRQNSTGIPYSRIEISA
26614	56982	Α	26765	201	632	NLLLCPLSAESRPEEGVRLFCSQ
						FRSRQRPQAHKSAWGTTALSES
						MNCFASFGASISSSADQEQLHL
						PGAVGSGRPGECLGPSGRCSK*
		1				GATFPGQKGRWKEARPSPVPAP
		1				AAGLQSRAGHPRGGIRPGRPHG
		1				ERDSAACWGR
26615	56983	Α	26766	197	777	LPSRGAGLRTCSPPCLSLPPTPW
1		ı				TPVRPEPPQRAPPPTPRRPVPST
						TQGLRNASARRGTGR/PAPP/VS
						PGAGSTR\EASWAPESAARAGL
						WGPSNSVQRAAESASRPHGFG
						QPPKAPARPGWLTGKFPASVPS
						ASRRAPPAAVTSARHYYLRQPP
1						PRPSSCPECNKIRLWPAFQLTPL
1						CQGPAASERDRRKPQKRR
L			<u></u>	<u> </u>	<u></u>	10 Correspondent Armer

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	1	1	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26616	56984	Α	26767	178	697	ATLFIQKHQSGVKSTNP*IGRRS
					LTPEITAELGLERLNPRRCSSCL	
						LGLKFEYHNSNLPLQLHGQAC
			ŀ			GDPTNSVQRAAESASRPHGFGQ
						PPKAPARPGWLTGKFPASVPSA
						SRRAPPAAVTSARHYYLRQPPP
					RPSSCPECNTIRLWPAFQLTPLC	
						QGPAASERDRRKPQKRR
26617	56985	Α	26768	1	858	
26618	56986	Α	26769	10	1332	
26619	56987	Α	26770	1	1086	
26620	56988	Α	26771	1	1392	
26621	56989	A	26772	1	987	
26622	56990	Α	26773	1	336	
26623	56991	Α	26774	46	302	APGAVKKTWFGKKGREREKQE
						RR*RQLGKENENIVALQLIRTD
	;					QEYWRHHSWHFFLSAAACQPE
						LFLLKHTAKNNRRIRVSQKWK
26624	56992	Α	26775	1	1839	
26625	56993	Α	26776	284	816	APGAVKKTWFGKKGRERGETR
						EKNNQPTVRTNSQTRDTFFKT*
						DLF*RMPSWELPSPASS*ASKTI
						KYLGIQLTRDVKDLFKEKYKTL
						LNKIKEDTNKWKNIPCSRIGIINI
						MKMAILPKSGPSAARLLEFAGG
						PLQTLFAWVSPEEAAEQQILPN
						SQSCYLILPLEASSQRGSWLY

	of peptide sequence	hod	in USSN	location of first	and an faulant aming anid	the Carrier and a second second
	sequence	1			codon for last amino acid	*=Stop codon, /=possible nucleotide
26626		İ	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26626 l:						
l'	56994	Α	26777	1	2547	MVKGSIQQEELTILNIYAPNTG
		ł				APRFIKQVLSDLQRDLDSHTLI
						MGDFNTPLSTLDRSTRQKVNK
						DTQELNSALHQADLIDIYRTLH
						PKSKEYTFFSAPHHTYSKIDHIV
ŀ						GSKALLSKCKRTEIITNYLSDHS
						AIKLELRIKNLTQSRSTTWKLN
ļ						NLLLNDYWVHNEMKAEIKMFF
1		ŀ				ETNENKDTTYQNLWDAFKAVC
						RGKFIALNAYKRKQERSKIDTL
						TSQLKELEKQEQTHSKASRRQE
·						ITKIREELKEIETQKTLQKINESR
						SWFFERINKIDRPLARLIKKKRE
						KNQIDTIKNDKGDITTDPTEIQT
						TIREYYKHLYANKLENLEEMD
						TFLDTYTLPRLNQEEVESLNRPI
					TGSEIVAIINSLPTKKSPGPDGLT	
						AEFYQRYKEELVPFLLKLFQSIE
1						KEGILPNSFYEASIILIPKPGRDT
						TKKENFRPISLMNIDTKILNKIL
		1				ANRIQQHIKKLIHHDQVGFIPG
						MQGWFNIRKSINVIQHINRAKD
						KNHMIISIDAEKAFDNIQQPFML
						KTLNKLGIDGTYFKIIRAIYDKP
						TANIILNGQKLEAFPLKTGTRQ
						GCPLSPLLFNIVLEVLARAIRQE
						KEIKGIQLGKEEVKLSLFADDM
						IVYLENPIVSAQNLLKLISNFSK
						VSGYKINVQKSQAFLYTNNRQ
				,		TESQIMSELP\FTIASKRIKYLGI
						QLTRDVKDLFKENYKPLLKEIK
		<u> </u>			<u> </u>	EDTNKWKNIPCSWVGRINIMK
26627	56995	Α	26778	1	489	SISWKLWFTEFTLFRFFQPSVSA
		1				VPVSTLAVVLGLKTLSLLFSHSF
						PGRHSWALRAISLLPSFLYTSSL
						MNSFSYTVHLYLGGLLRLCGSR
						DPHACGFPEGSPLPSGSAA*PFI
		İ				WGMRKPSCVLAPSCSRRDSFG
						CLSFSGHQCLHKSHVGSPSGPQ
						ERLYNG
26628	56996	Α	26779	354	685	YRGYLRGECFP*KALCCEPAAY
						LQTCPNPFSGPACSGHALHSLN
						VGDCVYLICPRYPPLRRAGKPR
						DTGIEGRTLSSGGPSVHSSFHSA
26622	56005		26700	1	967	VLFPYTSKLLWIERRRPAGQS
	56997 56998	C A	26780 26781	139	867 513	
	56999	C	26782	1	948	
	57000	A	26783	630	734	TAARSGYPGRAGTLTGLHPMQ
20032	57000		20,03	0.50		VCRCRR*PYSRGT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26633 57001	57001	A	26784	1	224	SRAGYDHVVEPVERGTSGVRW YACCGLMVCPANPQHFAHGY/
						VGKIPGYPARAGTLTGLHPMQ VCRCRRCPVYEI
26634	57002	Α	26785	112	254	
26635	57003	C	26786	1	567	
26636	57004	С	26787	i	543	
26637	57005	A	26788	165	633	RIPGLLLCPAYPQHFAHGYVDK IPGYPGR\GTLTGLHPMQVCRC RRQAPCMKSNNALIVILGTVTL DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDRFGRRPVLLASLLG ATIDYAIMATTPVLWIYPLVNS
26638	57006	A	26789	264	800	ISNFELCSRSIHLLCSSTGYPGR AGTLTGLHPMQVCRCRR*PAV
26639	57007	A	26790	1	738	
26640	57008	A	26791	84	162	AVLDLGPPTGRDPPQGSPDPYS GAFLLASCGAPLGQRSQRKEQ AAIFAVLQLLLVIPPGVGGTQT NRVWSGFPANHGNPGYPGRAG TLTGLHPMQVCRCRR*PPYRVI PQCGTPLGQGQPEVFVKQFWIL GLRLGETPHRGHQILIQGHSC
26641	57009	С	26792	1	531	
26642	57010	A	26793	216	519	QRESTIPSRPVERSNLGVRLYAC CGLLLCPAYRQHFARGYVDKIP GYPGRAGTLTGLHPMQVCRCR R*PDRRGTERVSARKHVCFVVV SLFVAACRPPLRA
26643	57011	C	26794	1	606	
26644	57012	С	26795	1	1059	
26645	57013	Α	26796	1	3285	
26646	57014	С	26797	1	1390	
26647	57015	A	26798	211	679	RIFKCKADLLLYDMLVYVTLWI HRAVTYTHRVPNHSYRRSNIKS ETTVPTRIVGPVERSNLGVRLY ACCGLLLCPAYPQHFAHGYVD KIPGYPGRAGTLTGLHPMQVCR CRR*PKPAPLPGSPQHLCSHQPH LAQRKTGQCFLQGHCFPEKNW GTV
26648	57016	С	26799	1	774	

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26649	57017	A	26800	542	1269	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQRKYP GCRLYASCELLLCPVNPQHFAH GYVDKI\PGY\PAGAGTLTGLHP MQVCRCRRQAPCMKSNNALIV ILGTVTLDAVGIGLVMPVLPGL LRDIVHSDSIASHYGVLLALYA LMQFLCAPVLGALSDRFGRRPV LLASLLGATIDYAIMATTPVLW
26650	57018	В	26801	1	1531	
26651	57019	Α	26802	1889	2154	
26652	57020	A	26803	147	162	APSLHLKDTVDRSNLGVRLYA CCGLLLCPAYPQHFAHGYVDKI PGYPGRAGTLTGLHPMQVCRC RR*PGAHTVVDIRPREDHLGSA GQPNCPENGCLQGFHTGLAYPE HHPCI
26653	57021	Α	26804	2381	3641	
26654	57022	Α	26805	1	2367	
26655	57023	A	26806	1	488	MDLLYMAAAVMMGLAAIGAA IGIGILGGKFLEGAARQPDLIPLL RTQFFIVMGLVDAIPMIAAIAFV LFVLFCMKYVWPPLMAAIEKR QKEIADGLSSAERAHKDLVLAK ASATDQLKKAKAEAQVIIEQAN KRRSQILDEAKA*GRQEPLVQV FLESARKR

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
140.	sequence	illou	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26656	57024	Α	26807	2125	2435	VSPRQKSARPDLT*IRTLLCKVL
						GVLFSVAGGKKGPTCILQILKG
						QRRQEA*CISVMAERVWASGQ
			<u> </u>			A*WEVWLHWAKSIDWFLFWK
			<u> </u>			QHVHALRVRLDTCLFSLEEGSS
				,		FWNQGLTWKVVRRTFSESINH
						TPRITLGVPYSVHGIQLPGLLNF
						GEFKVCFVLSPRIFNLTHENFLS
						SEGPERRGLLGATFNCLNKRLA
						KYRMRNVHPKPKLVRYLHSRL
						PPEPAAAP*AWCGPRHLSRRQM
						SSSSQIGNDSFQLQVTPVHLLPL
						SHTTRKNPEMYDLPLLIFNPQES
						AILQLFHQDGECLHCSPIVGDW
						CHLGHSQACPSFHVPSGLFVPS
				1		LLCGAAFGRLVANVLKRYSVC
						VRVCAHVHVCARVRVYACVC
					VRMTISLTVILIESTNEITYGLPI	
						MVTLMVSTLPPGPCQAQGHVR
						PTGPIFRSLLEWETEVEMDK*G
						HDFAHVLVSECISSEA*GMLLL
	,					GGGPDRSLFSTFRAVWSLSRLL
						DSVIAAGKQ*A*RT*SVGYSLL
						CPDLKGDPSAVFILRTTVHHAF
						PVVTENRGNEKEFMKGNQLISN
						NIKFKVKKTA*EERQVRDKRSR
						LTRLSALPIRNMCDEHIASEEPA
						EKEDLLQQMLERR*EPGGAPTA
				}		RRATQRWGEPLAQML*LTFHG
		l				LILRSQLVTLLVRGVCYSESQS
	:	l				VSLSEAEISQARPDEARGVGRC
		<u> </u>				RRADLTLLNPRMIVVRRAAPAC
26657 26658	57025 57026	A	26808 26809	24	369 371	
26659	57027	A A	26810	82	703	
26660	57027	A	26812	1	1692	
26661	57029	A	26813	293	563	NVWPSSSVRGRNE*GREGGRR
20001	37023	 	20013		303	RTQQAAGLGPAPSDLWWLWLS
		İ				WCLQKNMSQGGENLPAGPGSC
		l				CGREAQEGAGTSLEDAPFFEAQ
						LLQLH
26662	57030	A	26814	1	488	VARLYWKRPSLHACHFRDPRA
20002	1,000			1		GLSENPRLLQCSPSSSSGNVWG
						PHLYAVPCL*NGRIIPSPWNYRS
						LNSTTSSTCSSFAVVSSPSCPWV
					-	QLPGSCLLSRSLLQRVAWSQAP
				1	1	VPMRSEQDQLQKPPPPSAGLPA
				[1	SVHANL*PGDRKGSVWTPAGV
				1		AQIPSPWP
26663	57031	В	26815	51	90	
20003	121021	Г.	120013	171	120	l <u>. </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26664	57032	A	26816	299	707	
20001	31032	``	20010		, , ,	PLLS*MPLSHPQGPSQPPAGSMS
						SSPPATTSTCSCSPPAAGCTRGR
						TTGRPFWTASGPAELDWASGSS
]						VGL*SQGSQLGACGASYAGLG
						VPPRLLGPMTSCCMSLPFPSPAR
•						P
26665	57033	A	26817	146	330	TVARRMELTPALLRALLNGILPI
						SEPPSNRIFACWGKPAWTACCN
						SLRARR*RAISCCPSH
26666	57034	A	26818	1326	1694	IFGWFGACCSLGSCCVVFTAST
						CTTVCGGCAIKVGSCLSLATMG
	ł					CCVCCTSGLGCACSCWRGVSF*
						CLMESWGICGSLCWSWSACRW
		İ				MVCFCLVWKHCRVFTCS*VCS
		İ				SGGWLSFCCLADCD
26667	57035	Α	26819	1	1407	
26668	57036	Α	26820	75	1397	SRGSGREKFPAQLSYQTLLGKG
		1				PIEGTSLSNLAQQRCKEHHCHF
		1				LREQGPNCLIIERFMDRYTGKYI
		1				HMASHTTRCRPHVSRRPKARLL
		1				APATRSRSARARLRETRVRRGS
		1				PSCLWLNRRSRLPAEHSVRSPP
						RDMVFESLGLPSTKSSEFRSAA
						PEAAERAQPGDPCGLQTPAPLR
		1				PGFRRNQDPASAAAAAEEVRS
İ		1				GGGRGRILATTLWGCNTLCITQ
		1				YTRIRKLTLVYCGVESKQEWG
		1				EYHEGVQAGLTRPGRSPKLISK
		İ				FLEKELTDRNWDQEDEAEEVK
		1			Ī	SSFPKND*VLKNRAIKKAKRRN
						VGFEVSAPLQLLLFKGLVVPSG
	l					GGRFSGFGSGAGGKPLEGLSNG
						NNITSAPPFASAKAAADPKVAF
						GK*LPSPSRLLVDKVSNPKTNG
						DSQQPSSSGLASSKACVGNAYH
		1				KQLAALNCSVRDWIVKHVNTN
26669	57037	A	26821	3	89	AASGRSFRGYSRRHCYHRR*QL
						НАСНСР
26670	57038	A	26822	150	383	LCLGEVWKGSFFLTGTKRPGVF
					1	LSLHKKACYHHNHHRYHHHH
		1				HHQTKP*QQELNSLLLHFPPHQI
						QGDQFHHHLYYL
26671	57039	Α	26823	105	417	LCLGEVWKGSFFLTGTKRPGVF
		1	_			LSLHKKACYHHNHHRYHHHH
						HHQTKP*QQELNCENMPQYNF
					1	QNGSQSYQTLLL/SLSTKFM*YS
						KFFVVISVMFIASSPETDF
Ь——	1		1	<u> </u>	1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26672	57040	A	26824	89	554	AMNSCVTGDRYSPCGGFGFAF LYSSVSVSSSSEYQLSPLPPAKR PLAAQQSCSIPIASVFQQTIHSLF AKDKKEFSSNLLDSKVNMCHE AHQLISHS*ANFRSICHIPQRW* NLIFEKFSDVSMGSGTFG**AEN
26673	57041	A	26825	84	239	WS*TLSIAASLVYSLLHKIQ ACTKKACYHHNHHRYHHHHH HQTKP*QQELNSFRFSLSQPSLL AVFLFLRP
26674	57042	Α	26826	2	245	
26675	57043	A	26827	154	546	LIVTVHVNHLGVLINHRFRISGC GVCGTDCISHKFPGAADATGPS WTTHCAVITFSLTTGSATKKTE DNNTFVFNVDVKAN*HQITRA VKKLCDIDVPEVNTLPNVSISFR FLLCSTVFCTLTVFFLRENG
26676	57044	A	26828	331	612	NHRGLPFPDYIPGTYFLFFFFLF FSFSSFSSSSFSFPASGNHNSTLY FYGINFFSFHIGMRMGGIFLCLT CFT*HDVLQAHPHREGRQDLLF HD
26677	57045	В	26829	928	1617	
26678	57046	Α	26830	95	929	
26679	57047	A	26831	3	1128	LYNRRRRRCSHCRHRCRRLSS GLRKEEVISLGASLGRVFVPCSP PTVSAARGPTGAPGGPNSKPLS GCCDDGFNLGRQQWGNPLPFC SKTISSSLHWTWSQVNLVEILP AIFSSFLNLQHVNLWFLAAAM KAVTEQGHELSNEERNLLSVA YKNVVGARRSSWRVISSIEQKT ERNEKKQQMGKEYREKIEAEL QDICNDVLVRGQCFCFEQWFL NSINLMYKCRLSNYFRYLSEVA SGDNKQSK*YL*KEIRPVMEPV FFHRDFLTILIRLGLALNFSVFY YEILNSPEKACSLAKTVRKTLC DI*P*QNSACVINFILFLNILRDN LTVSTTSTGFIVSFLFTYLIIHCY LQEVCSVSLCTLNIYPLCDKKK
26680	57048	Α	26832	139	601	EGRGHLAQELLSERVFVPCSPP TGMTMDKSELVQKAKLAEQAE RYDDMACSSERHVTEQGHE\LS NEEKKSCSLVAYKECW*APRR\ SSW\RVISSIEQ\KTERNVEGSSR WGKEYREKI\EAELQDIC\NDVL ELLDKYLIPNATQPESKVFYLK MK
26681	57049	Α	26833	70	122	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26682	57050	A	26834	179	876	CIVILFFFSQFNFVGRILGPRGLT
						ANVNRYLELHTLYGYMNLFIV
						SIMKDVLSL*RE*F*SCTL*IF*E
1						EQNRGKPNWEHLNEDLHVLIT
						VEGV*I*LLYLWTVSNAFISCVF
İ						HV*AEGEDRYCCLYTSF*ISLLT
	ļ	1				VAALAFSLAATAQAAPRIITGP
ļ		1				APVLPPAALRTPTPAGPTIMPLI
		l				RQIQTAVMPNGTPHPTAAIVPP
						GPEAGLIYTPYIYIISKYLWLLSS
						CSPEP
26683	57051	A	26835	3	915	AEAHPRLPDAADERQEAHDSLP
		l		-		NFCGIFNHLERLLDEEISRVRKD
						MYNDTLNGSTEKRSAELPDAV
						GPIVQLQEKLYVPVKEYPDFNF
						VGRILGPRGLTAKQLEAETGCK
						IMVRGKGSMRDKKKEEQNRG\
						KPNW\EHL\NEDLHVLITV/EKV
						LQEQGQEIKLKRAVEEVKKLLV
ļ						PAAEGEDSLKKMHLMELAILN
						GTYRDANIKSPSLAFFLAGTAQ
						AAPRIITGPAPGLPPAALGTPTP
						AGPTIMALIRQIQTGGMPNGTP
						HPTAAIVPAGPEAGLRYTPYEY
						PYTL\APATSILEYPI\EPSGCI
26684	57052	Α	26836	1182	1360	KLSICVYIYICMFIYTHVSV*FYI
						YIYTHRHTENHYFCNSVQFVLY
						LFTFFCYYFIWPA
26685	57053	Α	26837	3	348	RNSKHVCRAEP*GHFCYK*HF
		ł				WNHTEHTAVLEI/EQINARDET
						DF\YLGNRCTYVCKEQHSGPGS
						KSNTTIVIWGKVTCAQGKNSV
		1		İ		VCAKFQSHPPAKAIGHRIHVML
						YHWRIQIH
26686	57054	Α	26838	264	527	NSKHVCRAVP*GHFC*K*HFW
						NQREHTTVLEIEGVYARDETEF
						YLGNRCTYVCKEQHSGPGSKS
		1				NKTRVIWGKERGSGWCRLSGR
26687	57055	В	26839	26	515	
26688	57056	Α	26840	92	341	
26689	57057	A	26841	224	1111	
26690	57058	Α	26842	2	592	HSLTGRCIFFLITGTSPGSPEMST
						TLKIMSSKEPSISPEIRSTVRNSP
		İ				WKTPETTVPMETTVEPVTFSPQ
						LVFARLMTGVGLGAALPNLIAL
				1		TSEAAGPRFRGTAVSLMYCGV
						PIGAALAATLGFAGANLAWQT
						VFWVGGVVPLILVPLLMRWLP
						ESAVFAWRSISNKRA*FRDCRC
L						CSAAIIW*RRFPFKSKPVM
26691	57059	A	26843	2	141	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26692	57060	Α	26844	1	978	
26693	57061	Α	26845	144	647	
26694	57062	Α	26846	1642	2652	FGILVLLALIVIWYNNFFGAETE
						AILPYDQYMHRFAAYFQQGNM
						ESNGKYVDRNGNVVDYQTGPII
						WGEPGTNGQHAFYQLIHQGTK
						MVPCDFIAPAITHNPLSDHHQK
1		ĺ				LLSNFFAQTEALAFGKSREVVE
				1		QEYRDQGKDPATLDYVVPFKV
						FEGNRPTK*ILLREITPFSKLNEV
						KAISDTICVIRDGQHIGTRDGIE
						HLTAWHPVNRHIKRVNDVSFS
						LKRGEILGIAGLVGAGRTETIQC
						LFGVWPGQWEGKIYIDGKQVD
						IRNCQQAIAQGIAMVPEDRKRD
		1				GIVPVMAVGKNITLAALNKFTG
	ļ	1				GISQLDDAAEQKCILSHPRCSW
		ļ				QGRHLLH
26695	57063	A	26847	52	137	MOLIVIDDIVIDLE ALIVORI TOO
26696	57064	Α	26848	<u> </u>	1858	MGLKVDDKVPLFAVVSRLTSQ
l						KGLDLVLEALPGLLEQGGQLA
						LLGAGDPVLQEGFLAAAAEYP
	ļ					GQVGVQIGYHEAFSHRIMGGA DVILVPSRFEPCGLTQLYGLKY
						GTLPLVRRTGGLADTVSDCSLE
1	•					NLADGVASGFVFEDSNAWSLL
		1				RAIRRAFVLCQGQFHHRTTDVE
						YKGDPKAVKIEESEINYLLNVY
						NTHFKKQLSRDDIVWTYSGVR
						PLCDDESDSPQAITRDYTLDIHD
						ENGKAPLLSVFGGKLTTYRKLA
						EHALEKLTPYYQGIGPAWTKES
					İ	VLPGGAIEGDRDDYAARLRRR
					1	YPFLTESLARHYARTYGSNQRA
						ACSAMREREARTLPOKLAGTL
						GMLSKVMRIPRQQEVTALRTY
						LQIRIGLHAAFNACEEMCQRVA
		1				LEROLDSEERALLIERSQTVIRO
		l				GRDLLHAWDATWNSAQALDN
						ALQPDRAGQFADALEKYAADE
						SFFAQLDKYDIPVVVIGKVEGQ
						YAHVYSVDTDNFGDSIALTDAL
		1				IESGHQNIACLHAPLDVHVSVD
						RVNGYKQSLAAHNIAVRDEWI
						VDGGYTHETALKAARQLLSQS
		1				PLPEAVFATDSLKLMSIYRAAA
		1				EKNI\AIPQQLAVRILFGLHL*IV
						LSTRAGFGNLAHY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26697	57065	A	26849	136	3261	I PMSPTIYDIARVAGVSKSTVSR
		-				VLNKQTNISPEAREKVLRAIEEL
		1				QYQPNKLARALTSSGFDAIMVI
						STRSTKTTAGNPFLLEVAQAFP
1						AKAE*KGFQVLVRTSHNPAEDL
						QKCESKIKQKMIKGIIMLSSPAD
						ESFFAQLDKYDIPVVVIGKVEG
	}					QYAHVYSVDTDNFGDSIALTD
			ŀ			ALIESGHQNIACLHAPLDVHVS
						VDRVNGYKQSLGAHNIAVRDE
		1				WIVDGGYTHETALKAARQLLS
		1				QSVSLSVAVSWSAC
26698	57066	Α	26850	73	174	
26699	57067	Α	26851	252	575	PGFPRGPPPPPGFAPFHVSIWDT
						DLSDPAARAGLGVRWTPDPPR
ļ						RAARSPVLPRGLSAGQRPAARL
	İ					LGGMEEGRFRQVAVFSES*SAV
	į				}	CPPPSPPPLSPLAPWTETA
26700	57068	Α	26852	1	462	AQSVNSQTFSELRATQTFYKTT
						SHNSPGVFHTSTKR\FIDGNPPGI
	:					FSAITA*RLMMP*RSSIFSASASI
	į					LSVSFSGSTCNNDQRPARFGVL
					ŀ	*DTRGETGCA*TGRPRRAR*LR
						RVEVRAV*LLRVRARNGAQMA
		<u> </u>				LVKTPCQTSAHNAPCRGRE
26701	57069	Α	26853	692	918	
26702	57070	Α	26854	1	2427	
26703	57071	Α	26855	1347	1978	LPHCVANHGCALR*QKWVHD
						KEQTTQTLKMVAENGRWVIDD
		1				IVSNHGSVLQAVNSENEKTLAA
						LASLQKEQPEAFVAELFEHIAD
						YSWPWTWVVSDSYRQAVNAF
			1			YKTTFKTANNPDEDMQIERQFI
						YDNPICFGEESLFSRVDEIRVLE
						KTADSARIHVRFTLTNGNNEEQ
						ELVLQRREGKWEIADFIRPNSG
26704	57072	ļ	26956	1	1722	SLLKQIEAKTAARLKQ LSEVDVDVRQSIHSAHAKTLDT
26704	57072	Α	26856	1	733	QGLRNEFLVEKVFVADEYTMV
						YSHIDRIIVGGIMPITKTVSVGG
						EVGKQLGVSYFLTSNRRTINKY
						`
						LVPDVLETCQSSMGLTELAPGN *WNTMPCHTHERRMEVYFYFN
						MDDDACVFHMMGQPQETRHI
						WMHNEQAVISPSWSIHSGVGTK
						AYTFIWGMVGENQVFDDMDH
						VAVKDLRANHHQRFIISQRSDI
						HLTTQWIKRAAQTIHPPVSIIQQ
					1	IVAFFE
26705	57073	A	26857	2	255	1 4 7 31 1 L
26706	57074	A	26858	1	597	
20700	13/0/4	14.1	120030	1.	1377	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
26707	57075	ĪA	26859	2	640	EARGRQPQLHHLPHPPRASSPP
20707	31073		20037	2	040	LALQPLGRSRRCPPPPGAAAPD
						PRPDMGDLPGLVRLSIALRIQPN
						DGPVFYKVDGQRFGQNRTIKLL
						TGSSYKVEVKIKPSTLQVENISI
		1				GGVLGPLELKSKEPDGDRAVY
			1			TGTYDTEGV\TPTKSGER\QPIQI
						TMPFTDIGTFETVWQVKFYNY
			•			HKRDHCQWGSPFSVIEYECKPN
						ETRSLMWVNKESFL
26708	57076	A	26860	218	426	TQPRVWSQAQ/RALQPDTELPQ
20708	37070	^	20800	218	420	PPQTPKSDTDQMLSVKKKKKR
						KKKKKKKKKKKKKKKKK
						KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
26709	57077	A	26861	1	423	RKKKKKKKKETQT
26710	57078	В	26862	1	252	
26711	57079	A	26863	1	171	
26712	57080	A	26864	5	254	
26713	57081	A	26865	16	220	ILDTSPMRWTQKNFSMILAQPE
		-				QQCKTLSQNKNKDRRIKKKEE
						KKKKKKKKKKKKKKKKK
		1				KKKKK*EKEKEKEKKKEKE
		1				EEKKKKKKKKKKKKKKK
İ						KKKKKKKKKKKKKKKKK
i						KKK
26714	57082	A	26866	32	286	
26715	57083	A	26867	1	847	EVKDLYDKTFKSLKKEIKEDLR
						RWKDLPCSWIGRINIVKMAILP
						KAIYRFNAIPIKIPTQFFNELEGA
						ICKFIWNNKKPRIAKTLLKDKR
						TSGGITMPDLKLYYRAIVIKTA
						WYWYRDRQVDQWNRIEDPEM
						NPHTYGHLIFDKGAKTIQWKK
						DSIFNNWCWHNWLLSCRRMRI
						DPYLSPCTKVKSKWIKELHIKP
						ETLKLIEEKVGKSLEDMGTGER
						FLNRTAMACSKKKEKKEEEED
						EEEKEKEKEKEEKEKEEEE\KK
						KKKKKKKKKKKKKKKKK
						KKKKKKKKKKKKK
26716	57084	A	26868	1	376	MLMKDPQWNSSIFISTHLALQQ
						KRRQAEYGAQEPSRRIVGGKGS
						GAQVDEEEEEEEEEEKEE\KK
		1				KKKEKKRKKKKKKKKKKK
						KKKKKKKKKKKKKKKLL
		1	[1	LSLPMIRPRLPHPRWASSPSSMV
				1	1	1
			İ			AKP
26717	57085	A	26869	1	2031	AKP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26719	57087	A	26871	171	495	SQLLDMRKPFQKPGLRQLKTLP QYLNTR/CILDYLDNISPQQIRK LFYVLSTLAFSKQNEASSHIQD DMHLVIRKQLSSTVFKYKLIGII
						GAVTMAGIMAADRSESPSL
26720	57088	Α	26872	1	3114	
26721	57089	Α	26873	173	397	
26722	57090	Α	26875	823	1194	
26723	57091	Α	26876	1	1263	MESNAVQLTRMEYAMKSLSLL YPKSLSRHVSVRTSVVTQQLLS EPSPKAPRARPCRVSTADRSVR KGIMAYSLEDLLLKVRDTLML ADKPFFLVLEEDGTTVETEEYF QALAGDTVFMVLQKGQKWQP PSEQGT*WRRTQRKDSPVSRPC STHGLQEIQL
26724	57092	Α	26877	128	317	
26725	57093	Α	26878	431	574	
26726	57094	A	26879	112	482	EGPEAKPKRSNCAPEKRSSPIPD WEPAFSEDGRARTVARLQHPPL GGPTHRYHHFLRRHDPPLRVHP AAERQEAHPGTSI*QSSPNSKQS PQGKWKITFPNSLSLTRKYYFQ QPRGWDFFKKT
26727	57095	Α	26880	3	179	
26728	57096	A	26881	977	1127	
26729	57097	Α	26882	121	708	
26730	57098	A	26883	38	828	GSRLRRLQAAAARPALPLPLPP WEWKHLPHVPEAKWWLTTAR HSAAYRADPLRVSSRDKLTEM AASSQGNFEGNFESLDLAEFAK KQPWWRKLFGQESGPSAEKYS VATQLFIGGVTGWCTGFIFQKV GKLAATACGEVDF/LLLQLANH TWVHQSLTGNEWEKDIEESPKS SLKIRKSQSDYLLRSGAKAAGR WCHFVKKNVLVTWGIFPEAFC LAWHPKEDDLHVPLFPGFFPSQ QPFTLHHRDIESLLLFFPWPSFP GHWEN
26731	57099	Α	26884	1	642	
26732	57100	Α	26885	1183	1349	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
:	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26733	57101	A	26886	1	1371	MSFLIDSSIMITSQILFFGFGWLF
					FMRQLFKDYEIRQYVVQVIFSV	
					1	TFAFSCTMFELIIFEILGVLNSSS
						RYFHWKMNLCVILLIL/VFPMV
Ì						PFLQLAYFIVSNIRLL\HKQRLLF
						SCLLWLTFMYFFWKLGDPFPIL
						SPKHGILSIEQLISRVGVIGVTL
						MALLSGFGAVNCPYTYMSYFL
						RNVTDTDILALERRLLQTMDMI
!				ļ		ISKKKRMAMARRTMFQKGEVH
						NKPSGFWGMIKSVTTSASGSEN
						LTLIQQEVDALEELSRQLFLETA
						DLYATKERIEYSKTFKGKYFNF
						LGYFFSIYCVWKIFMATINIVFD
						RVGKTDPVTRGIEITVNYLGIQF
						DVKFWSQHISFILVGIIIVTSIRG
						LLITLTKFFYAISSSKSSNVIVLL
						LAQIMGMYFVSSVLLIRMSMPL
	Ì					EYRTIITEVLGELQFNFYHRWF
			1			DVIFLVSALSSILFLYLAHKQAP
26734	57102	1	26887	1738	2140	DVIFLVSALSSILFLILAHKQAP
26735	57102	A	26888	81	733	
26736	57104	A	26889	1061	1154	
26737	57105	A	26890	1	3207	
26738	57106	A	26891	113	367	
26739	57107	A	26892	2	1391	
26740	57108	A	26893	154	647	
26741	57109	A	26894	40	747	
26742	57110	A	26895	1	3186	
26743	57111	A	26896	271	491	
26744	57112	A	26897	304	1836	
26745	57113	A	26898	1	2343	
26746	57114	A	26899	1	765	
26747	57115	A	26900	318	473	
26748	57116	A	26901	2	426	
26749	57117	A	26902	1	433	
26750	57118	A	26903	2	1004	
26751	57119	A	26904	125	199	
26752	57120	A	26905	3	156	
26753	57121	A	26906	2	397	VDGMGWSQDLFRALGRSLSRE
						GKEHVGTDQFGNKYY*SRSTK
						TGEVRWRRGQRLRGQ*LRGQT
						IREKRIVEAANKKEVDYEAGDI
Ī		1				PTEWEAWIKRTRKTPPFMEEIL
ŀ						KNEKHREEIKIKSQDFYEKEKL
26754	57122	Α	26907	1	1350	IN THE PROPERTY OF THE PROPERT
26755	57123	A	26908	1	582	333
20133	13/123	<u> </u>	20700	1.	362	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26256	157104	1	0.000		Icoz	C + D O M D O D O D O D O D O D O D O D O D
26756	57124	Α	26909	2	687	GARQVLPGESPCFSSS\AKIVKP
	İ	1	1			NGEKP\DEFESG/LSPQALLEL\E
						MNSD\LKA\QLREPELLRPA*GK
		1			}	LKVGGCSENLSI/ILLFPVPSN*K
						SFPENPQVRA*YRELEKK\FQW
						GSHVGLYRPQRRILP*AQLRKK
]			PVQKNKQKASPRARTLTAVHD
						A\ILEDLGLPQAKIVGARESRVK
						L\DGSRL\IKVHLDK\AQQNNVE
						HKV\ETFSGVYK\KLTGKDVNF
						EFPRSFNCKQK
26757	57125	С	26910	164	208	
26758	57126	Α	26911	2288	2625	GSEGHLPITKRWSSLWEWRKG
						LSEVGSCKRNLVRCLRTAI/LM
						GGEAGVIHCKGHQKASDPIALG
						NAYADKVARQAASSPTSVPHG
						QFFSFTLVTPTYSPAETSTYQSL
İ						PTQGK
26759	57127	Α	26912	1	400	
26760	57128	A	26913	3	277	
26761	57129	Α	26914	1	630	CEIKNRKAAEKVNKTKGKFFEI
						NTYPGPIKTGEPSGQTQKWLDI
			ŀ			VRNTLVEEDTSSWSWRAHQPK
	ļ					STLTGTGRPSTNGTMSSLARTV
ļ.		ĺ	ļ			REEPGNQPNYRGKPSPFWFPHL
		1				VRAASTQPVITRLLQHGRLKPI
						NSPYNFPILPVLKPDKPYKLVQ
						DLHLINQIVLPIHPVVPNPYTLL
						SSIPASTTHYSVLDLKHAFFTIPL
						HP*FQPLFTF
26762	57130	Α	26915	1	384	
26763	57131	Α	26916	1113	1319	GRDPVSAFYIWLASFPNTIY*IG
						NPFPIACFSQVCQRSDSCRYAA
						LFLRALFCSIDLYLCFGTSTMLF
26764	57132	A	26917	2	2144	
26765	57133	Α	26918	99	470	
26766	57134	Α	26919	636	1220	GPGFQAQNCAAIWADTKLAAG
						IFSHTPVAPGTPVRQNHLLPWD
				1		APAWSGEECLPLLRLVYVVFPS
				}		QCKQSCQEV*TGQSPPQLGKAF
				1		VARLPL*IPSLWAGHLFLEHPV
				1		YCCGCVTAGRQGSWKGQRRH
						GHPFPLPLLLLQMVCCSISYQY
				1		DYPESSFLLLFLSSLCSAGKSTG
						SHAILLGSAFVLPHLVALRS
26767	57135	Α	26920	10	161	RLRMVRDIKVLLNTRSLRNCLG
						DLTNKGRSIIGPPL*ELSKASVM
						VPVGF
26768	57136	A	26921	1	855	
26769	57137	Α	26922	5	1442	
26770	57138	Α	26923	1061	2332	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26771	57139	Α	26924	804	1100	SPKGGPPDPSHGTKFHSRPCEET
		ŀ				TKQAFCEQHGCLFHLGTLGALL
		ŀ				G*QRWLHQLSRPSLGCNESKSL
		ľ				FQ*PPLP*E*KEIQCKVPPNLGL
		:				GVRSGKGF
26772	57140	Α	26925	3	1186	
26773	57141	Α	26926	126	363	SRSKDQGLDPSGTWCKRAFSPG
						PWPIIPVAAGGGGHSGGGKSET
						PAHLQKGLHKVKNC*PSTYSVC
						QTPDAEHPVSNK
26774	57142	Α	26927	1	1125	
26775	57143	Α	26928	401	446	
26776	57144	Α	26929	332	499	
26777	57145	Α	26930	74	200	
26778	57146	Α	26931	300	416	
26779	57147	Α	26932	324	430	
26780	57148	Α	26933	60	381	
26781	57149	Α	26934	2344	2453	
26782	57150	Α	26935	131	274	
26783	57151	Α	26936	144	444	GGGENFSYPWYLLVGCGWFSS
						SPIVPDVPPFSLLLPAQKKKPAP
						PK\PEPKPKKAPAKKGEKVPKG
						KKGKADAGKEGNNPAENGDA
						KTAQAQKAEGAGDAK
26784	57152	Α	26937	540	811	
26785	57153	Α	26938	69	375	QHLRPAAVAAATMPKRKAEGD
	1					AKGDKAKVKDEPQRRSARLS\A
						KPAPPKPEPKPKKAPAKKGEKV
1						PKGKKGKADAGKEGNNPAEN
						GDAKTDQAQKAEGAGDAK
26786	57154	Α	26939	9294	9486	SLLYQPRCMAFRIKASS*RGMP
		1				GGSASAARKPTG/SPGREGAGR
						RGQWGPRNCCAGRLPGGESTV
26787	57155	Α	26940	248	613	
26788	57156	С	26941	94	234	
26789	57157	Α	26942	2157	2408	
26790	57158	A	26943	547	815	LADY TOTAL DESCRIPTION OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OWNE
26791	57159	Α	26944	254	467	VFLISVYNGLAISLYLGIHIRQK
						PVMPRNPLNCFGVLG*G*AGIG
						*IRSSLRTLVPLDNFSPKYLTFC
26792	57160	A	26945	238	391	EQS
26793	57161	A	26946	232	1659	
26794	57162	A	26947	1	951	
26795	57162	A	26948	1	2046	
26796	57164	A	26949	3	97	SVR/SKFYVREPPNAKPDWLKV
20/30	3/104	^	20343			GFTLSVEL*M
26797	57165	Α	26950	1	828	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26798	57166	Α	26951	224	475	AGPRKMAPSALLRPLSRLLAPA
						R\LPSGPSVR/STKFYVREPPNAK
						P\DWLKVGFT\LGTT\VFLWIY\L
		İ				IKQH\NEDILEYKRRNGLE
26799	57167	Α	26952	1	411	
26800	57168	Α	26953	442	2490	
26801	57169	A	26954	3	1592	
26802	57170	Α	26955	9	308	
26803	57171	Α	26956	153	227	
26804	57172	A	26957	1	411	
26805	57173	Α	26958	517	825	
26806	57174	A	26959	6	646	
26807	57175	Α	26960	1	275	
26808	57176	Α	26961	3	272	
26809	57177	A	26962	1	1002	
26810	57178	A	26963	1	1791	HMTTCLL ACCOUNTS ALVIET
26811	57179	Α	26964	2	160	HMTTSLLAQSGFQKTSALNKIT
						TKGSH*VQFTSLLPPPERVLVS
26012	57100	ļ. —	26065	1	902	MAERPWGG
26812	57180	A	26965 26966	1	892 549	
26813	57181	A A	26966	234	387	SCLEVCDEQGPEK\TRQRALRG
26814	57182	A	20907	234	367	VSSVTEDTLNICRLCWQPLPEPL
						ELWPKAL
26815	57183	A	26968	269	501	RARSEGAGLWSVVAPSAVSVFF
20013	3/103	A	20900	209	301	VSDPRCAPFHRSPSCCSP/RRPC
						LSLSA*SRPRASGVGACLLWQP
			}			LPEPLELWPKAV
26816	57184	A	26969	210	296	Di Li Ede Wi Kit
26817	57185	A	26970	71	283	LRLGDLPSEINPLSSCSLLREKD
20017	3,103	` `	20370	' *	203	PPTTSGPQT\TSPRNISPISNPDST
						GNRTVQLTWQPLPEPLELWPK
						AL
26818	57186	A	26971	1112	1180	
26819	57187	Α	26972	71	284	LILGDLPSEIKPLPSCSLLREKEP
						PTTSGPQT\TSPRNISPISNPDSTG
						NRTVQLTWQPLPEPLELWPKA
26820	57188	В	26973	1	663	
26821	57189	Α	26974	1	502	MLLTQSLFGGLFTRTHMKFGA
•	1					VTQIRGPPLGDKSPVLLLFALER
	-	l				QRRHVLSMDPKLRCWSRTGKA
						AFPWCLIIAEMPDYSPTFQRCQ
						TTQGRLPWSFTLSSKSRFSGEG
						ARACYKCQKSDHQAKECPQPG
						IPPKPCPICAGP\TGNRTVQLTW
						QPLPEPLELWPKAL
26822	57190	Α	26975	233	496	
26823	57191	Α	26976	226	543	
26824	57192	A	26977	1478	1744	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	,	in USSN	location of first	I .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26825	57193	Ā	26978	3	450	VRPRRDACLGPSPLAASPAFLG
						KGQVPQPLISLCPDPLFPHPNLIS
						LRPNPLCPHPDLVSLCPDPFPAF
						LEAHKNFQTTEPQQPGVPPEPP
:		i				PTGACYTCRKSGHWAKECPQP
						GIPP\NHVPSVWDPTENLTVQLT
						WQPLPEPLELWPKAL
26826	57194	Α	26979	615	724	
26827	57195	Α	26980	1	1968	
26828	57196	Α	26981	227	556	
26829	57197	Α	26982	400	548	
26830	57198	Α	26983	1	1968	
26831	57199	Α	26984	65	741	
26832	57200	Α	26985	ĺ	658	
26833	57201	Α	26986	1	666	
26834	57202	Α	26987	67	608	NPGKGGCFVL/VLDGLLRDRKA
<u>,</u>						V\IREETFDGWHPQDRPLPAHA\
						LVAG\IDRPTPPQK*TA\AMGKK
						KDRPKRSKIKSFCGKCYNY\NH\
ĺ						LMPHKGTLWDIPLGQNLFVQL
						RDVF\RDPGSLNRKA\RREGPRF
						KFE/EREYETGQETKWVLPRKL
						AGFKNAFGFDSLKIIKKKKKKK
						KKTTKKGRP
26835	57203	Α	26988	1	352	
26836	57204	Α	26989	1	1419	
26837	57205	Α	26990	2	878	
26838	57206	В	26991	75	2931	
26839	57207	Α	26992	229	724	IIFIVYSSQLTYVKISDSFQTFKF
		İ				CLDFCLFFSEMS\FLSLNISSCS*
						YSAKVNSCGKFGLTKGSFSAPL
		1				TPLFFLCFGSELVEGV*ELLAVG
						GLHLARIFLCLSISSLC*FTHSCC
						FTRVTPINLASNNSCLLGFRLQS
						SSIAPSLGLLDGGVCFIRDLAAA
26840	57208	Α	26993	737	1048	KKYNIQLEKPYFKHLYKNKLL
						KLSN*NMTSVQQFTIELEGNLS
	1					LSCIELVC/ILVTHCHLF/CMNK
						AW*QKKNT/WLSILTC*KHWQ
						YYNLVNSTDFNTSSSFLSKV
26841	57209	Α	26994	1	1209	
26842	57210	Α	26995	2	1683	
26843	57211	Α	26996	1	1386	
26844	57212	Α	26997	1	471	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26845	57213	ΙA	26998	2	514	VTARRRGTRWLRFRRASRVQK
						WLWLADFYLRYYVGHKGKFG
			1			HEFLEFEFRPDGKLRYANNH\N
						YKNDVMIRKEAYVHKSVMEEL
						KRIIDDSEITK\EDDALWPPPDR
						VGRQELEIVIGDEHISFTT\SKIG
					1	SLIDVNQSKDPEGLRVFYYLVQ
						DLKCLVFSLIGLHFKIKPI
26846	57214	Α	26999	1	570	
26847	57215	Α	27000	1	980	
26848	57216	Α	27001	270	356	
26849	57217	Α	27002	1	1032	
26850	57218	A	27003	1	1017	
26851	57219	A	27004	1	450	
26852	57220	A	27005	1	637	APIECGGIPSLPVLCQSRANDQE
						GVRLLEPSEAMPKSKELVSSSSS
						GSDSDSEVDKKLKRKK\QV\AS
						ENPVKK\QKTGETS\RALSS\SKQ
						SQPAARDDN\MFQIGKM\RYVS
						V\RDFKRQKCLI\DIREYWMDPE
						GEMKPGRKGISLNP\QQWEPSL
						KEQISGPLIDASKKTCKISEPILI
					1	KPCTVPVVLIWLFSIGFCFLNVL
	1-					RSYCMFGLQKNL
26853	57221	Α	27006	20	412	RFSPLSFLLAGDSCTCAGSCKC
		1			1	KECKCTSCKKSKWDPLFPLPLP
ļ						CPPACPLSTILRGIKAVWGCPIA
						RKLLPPQ*SLSGRAGILIPGVAS
						THLCRLLSAPR\CCSCCPVGCAK
		<u> </u>				CAQGCICKGASDKCSCCA
26854	57222	C	27007	32	505	
26855	57223	A	27008	854	1021	ALGGVAEYDLKEGLLLKH*AL
						VQSLVATEVRLVLCITSHTDML
		<u> </u>				QICFFVYATVTQ
26856	57224	A	27009	1	726	
26857	57225	Α	27010	99	537	
26858	57226	A	27011	1	963	LIVE DOTTO OFFICE A TO A LADVIOR
26859	57227	Α	27012	146	609	VYLRCTGGEVGATSALAPKIGP
	1					LGLSPKKVGDDIAKATGDWKG
]		LRITVKLTIQNRQAQIEVVPSAS
		1		1		ALIIKALK\EPPRDRKKQKNIKH
		1				SGNITFDEIVNIARQMRHRSLAR
						ELSGTIKEILGTAQSVGCNVDG
	<u> </u>	1				RHPHDIIDDINSGAVECPAS
26860	57228	A	27013	3	501	
26861	57229	Α	27014	1	1623	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26862	57230	A	27015	53	1227	QPPVHTTPASSPCDD\DIAAL\V
						VDN\GSGMCK\AGFAGDDAPRA
		1				VFPSIVGRPRHQGVMVGMGQK
		1				DSYVGDEAQSKRGILTLKYPIE
			j			HGIVTNWDDMEKIWHHTFYNE
						LRVAPEEHPVLLTEAPLDP\RAT
					ŀ	REKMTQIMFETFNTPAMYVAIQ
		i		ľ		\AVLSL\YASG/RVTTGIVMDSG
						DGVTHT\VPIYEG\YALPHAILR
						LDLAGRDLTDYLMKILTERGYS
						FTTTAEREIVRDIKEKLCYVAL
						DFEQEMATAASSSSLEKSYQLP
			,			DGQVITIGNERFRCPEALFQPSF
		İ				LGMESCGIHETTFNSIMKCDVD
						IRKDLYANTVLSGGT\NMYPGI
						ADRMQKEITALAPSTMKIKIIAP
						PERKYSVWIGGSILASLSTFQQ
						MWISKQEYDESGPSIVHRKCF
26863	57231	A	27016	2	438	ADLLQVSNCVVSSCQPPAFLVL
20003	3,231	'	2,010	-		FSSSRLPAGEGRGRPGQTQRPSS
						LEGAWHSVTLERRCLVSHLINL
				-		REAGMYPSRPCHHLFPDQLV*T
	-				Ì	EGGF*RPRLGWQRCHGTPQQA
						PSQPAFRSKHPRKGMPALQQQP
						GSGLCRPLPCRCR
26864	57232	A	27017	112	493	AHSRTPARPENRAAASAPRKPR
						RAMSSPPEGKLETKAGHPPAVK
						AGGMRIVQKHPHTGDTKEEKD
		Ì				KDDQEWESPSPPKPTVFISGV\I
						ARGDKDFRPADAQVAHQKPHA
						S\MDKHPSPRTQHIQQPRK
26865	57233	Α	27018	1	1176	
26866	57234	Α	27019	3	307	
26867	57235	Α	27020	86	179	SVKRRC*SLLTWIGMRLQRQHR
						ECLAEQVGS
26868	57236	Α	27021	1	948	
26869	57237	Α	27022	3	534	EGAHFRAAHHPRSTGSRCPGSL
	1					QPSRPLVANWLQSLPEMPVDFT
						GYWKMLVNENFEEYLRALDV
						NVALRKI/APTLLKPDKEIVQDG
						DHMIIRTLSTFRKLTSWNF\QVG
						KEFEEDLT\GIDDRKVHDKQ*A
						WDGDKL\QCVQKGEKEGRGW
						TQ\WIEGDELHLEMRVEGL\VC
	1.555	1	0.55.5	1	2400	KQVFKKVQ
26870	57238	A	27026	1	2400	
26871	57239	A	27027	294	425	
26872	57240	A	27028	1	797	
26873	57241	A	27029	1	173	<u> </u>
26874	57242	Α	27030		1047	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		·
26875	57243	A	27031	2	1019	PTSAPHSLSPRAVIERRSRALDW
						NASPSLSDPQGLDASLPFPSHKR
		1				SRTASPEPAEHPVMDKNE\LVH\
						KAKLAE\QAERYDDMAACMKS
						VT\EQGAELSNEERNL\LSVAYK
		1				N\VVG\ARRSSW\RVVS\SIEQKT\
		1	}			EGA\EKKQQMAR\EYREEIETEL
					:	R\DI\CNDVLSLVGKSSLIPNAFT
						SRRSKVF/YILENGKGDYLPFTL
						GWRVAAGWMDQERGLFDPVH
	İ					NKAYPRKAFWKSAKKGNGNPT
						HP\IRLGL\ALNFSVFYYEILNSP
						EKACSLAKTAFDEAIAELDTLS
		1	<u> </u>			EESYKDSTLIMQLLRDNFDIVG
						HRDTQGRRKLEGREEGRGENL
						TGPFPTFCSWPHS
26876	57244	Α	27032	177	477	
26877	57245	Α	27033	1	1290	·
26878	57246	В	27034	49	1112	
26879	57247	IA_	27035	98	245	
26880	57248	A	27036	1	351	
26881	57249	A	27037	3	471	MAKARIAGONE TA FOLODOGIO
26882	57250	Α	27038	1	440	MKMRVGCMLTAESLSDGGNS
						HQRTLSLFEESKESQCEARGEV
-						SKAGVWLVPLEPSSDALPKITS LVRPAVPWRPSSEAGLCEVRGG
1						
						VLGKASKAPIKEPQLDRGMGL GAQRRGSSGTEVQSGETLGASG
						SPRGLLEPRPDWVSNNGAGSLG
						FQQLPIVDKIRTIAQAVCGAKDI
						ELCPEAQVKIDRYTQQYYSC*N
						PKLPAPLFETQSGLGSKSPLGLP
			İ			LAPRVSPDCTSVP/GAP/SAAGP
						RAPCPDPAVAPLWGLCWPFPEL
26883	57251	A	27039	1	1113	MHQEDLRAWYLDLGLPSHQN
						AQPTAWKCQRAPSPYTHQDMA
	ł					LIPSPTARWLSPEKEPKQGEVG
						EKSLLPDPTLPLTDPRLTGSTEQ
						AHAEGLAALMSALRVSHLQGR
						GGVVTLVDSQLGVIAVSSTQFN
						KGPSYRLLADVQNRLLPKYDS
						QKEAELRSWIKGFTGLSIRPDFQ
						KGLKDGIILCTLVNKLQPGSVP
						KIN\ASV*NWH*LENLSNFLKA
		1				MVSYGM/NPVDLFEANNLFESG
						NNMQVRVSLLALAGKAKTKGL
						RSGVDIRDKYSEKQNFDDTTM
		1				KASQCVIRLQITNKCASQSGMT
						AYGTRRHLYDPKNRILPPMDNS
						TISLQMGTNKCASQVGMTAPG
						TQRHIYDTKLGIDKCENSSMSL
	1		1	<u> </u>	<u> </u>	<u> </u>

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26884	57252	Α	27040	347	1061	
26885	57253	A	27041	212	386	LQGSWVTSGLËRICGSILGTIPL AHEVTDTQHGRMVYQVATAG F*SSLGAASIGTQGL
26886	57254	A	27042		1017	MHSRRERARGLRGAHHPLVDN GPPQSLRAPPLLSPLKTAGAKSI WEPLASARRPETPERTPLQKTP EQVPTNFMGALHMKTSAPLSS RNGEGRRGGTSVASCPWVVGA VCSAERQPCTQRVREALMGGW RAGAQNNRAEDQVDEFTEVGF RRWVIKNYDELKEHVLTQCKE VKNLDKSIHPEISRLHEFITTTHT LPVIGGKVSLLSKCQDNAEQKQ SQGCSQEGHEVYDPRLNSSSSS SSSGGGQSPGLRRCSTSAAAAA ALEGAALKPMPVHAGLVGSGE GGGAGAVAGPCSRWGATTAA ASSAQPAQPVRGGSSGAQGHR GGRRRQAGKGGPAG*TAAAAA AP\GRGAEPGAAALLNLGGGSG GAG\SAALKPMPVHAGLVGSG EGGGAGAVAGPCSRWGATTA AASSAQPAQPVRGGSSGAQGH RGGRRRQAGKGGPAGSS
26887	57255	Α	27043	644	949	
26888	57256	Α	27044	811	1886	
26889	57257	A	27045	1	410	HAHSLNSIILPTPLEIHKV*IQIY A*GCKRISNNCWHCHQHLLSIS PDLRINEGKECGPSPWIGVEAR/ MGGELSSAVGLTSLLLYQQVPF HPHFQSPTFIPRESILLQHASCW RQHHLHTGIYSSYLPGWKQEFS
26890	57258	Α	27047	1	2445	
26891	57259	Α	27048	1	457	
26892	57260	A	27049	1	873	
26893	57261	Α	27050	2549	2728	ATSRSSALITSSKYPGKF*LILI* RSTLETANSISARLNNPFLRKYP SYFSLFMGTTRI
26894	57262	Α	27051	277	394	
26895	57263	Ā	27052	2	1394	
26896	57264	Α	27053	1	1091	
26897	57265	Α	27054	1	1404	
26898	57266	A	27055	2457	2674	ANHCYLLSELQHWSDCPVVLQ SAG*RH*DRN*DGNQY*SR/SLS *SR*STTK*RNTPCSQVSSLSRLS TRSAP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26899	57267	A	27056	716	1455	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGNYTSGDNHTLR/DPH YVEDKGHKYLVFEANTGTENG YQGEESLFNKAYYGGGTNFFR KESQKLQQSAKKRDAELANGA LGIIELNNDYTLKKVMKPLITSN TVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLG YVSNSLTGPYKPLNKTGLVLQ MVLIPNDVTFTYS\HFAVPQAK GNNVGIHQATLTN\RGFFEIKKA
26900	57268	Α	27057	66	197	
26901	57269	Α	27058	379	905	AGNFVHITVRKMLWIRRDQQQ S/DKQDIQTAHRSYSVLKGYND MYYGWPCCKVNEISGQLASEP A*SLVLPAAG*QAPASGSPWLS GGPQQVEDAGAGYGFAPGQPP PPPRTQPRSACSRRAAGSQFHG RPLLPRQAAKARAPRSLGCGSL GRFSTGVRPDKCIFPPETENAA
26902	57270	Α	27059	1	1608	
26903	57271	В	27060	1	1974	
26904	57272	A	27061	2712	3216	KTGRGPTDKFG\ANDPILKDQT\ QEWS\GSAPFTS\DGKFRLFYTD YSGKHYGKQSLTTAQNVQQFI DEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENGYQGE ESLFNKAYYGGGTPFFRKESQK LQQSAKKRDAELANGALGIIEL NNDYTLKKVMKPLITSNT
26905	57273	Α	27062	1	3066	
26906	57274	Α	27063	1	972	
26907	57275	Α	27064	14	273	
26908	57276	Α	27065	42	302	
26909	57277	Α	27066]	487	MGLSLKGPESAPIPKTPQFNKIL FKPIAVYNRFTQFRLSETKEITN PYAMRLYESLCQYQRYQLPQS YQR\SLTSAAASCRSVLMRSTA ELQCASHTLRKRKAARRLISLS EMPRKQGDYRTRIWKFEDGLS NVLVIQLNKLIICVMCLVRDCD VLKTYFHR
26910	57278	В	27067	1	1035	
26911	57279	A	27068	132	230	CHYFACMWSGCEVYS*SAPG** C*EDLSGMVR
26912	57280	Α	27069	1	2784	
26913	57281	Α	27070	855	980	LSCSGWRAG**ADGCIIQIG*RL SPNKCL*TWSALCKPIAE
26914	57282	В	27071	85	863	
26915	57283	Α	27072	345	500	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26916	57284	В	27073		1116	
26917	57285		27073	1	1173	
26917		A	27074	1	999	
26918	57286 57287	A	27075	771	908	
26920	57288	A A	27076	104	547	LFPRLLSCLTTPPHCSFSICFVIC
20920	37288	A	27077	104	34 /	SRTLILKGSSLMYVFCLPNTAIV
						MALSPRGWRSKFGMPVDSKGP
						PWLFKFLKNGLNFLLHSVGTRD
						LSRLSTILSPLYNTVAPGAN*CR
						ELKLVLDADDVLSTEVKRVITS
						SASNITPAFFCS
26921	57289	Α	27078	34	1353	
26922	57290	Α	27079	213	338	LSCSGWRAG**ADGCIIQIG*RL
			1			SPNKCL*TWSALCKPIAE
26923	57291	Α	27080	1	1246	MVKVGTSYVPINVSFSPKVGPG
					LPGINRDTRIYLFCEVIFRHRKD	
						RESADLGSDGQNGPRPWIGEA
						VAAAAADGVTFSVPVTPHTFR
			•			HSYAMHMLYAGIPLKVLQSLM
						GHKSISSTEVYTKVFALDVAAR
						HRNRFTQFRLSETKEITNPYAM
						RLYESLCOYRKPDGSCIVSLKID
						WIIERYQLPQSYQLYYFELAIPV
						GYFYPGSFSTASRILLLHPRGLR
						AITIAVFGKQNTYIRLEPFKINV
						LEQITKHIEKLQCGGVVKQLSR
						RGNNQHISSTYDINRADYPG*A
						RDPHLMLRLAIETVAHDYDVIV
						IDSAPNLGIGTINVVCAADVLIV
						PTPAELFDYTSALQFFDMLRDL
						LKNVDLKGFEPDVRILLTKYSN
						SNGSQSPWMEEQNSGCRGKTS
						RVEVPHRDSQFKVIKLVTLRQL
		l				VTLYDPVDFQRDDA
26924	57292	В	27081	1	1041	
26925	57293	Α	27082	1	1011	
26926	57294	A	27083	2	1007	
26927	57295	Α	27084	1	738	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
26928	57296	A	27085	1	1439	MAETAVINHKKRKNSPRIVQSN
20720	37270	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	27003	*	1437	DLTEAAYSLSRDQKRMLYLFV
						DQIRKSDGTLQEHDGICEIHVA
						KYAEIFGLTSAEASKDIRQALKS
						1
						FAGKEVVFYRPEEDAGDEKGY
]	ESFPWFIKRAHSPSRGLYSVHIN
		1				PYLIPFFIGLQNRFTQFRLSETKE
						ITNPYAMRLYESLCQYRKPDGS
						GIVSLKIDWIIERYQLPQSYQRV
						WTPGINCPEPCPGVWTPGINCP
						GAWGIHGPHGSAENTGPLHPG
1						QTSAQLETSLLPSLRSARELELA
						QLSPRRKQNRSLQNIGVTPSLR
						VPWPKASNVQQFIDEGNYTSG
						DNHTLRDPHYVEDKGHKYLVF
						EANTGTENGYQGEESLFNKAY
						YGGGTNFFRKESQKLQQSAKK
İ						RDAELANGALGIIELNNDYTLK
						KVMKPLITSNTVTDEIERANVF
						KMNGKWYLFTDSRGSKMTIDV
						PQAKSNNVGITSYMTNRSFFED/
						KKATFAPGFLWNIKAIKTS
26929	57297	Α	27086	345	563	
26930	57298	Α	27087	1	1188	
26931	57299	В	27088	1	1186	
26932	57300	В	27089	1	1090	
26933	57301	Α	27090	183	410	
26934	57302	Α	27091	1	1557	
26935	57303	Α	27092	888	1165	CTRERRIKARGPPAGKRWLLLS
ļ						GSSGRKHHL*QDPRPGSQTAGD
						LPEPAR\PIIVIGEGSQMGLDECQ
						FQFRNGRWNCSALGERTVFGK
						ELKV
26936	57304	В	27093	1	1027	
26937	57305	В	27094	1	1117	
26938	57306	В	27095	1	1377	
26939	57307	В	27096	1	1014	
26940	57308	A	27097	1040	1285	
26941	57309	Α	27098	901	2277	
26942	57310	A	27099	1	1122	
26943	57311	Α	27100	1	1137	
26944	57312	A	27101	1	1881	
26945	57313	В	27102	1	1211	
26946	57314	Α	27103	294	506	NRRPGSAATVWAAAAEPSERG
						NNPALENR*SSGFSWGFFSGYQ
						RCRESRATTAPGYGNSRTG*AT
						CWLYN
26947	57315	В	27104	1	1073	
26948	57316	Α	27105	1	1809	

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	i	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26949	57317	A	27106	1688	2187	SYFIMVKVGTSYVPINVSFSPKV GPGLPGINRDTRIYLFCEVIFRH RYLFAISSWSGVTVA\RKDRES ADLGSDGQNGQDLDWGGG\AA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS INSTEVYTKVFALDVAARHRV QFAMPESDAVAMLSF
26950	57318	A	27107	782	1402	LFPRLLSCLTTPPHCSFSICFVIC SRTLILKGSSLIKLLFYKIPSMLV SSVLLLEVKSHIVGPGLPGINRD TRIYLFCEVIFRHRYLFAISSWS GVTVA\RKDRESADLGSDGQN GQDLDWGGG\AAAAADGVTFS VPVTPHTFRHSYAMHMLYAGI PLKVLQSLMGHKSISSTEVYTK VFALDVAARHRVQFAMPESDA VAMLKQLS
26951	57319	A	27108	197	421	LAMPGAGFSSSLRMASIFSIHSV GTRDLSRVSTILSPLYNTVAPG AN*CRELKLVLDADDVLSTEVI RVITSSA
26952	57320	В	27109	1	934	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26953	57321	Α	27110	1	2047	MKLMETLNQCINAGHEMTKAI
						AIAQFNDDSPEARKITRRWRIG
ĺ						EAADLVGVSSQAIRDAEKAGR
				}		LPHPDMEIRGRVEQRVGYTIEQI
			ļ			NHMRDVFGTRLRRAEDVFPPVI
						GVAAHKGGVYKTSVSVHLAQ
						DLALKGLRVLLVEGNDPQGTA
ļ						SMYHGWVPDLHIHAEDTLLPF
1						YLGEKDDVTYAIKPTCWPGLDI
						IPSCLALHRIETELMGKFDEGKL
						PTDPHLMLRLAIETVAHDYDVI
						VIDSAPNLGIGTINVVCAADVLI
						VPTPAELFDYTSALQFFDMLRD
						LLKTVDLKGFEPDVRILLTKYS
1						NSNGSQSPWMEEQIRDAWGSM
]	İ				VLKNVVRETDEVGKGQIRMRT
						VFEQAIDQRSSTDTSLSTPAAP
						MVDSLIARVGVMARGNAITLP
l						VCGRDVKFTLEVLRGDSVEKTS
						RVWSGNERDQELLTEDALDDLI
						PSFLLTGQQTPAFGRRVSGVIEI
1						ADGSRRRKAAALTESDYRVLV
		İ				GELDDEQMAALSRLGNDYRPT
						SAYERGQRYASRLQNEFAGNIS
						ALADAENISRKIITRCINTAKLP
		ļ			_	KSVVALFSHPGELSARSGDALQ
		-				KAFTDKEELLKQQASNLHEQK
		•				KAGVIFEAEEVITLLTSVLKTSS
1		į				ASRTSLSSRHQFAPGATVLYKG
		İ				DKMALNLDRSRVPAYIIRSYIR
					ŀ	CGRKGFASAGVGGCRGWLNY
						AASEQIVLRVHHMRCEIPHRCV
26954	57322	Α	27111	1175	1298	LSCSGWRAG**ADGCIIQIG*RL
						SPNKCL*TWSALCKPIAE
26955	57323	В	27112	1	1056	
26956	57324	Α	27113	1979	2217	WLSVRVDGGANSGCLGKHGSK
						KCCT*NG*SW*RSDPDENCF*T
						EQ*STLFN\GAWRNALSIWEPV
						CN/GNFRSSD*TTLGD
26957	57325	В	27114	320	1633	
26958	57326	Α	27115	606	705	
26959	57327	В	27116	1	4118	
26960	57328	A	27117	4048	4051	
26961	57329	A	27118	1791	1884	ADGCIIQIG*RLSPNKCL*TWSA LCKPIAE
26962	57330	В	27119	1	2436	
26963	57331	A	27120	1	2449	
26964	57332	В	27121	173	4112	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
I	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
26965	57333	Α	27122	916	1568	HHSHEQQFQWPVGASGVDRW
20703	3,333		27.122			AGYLHQFRSLTQFQYGAEPDR
		İ				KE*CQIFIFMQKTLSCLSILGKR
			:			TMSLMQ
26966	57334	A	27123	1268	1773	SYFIMVKVGTSYVPINVSFSPKV
20700	3,334	' '	27123	1200	1,,,3	GPGLPGINRDTRIYLFCEVIFRH
						RYLFAISSWSGVTVA\RKDRES
	İ	1				ADLGSDGQNGQDLDWGGG\AA
						AAADGVTFSVPVTPHTFRHSYA
						MHMLYAGIPLKVLQSLMGHKS
						ISSTEVYTKVFALDVAARHRVQ
						FAMPESDAVAMLKQLS
26067	57225	 	27124	(0)	852	
26967	57335	Α	27124	606	832	HQILFDRTPVSVDQSVEKKG*D
				+		HSVRPQ*AAPGHVHYLTIPEKS
						SQHYHPRTTSE*TSGRYESSGG
		<u> </u>			2600	LSFSQCMRGALEFCC
26968	57336	Α	27125	1	2680	MKLMETLNQCINAGHEMTKAI
						AIAQFNDDSPEARKITRRWRIG
				1		EAADLVGVSSQAIRDAEKAGR
						LPHPDMEIRGRVEQRVGYTIEQI
						NHMRDVFGTRLRRAEDVFPPVI
						GVAAHKGGVYKTSVSVHLAQ
		1				DLALKGLRVLLVEGNDPQGTA
		1				SMYHGWVPDLHIHAEDTLLPF
						YLGEKDDVTYAIKPTCWPGLDI
					}	IPSCLALHRIETELMGKFDEGKL
						PTDPHLMLRLAIETVAHDYDVI
						VIDSAPNLGIGTINVVCAADVLI
						VPTPAELFDYTSALQFFDMLRD
						LLKNVDLKGFEPDAETSQGAL
į						GTLANVVTSLANLSESLNNGDT
						SEIQPEDQSASEITRAFDTLAKA
ĺ						LNTTDSSSSPSLADGIDTSGGGS
]	IHVISRDQSTPIIEVEGPLLSDTH
						VTFKSIREDRNGRSQKTVHTEG
İ						DMNMNIKKIVKQATVLTFTTA
ĺ						LLAGGATQAFAKENNQKAYKE
						TYGVSHITRHDMLQIPKQQQNE
						KYQVPQFDQSTIKNIESAKGLD
						VWDSWPLQNADGTVAEYNGY
					}	HVVFALAGSPKDADDTSIYMF
						YQKVGDNSIDSWKNAGRVFKD
İ						SDKFDANDPILKDQTQEWSGSA
						TFTSDGKIRLFYTDYSGKHYGK
						QSLTTAQVNVSKSDDTLKINGV
						EDHKTIFDGDGKTYQNVQQFID
						EGNYTSGDNHTLRDPHYVEDK
26252	15000	1.	07107	10014	2120	GHKYLVFEANTGTENGYQGEE
26969	57337	Α	27126	2014	2138	LSCSGWRAG**ADGCIIQIG*RL
		1	<u> </u>	1	<u> </u>	SPNKCL*TWSALCNPTAE
26970	57338	В	27127	1	7616	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<u> </u>				
26971	57339	Α	27128	240	719	HSKKLVTLSHGSVMAETAVIN
		}				HKKRKNSPRIVQSNDLTEAAYS
						LSRDQKRMLYLFVDQIRKSDGT
						LPEHDGFCYIHVAQSAEITGLTS
				ŀ		\GNPVRIYGRH*RVSRGRKVVL
	[YRPEEDAGDEKGYESFPWVIKR AHRPSRGLFSGHIPPISHSLLYR
26972	57340	A	27129	1505	3812	AHRPSROLFSOHIPPISHSLLYR
26972	57341	A	27130	471	566	
26974	57342	A	27131	1	229	
26975	57343	A	27132	121	303	
26976	57344	A	27133	183	524	MSTPRPPFVPAFVGRRPSLLFVP
						AARLTDVRGRKVRACGLLSPR
						LRSPSSSSATRVARHSIGRPRVA
		}				RLSTVFVAVCVESPSRQRRWCL
						FALAATPRAPGTLA*SCLTDSFS
i		1				A
26977	57345	Α	27134	1	1025	MIFVLQIRVRGHDDSFLKNHLV
						FLVIYGTNGTFNQTLVTDNNGL
					1	APFTLETSGWNGTDVSLEGKFQ
						MEDLVYNPEQVPRYYQNAYLH
						LRPFYSTTRSFLGIHRLNGPLKC
		1				GQPQEVLVDYYIDPADASPDQE
		1				ISFSYYLIGKGSLVMEGQKHLN
		1				SKKKGLKASFSLSLTFTSRLAPD
						PSLVIYAIFPSGGVVADKIQFSV
						EMCFDNQGTDLTSTVRVTRSSA
						SVMVYGASEAIGQRQSSAAKP
						RRSQSDSLGPEFQGLWERLPGL
						RINGELITAYPQVVVVRVPTPW
						VQSDSDITVLRHLEKMGCRLM
						NRPQAILNCVNKFWTFQELAG
						HGVPLPDTFSYGGHENFAKMID EAEVLEFPMVVKNTRGHRGMY
						ELLVSTMGCSNSGMVTTPIKWL
						SMISVQCLANGTFLSPSLTKCPK
						GIRASVPLSGGPRSLKARTFSAF
						SGPVRSDEQAEALPEAYEPIEV
						NEFGEIDLLAMVEDEILALPVV
						PVHDSEHCEVSEADMVFGELPE
						EAQKPNPFAVLASLKRVRSMA
						VQQNKPTRSKRGMRRSHDALT
				1		AVTSLSVDKTSGEKHLRHH*SA
						DLAAAPRAPGTLAQGCLTDSFS
26978	57346	A	27135	79	306	SGDLPWEINPLSSCSLLREKDPP
		1				MTSGPQTNQPKKHLINFKSGPH
				1		WKSDCSTHLAATPKAP\GTLAQ
				1		GSLTDSFSA
26979	57347	A	27136	159	254	
26980	57348	С	27137	63	370	
26981	57349	С	27138	107	408	
	1		1	1	<u> </u>	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
26982	57350	A	27139	210	291	
26983	57351	A	27140	395	680	
26984	57352	A	27141	157	485	
26985	57353	Α	27142	1	507	
26986	57354	A	27143	1	1041	
26987	57355	Α	27144	I	671	GASGAAAYGADMAKSKNHTT HNQSRKWHRNGIKKPRSQRYE SLKGVDPKFLRNMRFAKKHNK KGLKKMQANNAKAMSARAEA IKALVKPKEVKPKIPKGVSRKL\ DRLAYIAHPKLGKRARARIAKG LRLCRPKAKAKDQTKAQAAAP PSVPAQAPKDKDTSNIFISNRKR GCDFTKKETNIPKVLTISMAPSL MSLYSVTRNQTTKPPSRHKNLT KGQLEPLY
26988	57356	A	27145	6	448	
26989	57357	A	27146	930	1307	
26990	57358	A	27147	1	675	
26991	57359	A	27148	142	456	
26992	57360	Α	27149	3	175	
26993	57361	С	27150	378	434	
26994	57362	Α	27151	1	792	
26995	57363	A	27152		578	MVRCVRLVEAGSVVRYLSTSIC RPVVDAGSRALCLQEWADSQQ VKEKQYSSRDVQRAAALNIYRI PPSSRKPALCPTPRDRLEYDEDR LEHIAYVRARELHTLEVTGLET VAQSKAHVASLEGLIPEDKVVL LAGSPLQNEATLGQCGVEALTT LEVVGRRLGASL/HTSASKHTM VRALTYCSSREETFTAI
26996	57364	A	27153	1239	1905	SAAAAPATGVPACRAGAWVSA APPAEGRPARARRHPGRCLEAA GPRGQRGAAHGH*ARAGSPQP GAPPCHPLGIPARQPLGLPRRTR CFGGIAQRGRAARHCLLSRPSA KAKRNSSYREPGMGGWRSPQA LGEYGKGSQAGSARLSGAASQ GRRARHLRGKAPAWNPAPPPSP PPPALGLPLRTQREATRKPRRE EARRPRPRPLRPGGANGSPGPP RAARA
26997	57365	Α	27154	1	1275	
26998	57366	A	27155	3	92	EAVDPHSECYSS*RWCVRSFFIL VGLWSH
26999	57367	Α	27156	2	367	•
27000	57368	A	27157	98	293	GQTFATASISLLRYATGCGVFP RV*IRSPRAIPALSGDWPAPFSV LSEPPRFVCLRAMTKAAAFL
27001	57369	A	27158	3	211	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			:	sequence		
27002	57370	A	27159	1	519	GQLI/LKDTFITQSAADIRRKFQ
27002	3,3,0	l'`	27(3)	'		KQALGPEHNLEALLNLAILVFY
						NRDQEEQAQKEKRDQRKAAPL
		l				IMALRQTLVVQRGQKMEQANH
		1				LIPGYSEIARPLYTLIKEIQRANT
						,
		1				HQVEWEPEAETAFKPLKQALV
						QAPALSLPTGQNFSLYITERAGI
		<u> </u>				ALGVLTQTHGTTPQLVAYL
27003	57371	Α	27160	72	381	DSHTRSGTTRWGIRCRSGSSPSR
	ļ					RARWGRWGGLAAVALRRPAP
				İ		AAGGTAPRGCLPAA*GSPPAPP
	1					SGS*SGSSDRPARMPLVVGLSH
	[EFE*GLAGVDGEVLPPSRCVAL
						LLLRVERLHVAVYLPREALHQL
						HPLALDLDLLIARLVCHWLWG
		1				CPTSLSKDSKSYSCSLCDV
27004	57372	Α	27161	515	747	SHGNSGNFQGTRDTISLS*AQLT
						TSTKDPWTDPPALWPRVFPSGG
1	į.			-		HYNCRAPSSP/TIQQEVARAVIT
						QFPTAAGVSCL
27005	57373	A	27162	1	663	
27006	57374	A	27163	1	1980	
27007	57375	A	27164	1	672	
27008	57376	Α	27165	1	691	
27009	57377	С	27166	1	1491	
27010	57378	Α	27167	830	2592	
27011	57379	Α	27168	1	3744	
27012	57380	A	27175	2	365	QWDWAPWSRGWCSSGRLGPH
		1				RSPRSGGGSG\RRAAGPKPCPSP
						RSDAPAQPRGRSRRVLPLPQVQ
				1		AEPPEPWPVLPAAPKPLARPEA
	1	1				GMAGPGGRRTTSLPRRRGCGC
}						CCPASSCFSSLSC
27013	57381	В	27176	1	1392	
27014	57382	Α	27177	79	1241	·
27015	57383	Α	27178	3	299	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
27016	57384	Α	27179	1	812	MPTVLACPAFDSRGSPICRFDPP
						ELTSGVRALEESPNAITLPVCGR
						DVKFTLEVLRGDSVEKTSRVW
						SGNERDQELLTEDALDDLIPSFL
						LTGQQTPAFGRRVSGVIEIADG
						SRRRKAAALTESDYRVLVGEL
						DDEQMAALSRLGNDYRPTSAY
						ERGQRYASRLQNEFAGNISALA
						DAENISRKIITRCINTAKLPKSV
						VALFSHPGELSARSGDALQKAF
						TDKEELLKQQASNLHEQKKAG
						KRSRRLHHTLLRVVAEIDKPDP
						RDELAGLLQFAGGPLQTLFAW
						VSPVEAAEQQRLLLAPSSGSFIP
						EG*DHPVRPQ*AAPGHVHYLTI
27017	57205	A	27180	306	701	PERSSQHYHPGALQE
27017 27018	57385	A	27180		396	
27018	57387	A	27181	1	1263	
27020	57388	A	27183	1	873	
27021	57389	A	27184	149	421	
27022	57390	В	27185	23	268	
27023	57391	A	27186	1	363	
27024	57392	A	27187	2	398	TKFAARRPALAACAAISKIKAR
						DLRGKKKEEL\LKQ\LDDLKVE
						LSQLRVAKV/TQGGAASKLSKI
						RVVRKSIARVLTVINQTSGKKT
						FREILTRGKKYKPLGPCGP*GRT
				ĺ		RAMRRRFKPSTEGEP*RTQGSR
27025	57393	A	27188	224	547	
27026	57394	A	27189	1	888	
27027	57395	A	27190	280	1170	
27028	57396	Α	27191	1	191	
27029	57397	A	27192	438	1240	
27030	57398	Α	27193	168	378	
27031	57399	Α	27194	1	1362	
27032	57400	Α	27195	2	918	
27033	57401	A	27196	38	397	RRCRPTMPRP\WCTCRGYQGPR
						KAQGG*AQDPKGCQPQARSTC
						LHCPPQAWE/RVLVPVLPRGSG
						CAGQ/MAKAKAKAKDQTKAQ
						AAAPASVPAQAPKRTQAPTKA
						SE*ISLPT*GQKDWCDP
27034	57402	A	27197	1	1206	
27035	57403	A	27198	734	913	
27036	57404	A	27199	3	778	
27037	57405	С	27200	164	274	
27038	57406	Α	27201	1	2700	
27039	57407	A	27202	1	747	
27040	57408	Α	27203	164	409	
27041	57409	A	27204	152	380	

27042 27043 27044	SEQ ID NO: of peptide sequence 57410 57411 57412	Met hod	SEQ ID NO: in USSN 09/540,217 27205 27206 27207	Nucleotide location of first codon for peptide sequence 230 1	Nucleotide location of last codon for last amino acid of peptide sequence 2579 2433 528	deletion, \=possible nucleotide insertion) NHQIRNDFTISPGVKADSRTSPI PQQPASSFDITEAAVSFAKDSLA
						GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP\ TQALNFTFKDKYKQIFLDGVDK RSQFWRYFAGNLASGGATGAT SLCFVYPLDFAHTRVAADVGK AGAERELRGFGDCLVKIYKSDG IK
27045	57413	A	27208	1	292	MTSKDKTSRGTIRQQHSRFKKI RCSAATTAGTQANRVWSGPLA NSNRPAAEAGVSTAAAPDGPPP PSVPTVDSDSLESAQFKCDNLK TCHTSHGSVMAETAVINHKKR KNSPRIVQSNDLTEAAYSLSRD QKRMLYLFVDQIRKSDGTLQE HDGICEIHVAKYAEIFGLTSAEA SKDIRQALKSFAGKEVVFYRPE EDAGDEKGYESFPWFIKRAHSP SRGLYSVHINPYLIPFFIGL*PDK EGNEIWVDMYTVKPSGWTVRT FDKPRKRFIAFFIAGILFRAIKNH FLPRETLQCLPYILTGFRRGQSE YFSIFSNMDLADTVMFL
27046	57414	Α	27209	1	1452	
27047	57415	В	27210	53	844	
27048	57416	A	27211	281	624	ACSDVWSKFRLRWSPNPRCQE RPSAEKMSPHPPSAARHQASWS ARRLTQWPRPCHTQ*GQSEEH GHRSGLMPAG\THQLPDEHAIT PHLQSTAPIIPEPKTLSHKDSSLQ GTGK
27049	57417	Α	27212	3	411	
27050	57418	A	27213	265	480	LDTILTASDGRPTYTPP*FLLLS/ CFCYGFFCYIFGCSCRALARAR AGGGGVPAAHRAAGRGSRAPE RIPPH
27051	57419	Α	27214	294	620	
27052	57420	A	27215	1	420	
27053	57421	Α	27216	1	342	
27054	57422	Α	27217	175	244	DLLIEMGSFFVQCRTAIL*RKQN
27055	57423	Α	27218	11	951	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27056	57424	Α	27219	20	1654	ELRFPAACSQLQFSDGLHRVDQ
						PPSSMCVSAADLWLC\EAGKLL
						VVPMDGSHWFTMRSVVEKLIL
		l			:	RGHEVVVVMPEVSWQLGRSLN
				1		CTVKTYSTSYTLEDLDREFKAF
		1				AHAQWKAQVRSLFSLFLSSSNG
		1				FFNLFFSHCRSLFNDRKLVEYL
		1				KESSFDAVFLDPFDACALIVAK
						YFSLPSVVFARGIGCHYLEEGA
						QCPAPLSYVPRILLGFSDAMTF
		ŀ				KERVRNHIMHLEEHLFCQYFSK
						NALEIASEILQTPVTAYDLYSHT
						SIWLLRTDFVLDYPKPVMPNMI
						FIGGINCHQGKPLPMEFEAYINA
						SGEHGIVVFSLGSMVSEIPEKKA
						MAIADALGKIPQTVLWRYTGT
	1					RPSNLANNTILVKWLPQNDLLG
						HPMTRAFITHAGSHGVYESICN
		l	ļ			GVPMVMMPLFGDQMDNAKR
						METKGAGVTLNVLEMTSEDLE
1						NALKAVINDKSYKENIMRLSSL
						HKDRPVEPLDLAVFWVEFVMR
						HKGAPHLRPAAHDLTWYQYHS
						LDVIGFLLAVVLTVAFITFKCCA
						YGYRKCLGKKGRVKKAHKSK
27057	57425	Α	27220	1	2022	
27058	57426	Α	27221	124	205	
27059	57427	Α	27222	248	443	
27060	57428	Α	27223	263	415	
27061	57429	С	27224	1	717	
27062	57430	A	27225	349	1125	
27063	57431	A	27226	629	796	
27064	57432	В	27227	1	388	
27065	57433	Α	27228	2	346	
27066	57434	Α	27229	448	555	
27067	57435	Α	27230	2	423	CEPIKVYVVGN\GAVGKTCLL\I
						SYTTNAFPGEYIPTVFDNYSAN
						VMVDGKPVNLGLWDTAGQED
						YDRLRPLSYPQTDVFLICFSLVS
			[PASFENV/LCKGAVKYLECSAL
						TQRGLKTVFDEAIRAVLCPPPV
						KKRKRKCLLL
27068	57436	A	27231	1	1503	
27069	57437	Α	27232	[1	635	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27070	157420	<u> </u>	Togges	Ta	11107	AVELORGIVANDI DOLORGO A FOR
27070	57438	Α	27233	3	1107	AVFLSFGWWPLPGIGFQSAEGE
						AAWTAAPAPSAPPPSKPRARPP
						RPEPAASYLSALPPPPRPSERPS
						MQAIKCVVVGDGAVG\KT\CLL
						I\SYTTQCHFLGEYIPTVFDN\YS
						A\NVMVDGKTGEIWGLWDTAG
						QEDYD\RLRPL\SYPANRMCS*I
						CFS\LVSPA\SFENV/LVQKWYPE
						VR\HH\CPNTPI\IPVGT\KLDLRD
						DKRHDSRNLKEKKLT\PITYPA
						GS*AMAK/ERLGAVKYLG/CAP
						AAHTSEGLKTVFDEAIRA\VLCP
:						PPVKERGRENCLPVVNVSAPSF
						LGSCPLGTFCRLCSKKNKKKKQ
						KKKNNGGAFALNANFLLQINFS
						IKPFFEPISNFKVLFVLNVRVQT
						HILLKFSPKMTSLLKALFFK
27071	57439	A	27234	3	203	
27072	57440	Α	27235	1	112	LGNTWG*QPCKRLKIWLSLEFT
		1				KINVIRHMWKKFKRL
27073	57441	Α	27236	1	513	QHWGRYLKRAFEQWQVPRFG
						HMPDPGPVKPLQPVEVETRGN
		1				DYKFLLFHFWDEWLYKFSADE
		1				FFIPGKLCAIVF*KRL*RPGAVA
						YACNPSTLGSRGRWIT*GQEFE
		1				TSLTNKEVKVLSIDQRNFKLRSI
		1				GWGEEFSLSKHPQGTEVKAITY
		1				SAMQVYNEENPEVFVIIDI
27074	57442	В	27237	125	302	
27075	57443	Α	27238	93	432	
27076	57444	Α	27239	3	279	
27077	57445	Α	27240	263	446	
27078	57446	Α	27241	237	369	
27079	57447	Α	27242	389	836	
27080	57448	Α	27243	1422	1580	
27081	57449	Α	27244	103	444	RSLTCPGDMFPVVLVINIQLLLT
						YANFCSWLESLPRKWDFLFYCI
						VRLQIFQTFMLCFLLNTLPLRNF
						FYQIP*IISLKFKVPQISKAEAKC
						HQSLCIGRVTFIPVPNKFFISI
27082	57450	Α	27245	3	242	MHRNAQHHVKTAKPWGLHPL
						KPQPK*YSGPF*PPLEQLRCKAT
				1		GP*GCTQQGGPGPGPQNNFSLL
						GLQACDGRDCHEGL
27083	57451	Α	27246	506	664	-
27084	57452	Α	27247	1	1515	
27085	57453	Α	27248	269	541	RFPNLNS*LLYTRGLTPHESCQ
						GLGLAPSEAMAQTIPWPLLATA
						RLAVTGNQILMQISAAGLNFSS
						ENGAFISIALSGCKFFKLLCSAS
27086	57454	A	27249	1	564	
12,000	13,434	1,,_	12,27	<u> </u>	1201	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27087	57455	A	27250	2	235	
27088	57456	A	27251	3	1393	, , ,
27089	57457	Α	27252	28	271	
27090	57458	A	27253	12	485	RMAFCRASQADQDRFICIYPAY
						LNNKKTIAEGRRIPISKAVENPT
						ATEIQDVCSAVGL\NVILRKIKM
						YF*EWNRDVQYR\GRVRVQLK
						QEDGSLCLVQFPS/RLYTKPNF
						WFLGKSVMLYAAEMIPKLKTR
						TQKTGGADQVFQQGEGS*KGK
!						GKQKEVT
27091	57459	Α	27254	1689	2176	APPGMGAASLCAFGLLVTFAT
						ASPRYAMVQPSFRLGTKLGQA
						EADEPFVSSGSVPPSFLSPLLPA
						APGARRG*LQRGDLGRQAPPPA
						PGCAPGLA*GRPPAPHL*RLCSR
						PTFFPPPANSSRLALADSPPPRQ
1						LQGARP*PVPGRLLTSTGTPRPL
						PRPLGP
27092	57460	Α	27255	263	439	
27093	27093 57461	A	27256	1	499	MSELPFTIATKRIKHLGIQLTRD
					VKDLFKKNYKPLFNEIKDDTNK	
						WKNIPCLWIGRINILKMAILPKV
						IYRFNAIPIKLLMTFFTEMENTT
						FKFMWNQKR/CPHCQDNPKPK
						EQSWRHHAT*LQTILQGYSNQN
						SMG/TWMKLETIILSKLSQGQK
						TKHRMFSLIGGN
27094	57462	A	27257	1940	2062	
27095	57463	A	27258	1232	1432	
27096	57464	Α	27259	168	1189 1760	
27097	57465	A	27260	<u> </u>	543	
27098 27099	57466 57467	A	27261 27262	453 873	962	
27100	57468	A A	27263	8	411	FSRCRCSGR/YLCMASCL\CFHH
2/100	37408	^	27203	°	1411	CWWMASHHWPI*RTQV*CAC
					<u> </u>	WEGRHLG\CAPKCLSLLGFTRL
						LACVLWLPILQSVIPIHIQVSITV
						RVLFAAAHDEARASEATFQESG
						GPYPLLSTPLILLKAVVVLMLD
		ľ				AHAS
27101	57469	A	27264	<u> </u>	552	ALLAS
27101	57470	A	27265	828	1211	
27103	57471	A	27266	428	655	DQKVPPLEMYFGIEVKSLKQLR
[[ļ.,				SISA*SLFSSRALKEDSGLLKLK
	}					QPRSSGVIPRRFIVSWPWKMVR
						QPVLFSVG
27104	57472	A	27267	1	855	
27105	57473	A	27268	1	1261	
27106	57474	Ā	27269	164	260	

SEQ ID	ISEO ID NO:	TMet	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	· · · · · · · · · · · · · · · · · · ·
27107	57475	A	27270	147	224	RLTLPDHLGSLLDHHR\ALGNS YSGG
27108	57476	Α	27271	1	837	
27109	57477	В	27272	184	288	
27110	57478	Α	27273	1	286	
27111	57479	Α	27274	1	699	
27113 27114 27115	57481 57482 57483	A A A	27275 27276 27277 27278	1059 2 415	1229 4735 825	MTGICYTEDERSYKKNAQPTA ASKKQKETQKFCLRVDGQQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPPED PVALETRSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPVRVDTVRVVEGPREVEVV ASTAAGAPAQRAQSLEPYGTG LRALAMPGRPESPPVFRSQEVV ETMCPVPAAATSNVHMVKKISI TERSCDGAAEMKWEDQNIGD SCADFQDYWDQREYTYNRPHT ASRRIVLDFLLFPEW/PTFVAFW APLFNPSKRASLYRFSLCISSLSF GSHWGSVPGNWVLTYSWG/SL
27116	57484	A	27279		1326	VISRCMFL*PLSCCLEHSPPFICV KEEHEQLVAISPSGVMGLDNSL EQIN
27117	57485	A	27280	2976	3068	VWTALTNRLGQQVSICG*PGTE DSKGDWLL
27118	57486	A	27281	78	220	APTSLHS*SYFKNCGHGRLRWV ITHIRLVISWATYLVQNNIIQTR LF
27119	57487	Α	27282	1	1077	
27120	57488	A	27283	307	922	QVVPSSLSAISQSPAPCG/CSP*G PSPGAT
27121	57489	A_	27284	1	4560	
27122	57490	A	27285	87	237	LLFFQLGGDAFSFKFSSGVNF\R NSLICQAWGKRVFSALLCIILSE YTSPL
27123	57491	A	27286	1	246	
27124	57492	A	27287	46	396	
27125	57493	A	27288	1	552	
27126	57494	A	27289	3	418	AEKCPCLGAFGFGWDHPRRPG SWGAWSEGSGSPPARIVKMSLR KQTP\SDFLKQIIGRPVVVKLNS GVDY\RGVLACL\DGYMNIALE QTEEYVNGQL\KNKYGDAFI\R GNNVLYI\STQKRPDVRTPKRA TLFIVGYIFL
27127	57495	Α	27290	202	450	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27128	57496	Α	27291	304	642	
27129	57497	Α	27292	75	393	
27130	57498	A	27293		678	VFGLGSVAHMLLNKTFGSYLG VNLGFGFGVTMGVHMAGRTS GAHMNAAVSLTNCALGRVPW RKFPVYVLGQFLGSFLAAATIY SLFYTAILHFSGGQLMVTGPVA TAGIFATYLPDHMTLWRGFLNE AWLTGMLQLCLFAITDQENNP ALPGTEALVIGILVVIIGVSLGM NTGYAINPSRDLPP\RIFTFIAGW GKQVFRWHHLPGLHWLHHPT GAPEIGGFCGV
27131	57499	A	27294	2	1694	
27132	57500	A	27295	1	356	GIFVTYLPDHMTLWRGFLNEA WLTGMLQLCLFAITDQENNPA LPGTEALVIGILVVIIGVSLGMN TGYAINPSRDLPP\RIFTFIAGWG KQVFRYFPCPGPIPLSFSVGPLC VEGWGVM
27133	57501	Α	27296	1	544	_
27134	57502	A	27297	320	610	LREYTINIHTAHPMEWASKKRA PRALKEIRKFAMKEMGTPDVRI DTRLNKAVWAKGIRNVPYRIR VRLSRK\RNEDEDSPNKLYTLV TYVPVYHFQK
27135	57503	Α	27298	1	303	
27136	57504	Α	27299	1	1311	
27137	57505	Α	27300	1	3126	
27138	57506	A	27301	2	779	NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKGPRGTA*FSLL* ATGEKGFGL*GVPCFHRIIPGFM \CQG\GDFTRH\NGT\GGKSHLW GRNLKDENFI\LKHTGPGILSHG KMLDPNTNGSQFFICTA\KT\EW LDGK\HVVFGKVKERHEILWEA MGALLGPRNGKTQQEESPIVPG GQLRIKFDLVFYSLTTKIIPFCSF KESTPPPHLLASILESLCSRLQFP FGFHVFLVPCHA
27139	57507	Α	27302	143	390	
27140	57508	Α	27303	249	1516	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		İ		sequence		
27141	57509	Α	27304	2	645	NRVLLAMVNPTVFFDIAVDGEP
				l		LGRVSFEVRGLDTKK*LLI*SIK
1						LC*QIG\LFADKGPRGTA*FSCL*
				İ		SIEEKGFGL*GVPCFHRIIPGFM\
						CQG\GDFTRH\NGT\GGKSHPM
						GKKFE\DENFI\LKHTG\PG\ILSH
					}	GKCLDPNTNGSQFFICTA\KTEV
						VGMAKHVVFWQK*KKGMKYC
		ļ				GRPWERFG\SR\NGKTQQRKITI
		ļ				C*LVGQLRNKVLTWWF
27142	57510	Α	27305	72	387	VCLQHGPWSSLKHVQGWRDD
						CHGLSLGPRTHVQAGTLPKPTL
						WAEPGSVITQGSA\VTLWCQGI
						LQTQEYRLYREKKTAPWITRIP
						QEIVKKGHDPIPSITWEHTG
27143	57511	A	27306	1	322	
27144	57512	A	27307	1	1125	
27145	57513	Α	27308	1	1419	
27146	57514	Α	27309	198	1634	
27147	57515	Α	27310	78	216	
27148	57516	Α	27311	1	489	
27149	57517	Α	27312	18	463	AEGVEPGSPRVVLLESEQFLTE
						LTRLFQKCRTSGSVYITLKKYD
						GRTKPIPKKGTVEGFEPA\DNKC
						LLRATDGKKKISTVVSSKEVN*
						VFRWLISNLPLGANMDGLKKR
						DKKNKTKKTKAAAAAAAAGP
07150	57510	١.	07212		1242	AAAATAATTAATAAQ
27150	57518 57519	A	27313 27314	147	1242 1965	DPPSPVPAPPSSPRDGHFLVPDA
27151	13/319	Α	2/314	14/	1903	TMAEEQPQVELFVKAGSDGAK
						IGNCPFSQRLFMVLWLKGVTFN
l						VTTVDTKRRTETVQKLCPGGEL
						PFLLYGTEVHTDTNKIEEFLEA
						VLCPPRYPKLAALNPESNTAGL
						DIFAKFSAYIKNSNP\ALN\DNLE
	İ	1				EGTPGKP*RFLDNYLTSPLPEEV
ŀ						DET\SAEDERCLSDGTFLDGNEL
	1	1				
Į.						TLADCNLLPK\LHIVQVVCKKY
						RGFHHPPRPFRGVAFGYL\SNA\
						YARENFRFPPVPDDEEIELAYE
27152	67500	 	27215	1	933	QVAKALK
27152	57520	A	27315	<u> </u>	ננדן	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27153	57521	A	27316	63	641	FAKMTDHKGERGEATRYMFSR
						PFKKTMGVVPCGHNN*RFYK\K
						GDIVD\IKGMGYCVQNGMP\HK
						CY\HG\KTGRSLTIVTPACLLPLL
						*TNQF*GKVFS\KRINVRIEHIKH
						\SKSRDSFLKRVKENDQKKKEA
						QEEGT\WVQLKRQPAPPREAHF
						V\RTNGKEPEL\LEPIPYEFHGIN
						RCPKKKIKDLWATKKKKK
27154	57522	Α	27317	1	390	
27155	57523	Α	27318	75	394	IWGDVEKGKK\IFIMECSQCHT
					:	VEKGGKHKTGPNLHGLFGRKT
						GQAPWDTPYTAANKNKGIIWG
						EDTLMEYLENPKK\YIP\GTKMI
	1					F\AGIKKKEERADLIAYLKKSY
27156	57524	A	27319	2	529	ERQTRHAGGVRRGPRPKLQRD
						KAAAAAVLGAVRKRPSVVPM
						AGQDPALSTSHPFYDVARHGIL
						QVAGDDRFGRRVVTFSCCRMP
						PSHELDHQR\LLEYLKYTLDQY
						VENDYTIVYFHYGL\NSRNKPS
						LGWLQSAYKEFDRKYKKNLKA
						LYVVHPTSFIKVLWNILKPLISH
						KFGKK
27157	57525	Α	27320	287	445	
27158	57526	Α	27321	2	362	
27159	57527	A	27322	30	365	EEAETVLVGQLKQLSSCLAVH
						KYRPETKQEKKQRLLARAEKK
						AAGKGDVPTKRPPVLRAGVNT
						VTTLVENKKAQLV\CRKMGVP
						YCIIKGKARLGRLVHRKTCTTV
		<u> </u>			105	AFTQVN
27160	57528	A	27323	3	432	NSRVDDFVAAQDAKGKKVAP
						APAVVKKQEAKKVVNPLFEKR
						PKNFGIGQ\QRLLARAEKKAAG
						KGDVPTKRPPVLRAGVNTVTT
		1				LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR
						LGRLVHRKTCTTVAFT
27161	57520	<u> </u>	27224	62	217	LUKLVIKKICI I VAFI
27161	57529	C	27324	62	217	
27162	57530	A	27325	1	1545	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27163	57531	A	27326	2	801	I PKGKKAKGKKVAPAPAVVKK
2,103	3,331	l'`	27320	[QEAKKVVNPLFEKRPKNFGIGQ
Ė						DIQPKRDLTRFVKWPRYIRLQR
						QRAILYKRLKVPPAINQFTQAL
		1				DRQTATQLLKLAHKYRPETKQ
		l				EKKQRLLARAEKKAAGKGDVP
						TKRPPVLRAGVNTVTTLVENK
						İ
						KAQLVVIAHDVDPIELVVFLPA
						L\CRKMGVPYCIIKGKARLGRL
						VHRKTCTTVAFTQVNSEDKGA
						LAKLVEAIRTNYNDRYDEIRRH
						WGGNVLGPKSVARIAKLEKAK
						AKELATKLG
27164	57532	Α	27327	550	827	DVSWAGRSEDHRWIFLKEQRT
•		l				GGPPK/ERSRSESRHQISCMCAA
l		1				STWMERTAYGGSHRELLLQQL
		1				PQEHTRKTLPLQQTSAWTYRLF
						HTSCEI
27165	57533	Α	27328	908	1331	GDMRGRREGGFGLGRRTAMRC
		İ				GCSPGIVREADNLVKLSRPSTV
1						RVTRSSASVMVLTMPLAPATFL
						RVNCWAG/RGR/C*SQNETVSR
						TRCEEGR**KDYRVEEQRLRKN
						WDLARPGEEQLAPSPEKRDLPL
						RVKDQGRHPCVV
27166	57534	Α	27329	1	1134	
27167	57535	A	27330	62	310	
27168	57536	Α	27331	243	578	
27169	57537	Α	27332	324	995	NLVPRPGTWIRGLPLGDHSPVL
						LLFAP*ERSTYDLRSSDRPAQET
						SHQFQIRERQRRHVLSVDPKLR
						RRSRTGKAAFPWCLIIAGTPL*L
						YTHVSRVSDHAGMPALVLHP*
						R/LSPTFLGKGQHALKGLKPVIT
						RLLQHGLLKPINSPFPSPILPVLK
						PDKAYKLVQNLRLINQIVLPIHP
ł						VVPNPYTLLSSIPPSTTHYSVLD
		<u>L</u>				LKHAFFTIPLHPSSQPLFAFT
27170	57538	Α	27333	1	1860	
27171	57539	Α	27334	1	957	
27172	57540	Α	27335	97	826	
27173	57541	Α	27336	245	392	
27174	57542	Α	27337	736	1300	
27175	57543	Α	27338	590	891	
27176	57544	Α	27339	1256	1654	VQPVRLVSGMQHPGSGWRRL
		ļ				WGQHSTSLTSKEHLHISKRGNI
						DNLVQRNMP\SNEKPKCPELPP
1						FPSCLSTVHFIIFVVVQTVLFIGY
					1	IMYRSQQEAAAKKILLTTIFLCT
				<u> </u>		SSICVQNDVVLREFKYLNCFIV
27177	57545	Α	27340	295	852	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27178	57546	A	27341	3	446	ILAWFGSIAEAPSAAWLCGSSQ GRYCSSFNRVVRQNSSDAKVV NVPKTRITFCKK\CGKHQPHKV TQYKKGKDSLYAQGRRRYDRK QSGYGGQTKPIFRKKAKTTKKI VLRLECVEPNCRSKRMLAIKRC KHFELGGDKKRKGQVIQF
27179	57547	Α	27342	1	565	
27180	57548	Α	27343	1	1050	
27181	57549	В	27344	1	2109	
27182	57550	A	27345	2916	3229	· · · · · · · · · · · · · · · · · · ·
27183	57551	A	27346	3	671	AGILAAIREANMGAYKYIQEL W/RKKPSDVHAFFLRV\RCGQT RSFFVFTGVPRPTRPDKARRLG YKAKQGYVIYRIRVRRGGRKRP VPKGATYGKPVHHGV\NPA*KF ASKALQVPLPEGTEAGR\HCGG S*ESLNSYWVGEDS\TYKFFEVI LIDP/YSHKAIRRNPDTQ\WIT\K PVHKHREMRGLTSAGRKSRGL GKGHKFHHTIGGSRRAAWRRR NTLQLHRYR
27184	57552	A	27347	1	1646	
27185	57553	Α	27348	2	2600	
27186	57554	Α	27349	1	2403	
27187	57555	Α	27350	100	520	
27188	57556	Α	27351	1	570	
27189	57557	В	27352	1	837	
27190	57558	В	27353	1	1434	
27191	57559	A	27354	1	2379	
27192	57560	A	27355	3	952	IDWAPKSDRIVTCGADRNAYV WSQKDGVWKPTLVILRINRAA TFVKWSPLENKFAVGSGARLIS VCYFESENDWWVSKHIKKPIRS TVLSLDWHPNNVLLAAGSCDF KCRVFSAYIKEVDEKPASTPWG SKMPFGQLMSEFGGSGTGGWV HGVSFSASGSRLAWVSHDSTVS VA\DASKS\VQVSTLKTEFLPLL SVSFVSENSVVAAGHDCCPMLF NYDDRGCLTFVSKLDIPKQSIQ RNMSA/LWERFR\NMDKRATTE DRNTALETLHQNSITQVSIYEV D\KQDCRKFCTTGI\DGAMTIW DFKTF\ESSIQGLRIM
27193	57561	A	27356	3	134	
27194	57562	A	27357	1	478	
27195	57563	A	27358	1	623	
27196	57564	Α	27359	425	667	
27197	57565	Α	27360	121	401	
27198	57566	Α	27361	1	1818	

SEQ ID NO:	SEQ ID NO: of peptide sequence		_			Amino acid sequence (X=Unknown,
	sequence	nou.	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27199	57567	A	27362	552	2325	
27200	57568	Α	27363	693	1270	
27201	57569	Α	27364	18	146	
27202	57570	Α	27365	270	683	
27203	57571	Α	27366	1	1398	
27204	57572	В	27367	1	1152	
27205	57573	A	27368	40	538	SPSPKDSPGVRVGISCYIGGPCQ QRLLSPVRASKMTKKRRNNGR A\KKGPRHVRGPSPLKFLPPSSC HLTVPRCRAQGTRPIKKF\VISK P*VEAAAV\RDISEASVFDAYL\ LPKLYVKLHYCVSCAIHKQK*S
						GNRS\REA\RKTRTPPPRFR\PGG *LPHGPPTKSP
27206	57574	A	27369	204	401	LEHUFFIKSF
27200	57575	A	27370	3	980	
27208	57576	A	27371	2124	2836	
27209	57577	A	27372	139	8892	
27210	57578	A	27373	1	2592	MAGLGASLHVWGWLMLGSCL
27210	57579	A	27374	2	2138	LARAQVRASAPRHLFSRSLRRG LSFSDTEARCARELIHVHTSTN APARTEAYPAGSAEPPRRPRAG REHSFFSQRYVPLPPLGGALGS GPAKLPPPRAPCPVRFCADLET LCGALDCYKVRGGAAPARPAP RPAGGIQVSSLSGFGTESLPGGN PFPHRDHRESGTMDSPSLTVAT PLSLTPPIPRELACGDWRRVGG GAGGGGLRRRGLGGDKAGKR KSSDLPCGPGFLQSLLQKRRHW ESGLGLPGCGCESELVSGCGAP TLRQHIIPAEGRNGVKEKSADL GCGGSQGLRAKKGTNPGIENG KRKGKEGMLDAWICRRSAFGP GREKLGGEEVGCNDKGKIRFIE VKMSKKISGGSVVEMQGDEMT RIIWELIKEKLIFPYVELDLHSY DLGIENRD/ATNDQVTKDAAEA DKKHNV\GVKCATITPDEKRVE EFKLKQMWKSPNGTIRNILGGT VFREAIICKNIPRLVSGWVKPIII GRHAYGDQGFGSNMQNAIMK KLKWLHLARVGKFSDANAKFY CRLYYAGEFHKMREVILDSSEE DFIRSLSHSSPWQARGGKSGAA FYATEDDRFILKQMPRLEVQSF LDFAPHYFNYITNAVQQKRPTA LAKILGVYRIGYKNSQNNTEKK LDLVMENLFYGRKMAQVFDL KGSLRNRNVKTDTGKESCDVV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	į	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		-
27212	57580	A	27375	1	2355	
27213	57581	A	27376	249	1544	EIYSLSRFIEVKMSKKISGGSVV
2/213	37301	l'`	27370	247	1344	EMQGDEMTRIIWELIKEKLIFPY
					VELDLHSYDLGIENRDATNDQ	
						VTKDAAEAIKKHNVGVKCATI
						TPDEKRVEEFKLKQMWKSPNG
						TIRNILGGTVFREAIICKNIPRLV
						SGWVKPIIIGRHAYGDQYRATD
						FVVPGPGKVEITYTPSDGTQKV
		į				TYL\VHNFEEGGGVAMGMYNQ
						DKSIEDFAHSSFQMALSKGWPL
						YLSTKNTILKKYDGRFKDIFQE
İ						`
	1					M\YDKQYKSQFEAQKIWYEHR
						L\ID\DMVAQAMKSEGGFIWAC
						KNYDGDVQSDSVAQGYGSLG
			:			MMTSVLV\CPDGKTVEA\EAAH
	ı					GTVTRHYRMYQ\KGQGDVHPIP
						LASIFAWGPEGL\AHRAKLDNN
						KELAFFANALEESFYETHE\AGF
						MTKDLAACIKGLPNVQRSDYL
25014	55500	 	05055	1,	(00	NTFEF\MDKLGENLKIKLAQAK
27214	57582	A	27377	1 251	692	
27215	57583	A	27378	251	2150	
27216 27217	57584	C A	27379 27380	93 308	293 534	
27217	57585 57586	A	27381	2	856	
27219	57587	A	27382	3	327	AQELHTFEVTGQETVAQIKAHV
21219	37367		2/362]3	321	ASLEGIAPEDQVVLLAGAPLED
						EATLGQCGVEALTTLEVAGRM
						LGG\AKQEKKKKKTGRAKRRM
						QYNRRFVNVVPTFGKKKGPNA
27220	57588	A	27383	150	456	Q Tridd VIV VI II Gleicico III/I
27221	57589	Α	27384	651	835	
27222	57590	В	27385	1	2193	
27223	57591	В	27386	109	714	
27224	57592	Α	27387	150	458	
27225	57593	Α	27388	1	2055	
27226	57594	Α	27389	1	804	
27227	57595	Α	27390	645	1828	
27228	57596	Α	27391	899	1216	
27229	57597	Α	27392	79	156	
27230	57598	Α	27393	1796	2215	
27231	57599	Α	27394	107	724	
27232	57600	Α	27395	854	926	PLEIPHEPPPGRG*HAPQLPRGQ
27233	57601	Α	27396	2	413	
27234	57602	Α	27397	54	442	FAKMTNTNLNRRGTRYMFSRP
						FRKHGVVPLATYMRIYKKGDI
		1				VHIKGMGTVQKGMPHKCYHG
1						KTGRVYNVTQHAVGIVVNKQG
	1					KGKILAKRINVRIEHITHSKSRH
	-					SFLKRAKENDPEYE\EALENGT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27235	57603	Α	27398	1	490	
27236	57604	A	27399	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQLKR/QGKNLVYISLVLRA L*G*DLTHHIIILFPFFFL**PAPP REAHFVRTNGKEPELL
27237	57605	Α	27400	336	928	
27238	57606	A	27401	13	724	INPPPPPFRPEPPSSSKFAKNDGP QRGKRRGTPIIMFS/RGPFKKTM GVVPLAHIFMR\IYKQRCDFVDI QGEWGTLFQKGNCPHKVVTHG QNLEGVLPMVTPAMLVGHLL* NKQV*GQRFLPKRNLMWRI*A HLRHF*GARD/RASLKTCGREN GSRKKERKPKGGKVTWGFQLK RRHLGFPPQEEATFLLKEPIGGR EP*ACLEPYFPYWISWGINRVF KKKIKGPSGLQKKKKKKVD
27239	57607	Α	27402	1	759	
27240	57608	В	27403	1	372	
27241	57609	A	27404	1746	2966	DMKNGAKEGESYLLLQCLPPSP LPSPPPSPSPPPPPPPPPPSPSSPSPP PSPPPPSPSPPPPPP
27242	57610	A	27405	150	462	ICEGRTCIFEEPCNCSSLYVRSN GGNHSHSTTTFKYNGSNWIPR WQGPSGSTQPSKARRPVAFSQG NCAMEKGN*SDILGTTEHWL*A DIDSRGPKMSLQSSS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
•				sequence		
27243	57611	Α	27406	142	1285	SRMSKAFGLLRQICQSILAESSQ
					- -	SPADLEEKKEEDSN\MKREQPR
						ERPRAWD\YPHGLVG\LHNIWT
1						DLACLNSLIQVFVMNVDFTRIL
ŧ						KRITVPRGADEQRRSVPF\QML
						LLLEKMQDSRQKAVRPLELAY
						CLQKCNVPLFVQHDAAQLYLK
						LWNLIKDQITDVHLVERLQALY
						TIRVKDSLICVDCAMESSRNSS
						MLTLPLSLFDVDSKPLKTL\EDG
						LHCFFQPRELSSKSKCFCENCG
						KKTRGKQVLKLTHLPQTLTIHL
						MRFSIRNSQTEKDLATPLYFPQS
						LDFKPRSFQLKRESC\DA\EEQS
						GGQYELFAVIAHVGMADSGHY
						\CVYIRNAVDGKW\FCFNDSNIC
		l				LVSWEDIQCTYGNPNYHWQET
	ļ					AYLLVYMK\MEC
27244	57612	Α	27407	1	1077	
27245	57613	A	27408	3	242	
27246	57614	A	27409	213	928	EGPARQRLLSPVRASKMTKKR
						RNNGRAQKRAAAHVRGPSPLK/
İ		1				CFPSGPLPPNCAR\CVPQGTRPI
						KKF\VIR\NIVGGRSRQGHISEAS
						RLRMPISLPKL\YVKLH\YC\VSC
Ì						AIHKQK*FR\NRS\RESPAKTRTP
						PPRF*DLAGGCPTVPPPKAHDL
						GPEYCRHQTCVNWVCCRQATI
						LGKELCGQIRKLPSQQMSPGWL
1						PSGYSCWLYKYKTEATTALQS
İ						RGEVYHPLQALWSRPPGRDPL
27247	57615	A	27410	1	267	
27248	57616	Α	27411	257	322	
27249	57617	Α	27412	2	176	
27250	57618	Α	27413	218	923	
27251	57619	Α	27414	2	429	TKFAARRPALAACAAISKIKAR
						DLRGKKKEELLKQ\LDDLK\VE
						LSQLRVA*VTGGAASKLSKIRV
						VRKSIARVLTDINQTSGKKTFR
						EILTRGKKYKPLGPCGP*GRTR
						AMRRRLNKHEENLKTKKQQRK
						ERLYPLRKYAVKA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27253	57621	A	27416	2	670	IAGEITRRGSRARPRPGPQCPPG PPGTAMIKAILIFNNHGKPRLSK FYQPYSEDTQQQIIRETFHLVSK RDENVCNFLEGGLLIGGSDNK\ LIYRHYATLYFVFCVDSSESEL GILDLIQVFVETLDKCFENVCEL DLIFHVDKVHNILAEMVMGGM VLETNMNEIVTQIDAQNKLEKS EAGLAGAPA\RAVSAVKNMNL P\EIPRNINIG\DISIK\VPNLPSFK
27254	57622	Α	27417	5	379	
27255	57623	A	27418	536	675	LEWSSAKFPTAVGVSLLLSSVC RSQ*FLMDAMSRMDLVRYTSA RVS
27256	57624	Α	27419	2	1220	
27257	57625	Α	27420	435	552	
27258	57626	Α	27421	5	379	
27259	57627	Α	27422	1	1062	
27260	57628	Α	27423	17	467	
27261	57629	Α	27424	105	355	
27262	57630	A	27425	283	466	APRSARPIVHGVKATRPKPRNL LDKDMFSKSDPLCVMYTQGME NKQWR\EFGRTEVIDNTLN
27263	57631	C	27426	167	379	
27264	57632	Α	27427	164	1185	
27265	57633	Α	27428	1	873	
27266	57634	В	27429	20	523	
27267	57635	A	27430	3	1225	
27268	57636	A	27431	1	884	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILP\L FADKVPKTAENFRALSTGEKGF GL*GVPCFHRIIPGFM\CQG\GDF T\RH\NGTGGKSIYGEK\FEDENF I\LKHTGPGILS\MANAGP\NTNG SQFFICTAKT\EWLDGKP\VVFG KVKE\GMNIVEAMERF\GS\RNG KT\SKKITIADCGQLRIKFDLVF YSLTTKIIPSGSPRESTPPTHLLA SILESLCSRLQFPFGFHVFLVPS
27269	57637	A	27432	27	410	LQDEATGCQKLIEVDDERKLRT FYEKRMATEVAADALGEEWK GYVVRISGGNDKQGFPMKQGV LTHGRVRLLLSKGHSCYRPRRT GERKRKSV\RGCIVDANL\SVLN LVIVKKGEKDIPGLTDTTVPR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid of peptide sequence	
	sequence		09/340,217	sequence	or peptide sequence	deterion, (-possible nucleotide insertion)
27270	57638	A	27433	93	866	TVSFPATGC\QKLIEV\DDERKL
						RTFYEKRMATEVA\ADA\LGEE
						WKGYVVRISGGNDKQGFPMK
						QGVLTHG\RVRLLL\SKGHSCY
						RPRRT\GERK\RKSSSVGCI\VDS
						KSWSVLQLGLLLKKKKK*RRIF
					}	PG\LTDTTVPRRLGPQK/RASRIR
						KLFNLSK\EDDVRQYVVRKPLN
						KEGKKPRTKAPKIQRLVTPRVL
						QHKRRRIALKKQRTKKNKEEA
						AEYAKLL\AKRMKEAKEKRQE
						QIAKRRRLSSL\RASTSKSESSQ
27271	57639	A	27434	2	401	
27272	57640	Α	27435	1373	1838	
27273	57641	Α	27436	1	257	MNRQLSDSYTEDTKEPSDVTTS
						ERTRSPPGSAKTTMIDTLKKLQ
ļ						DV\QKLRTPKIPQSQQQICWNN
						MSRLRDQS*RSSKKRQRLWK
27274	57642	Α	27437	247	831	
27275	57643	A	27438	1	993	CHOPHERA BUILDIA WOLCHWIDT
27276	57644	A	27439	267	281	CNCPNIFEARWVNLKSLSKIHE* RPFQP
27277	57645	A	27440	274	482	
27278	57646	Α	27441	1	219	
27279	57647	A	27442	1	681	
27280	57648	Α	27443	11	1094	
27281	57649	Α	27444	51	65	NNTFLKYC*IDFND*DCGGEDIS PN*LGLPIPLSMVLCEIIHF
27282	57650	Α	27445	1	1563	
27283	57651	Α	27446	3	318	
27284	57652	A	27447	1	294	
27285	57653	Α	27448	7	259	
27286	57654	Α	27449	29	191	
27287	57655	Α	27450	2	519	KSQDYKSLNATCAGGTSFSGC
						ARRLLLSTCSSGWRSGGLSLRG
		1				GKMELEA\MSRYTQPSEPQLSS
						PHLTVVLLAIGMFFT\AWFFVY
						EVTSTKY\TRDIYKEAPHPP*VA
						LTPSMGFGVLF\LLL\WVGIYRV
						SHPRVTTQNGFHWKPAFCKINF
27700	55.56	<u> </u>	25.51		206	FFYLFAWEVFPPAAHNKVQML
27288	57656	Α	27451	144	386	VCECKMPKVQPNFTHWSRS*N
						DDLNRSSLWQA*PQAASVEIIIL RS
27289	57657	A	27452	462	672	NO .
27290	57658	A	27453	1	475	
27291	57659	A	27454	1	741	
27292	57660	A	27455	62	390	
27293	57661	A	27456	549	641	
27294	57662	A	27457	456	774	,
27295	57663	A	27458	2852	2935	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27296	57664	Α	27459	699	761	
27297	57665	A	27460	399	434	
27298	57666	Α	27461	683	1661	
27299	57667	Α	27462	1	95	
27300	57668	Α	27463	3	517	
27301	57669	A	27464	6	401	RGLTEVPETSGGRVSVGAMAK HHPDLIFCRKQAGVAIGRLCEK CEGKCVICDSYERPCTLVRICDE RNYGSYQGRCVICGGPGVSDA YYCKEVHHPGERTRDGC\SKIV NLGSSKTDLFL*TAKNTGFQER
27302	57670	Α	27465	1	321	
27303	57671	Α	27466	67	348	
27304	57672	A	27467	1	642	
27305	57673	В	27468	193	445	
27306	57674	A	27469	32	216	AGPSQPTNQTTGKSPQLQQDYF PRRSYRCSHRLIICLNVIGDAV* STVQLKALMLRGRNYK
27307	57675	A	27470	214	440	QDRWGLAPHPPAPGLPLPGPTN QTTGKSPQLQQDYFPRRSYRCS HRLIICLNVIGNAL*STVQLKAL MLRGRNYK
27308	57676	Α	27471	35	3801	
27309	57677	Α	27472	1	2901	
27310	57678	A	27473	1	1317	
27311	57679	A	27474	1698	3255	RVACPCVVWLCWAHWELWRT EEVEGGIAGTDVAR/EASDFILT DAIFSSIVKAVMASLQRRGSRE L*LPAAGVWKLQTDF*AQSI/AE EGIECKSIKPVLAKYLVWTRLF VGLLAELRDESAPETTPAGRRR QPQVWSGARQTCGQRTERLAG GLGEMQACSGNLGAEKEKQSK KLAGGWPMSPTSLHALGPKLV PAKSQRHRAEHMSTWQVGVVS SSYFTGNLVGTLLTGYVIKRIGF NRSYYLASFIFAAGCAGLGLMI GFWSWLAWRFVAGVGCAMIW VVVESALMCSGTSRNRGRLLA AYMMVYYVGTFLGQLLVSKVS TELMSVLPWVTGLTLAGILPLL FTRVLNQQAENHDSTSITSMLK LRQARLGVNGCIISGIVLGSLYG
						LMPLYLNYKGGKSSPTPAVRPA RHNSLPGPEAKKYRPGFIIGLTS CIAFSVQAANVDEYITQLPAGA NLALMVQKVGASAPAIDYHSQ QMALPASTQKVITALAALIQLG PDFRFTTTLETKGNVENGVLKG

SEQ ID	SEQ ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27312	57680	A	27475	152	468	GLGIQ*LLCCSSFCFQLLPEKKE GRLAGDAGAARPAKSGRFLGL TSGLPSEWSARTGPEPPKSLSG GGELNGSSLGFGTQDGRGTRE GRDRGLHPARPPQYQHSP
27313	57681	Α	27476	541	4172	
27314	57682	Α	27477	3	1110	
27315	57683	Α	27478	340	1032	
27316	57684	Α	27479	2	779	
27317	57685	Α	27480	3	281	
27318	57686	Α	27481	519	737	VPDLLLQLPNAGLCGHFCDPGD SLQCLCHQGPGFQAQNWAAV WADTKPAAGAEAREPGDLA*L VPPTWSPTR
27319	57687	В	27482	1	915	
27320	57688	Α	27483	68	145	
27321	57689	Α	27484	1281	1433	
27322	57690	Α	27485	171	708	
27323	57691	Α	27486	1	270	
27324	57692	A	27487	278	588	VYIKRMPKKKV/SEGTIKEEPKR RLAQLSAKPAPAKVEAKLKKA AAKDKSSGKNVQTKGKRRAK GKQAKVANQETKEDLPAENGE MKTEESPASDEAGEKETKSD
27325	57693	A	27488	304	513	PVRHGAFFQDKSSDKK\VQTKG KRGAKGKQA\EVAN\QETKEDL PVD\SGETKT\EESPSLLIEAGEK EAKS
27326	57694	Α	27489	1	435	
27327	57695	Α	27490	3	273	
27328	57696	Α	27491	9	293	
27329	57697	Α	27492	1	504	
27330	57698	A	27493	1	529	IPPPRLFLPVATEVARVRLLPPP PPQNAARDALTSPSYLAWASPR KQTPSPPAAKDIK\KILEQRGYP KADDDR\LNKVI\SEAEWKYTL KDVIAPGVLASLPSVP\AGGAV AVSACPQALAAPCCLGSAPA\A AEGEEKMKKKEEVLKES\DDD\ MGFGPFELKSLPPLQIKGLFYTS R
27331	57699	Α	27494	1	396	
27332	57700	Α	27495	2	398	
27333	57701	Α	27496	1	702	
27334	57702	Α	27497	1060	1446	
27335	57703	A	27498	46	216	HPLQLSVIPFLPVK*HVDQMGF AD/CVLSN*VNCLASRFLAVSV ALRSSRFIFTMVP
27336	57704	Α	27499	1	1152	
27337	57705	Α	27500	126	184	
27338	57706	A	27501	238	498	

27339 5 27340 5 27341 5	57707 57708 57709	A A	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27340 5 27341 5	57708 57709			sequence		,
27341 5	57709	Δ	27502	1	852	
		l /*\	27503	3	171	
27342 5	7710	A	27504	1064	1302	
	57710	A	27505	449	668	SPGDYFISLMAAMGRPQVGYW APELLQKMMRKRMNR/VKKLI QNYKQLK/CSLTLNNHVKLVRT NLRFHLAGLLG
	57711	Α	27506	1	2454	
27344 5	57712	A	27507	2	408	
	57713	A	27508	205	715	
	57714	A	27509	1	813	
	57715	A	27510	1	864	
	57716	Α	27511	17	396	
27349 5	57717	A	27512	3	428	LTNYAAAYCTGLLLARRLLNR LGMDKIYEGQVEVPGNEYNVE SIDGQPGAFTCYLVADLARTTT GNKVFGAPEGAVDGGLSNPHS SKRFLGLSIPHSTK*ILGYDSEN KEFNAEVRRKHIMGQKFADDL HCLIEEDENASKK
27350 5	57718	Ā	27513	164	431	EFFFSTSNIGVYLQIIHIVGKPI*H /YLV*ILSY*HLAARTISSKIKSN SLVPCASNRGDVGSTRRPRVTR RSVRYSAPAAPLRSPLFAR
	57719	A	27514	1307	1947	TNEGSGNSAPLFSGARNQTRMI VRGTNR/DIICQIAYARTEGDMI VCTAYVHELPKYGVKVDLTNY AAAYCTGLLLDRRLLNRFDMD KIYEGQVEATGDDYNVVSIDG QPEVHRKHIMGHNVADYMCY LMEEDEDGYKKQFSQYMKNSV TPDMMEEMCKKAHAAIRESPV CEKKPKKEVKKKKWNRPKMS LAQKKDWVAQKKASFLRAQE RAAES
	57720	A	27515	1	987	
	57721	A_	27516	1521	1641	W OD W WIDDLY OF THE STATE OF T
27354 5	57722	A	27517		614	ILSRVVEFPLTAEVPPELLAAAG FFHTGHQDKVRCFFCYGGLQS WKRGDDPWTEHAKWFPSCQFL LRSKGRDFVHSVQETHSQLLGS WDPWEEPED\EPLWPPPSLPLG TLSCPHPGERSSLKVPRSQEGSV QPRPRGRGGFLSPQ/DARDVEA QLRRLQEERTCKVCLDRAVSIV FVPCGHLVC\AECAPGLQLCPI WQKPPSRSR
27355 5	57723	A	27518	3	89	<u></u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
ļ				sequence		
27356	57724	IA	27519	1	1618	ASSHVETRAHAEERLLKKLFSG
2,000						YNKWSRPVANISDVVLVRFGLS
						IAQLIDVDEKNQMMTTNVWVK
		1				QEWHDYKLRWDPADYENVTSI
						RIPSELIWRPDIVLYNNADGDFA
						VTHLTKAHLFHDGRVQWTPPA
						IYKSSCSIDVTFFPFDQQNCTMK
		ł				FGSWTYDKAKIDLVNMHSRVD
l						QLDFWESGEWVIVDAVGTYNT
						RKYECCAEIYPDITYAFVIRRLP
ł						LFYTINLIIPCLLISCLTVLVFYLP
	į					SECGEKITLCISVLLSLTVFLLLI
						TEIIPSTSLVIPLIGEYLLFTMIFV
						TLSIVITVFVLNVHHRSPRTHTM
1						PTWVRRVFLDIVPRLLLMKRPS
1						VVKDNCRRLIESMHKMASAPR
						FWPEPEGEPPATSGTQSLHPPSP
						SFCVPLDVPAEPGPSCKSPSDQL
						PPQQPLEAEKASPHPSPGPCRPP
ŀ						HGTQAPGLAKARSLSVQHMSS
ļ						PGEAVEGGVRCRSRSIQYCVPR
1						DDAAPE\QMARLPAPWPLATPT
1		ļ				RLSSHPQTSPLRANAHARRSPL
					,	RCPRVPRSRPAAPKHRPRTCPC
27357	57725	$\frac{1}{A}$	27520	1	3158	Ref RVI RSRI AAI RIIRI RTELE
27358	57726	A	27521	2	237	
27359	57727	Α	27522	76	254	PLHITFFSRACFPSLHNCCEY*Q
						PGF*TS\KTPQLWCQLRQYSFK
						HSFLVVPTCPVPLLG
27360	57728	Α	27523	86	376	SLEGRLSDYTPTFQGCQTTQGR
1						LPWSFTLSGKSRFSGEGARACY
	ŀ					KCQKSDHQ\ARNACSPGFLLSRI
				1		PSVRDPTGNRTVQLTWQPLPEP
						LELWPKAL
27361	57729	A	27524	1	167	MPEPQRPGVPPEPPPGACYAC
						RKSGHWA\RNARSPGFLLSRVP
						SPPGPSRTPSFG
27362	57730	С	27525	1	381	
27363	57731	Α	27526	243	437	VTSTVRQTPATSPAHKNFQMPE
						PQRPGVTPEPSPPGACYKCQKS
						DYQA\RNACSPGFLLSRVPSV
27364	57732	В	27527	88	1485	
27365	57733	Α	27528	1	3759	
27366	57734	Α	27529	36	438	RNDRVRPHRDVYSLQGRLSDH
						SPTFQGCQTTQGRLPWSFTLSG
						KFRFSGEGATTSPAHKNFQTPE
						PQWPGIPPEPPPTGACYTCRKSG
						HWA\RNARRPGFLLSRIPSVWD
						PTENRTVQLTWQPLPEPLELWP
I				1	ŀ	KAL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27367	57735	A	27530	314	691	SLQGHLSDYTLTFQGCQTTQGH
2/30/	37733	^	27330	514		LPWSFTLSGKSRFSEEGTKGDV
		1				SGSQDNCGERVSRQTREQRSLH
		1				
						HRQGACYTCRKSGHWA\RNAR CPGFLLSCVPSVWDPTENRTVR
		1				
27368	57736	A	27531	383	2907	LTWQPLPEPLELWPKAL RSPTSKTKDICHRSWRRGL/WV
2/308	37730	A	2/331	363	2907	NKASEDGEDLDRDVSVASNIEP
		1				WTGWCRAAPLQADLGPNSSSA
		1				SAPPPYNPFITSPPHTWSGLQFR
		1				SVTSPPPPAQQFTLKKVAGAKG
						IVKHALKRLKPVITRLLQHGLL
						KPINSPYNSPILPVLKPDKPYKL
		1				VQDLRLINQIVLPIHPVLGIIGLT
		1				SSVRRDAGQDLKRDRAEFLLG
		1				DEVHHPHRRRIAEARRLLLGQH
		1				FDPLHRLIGQVLELGEARYAPP
						VEQHHRLAPARRTGQRLHPLE
						QFGQAGRAQRRNRLGIEHRDR
		1				LDRPDDGAGNALAGDGDFRRG
						CLFAGIGIRPRYCRYRQSQDDR RPSHAAPRPRALPIPHRPATPIA
						·
						DVMVMFSVAIMSQLRLVLRHI DGISRWPPAVVFITDVKIWLVY
		1				PSDDCRIRSNDRDDMQGEAPA
						MSMNAAARVGDPIGHSFSQGL
						FGEALDGLFFARRSEVDMRAG
						NLGRLIARGLSGGRWTPADGQ
						LTLGSRDVFINGPPATMTIRSTG
						QCRQHSGLRTVTRTETDSIGPIE
		1				VPADAYWGAQTERSLENFPFG
		1				AREOMPIGIVHALAIVKKAAAR
		l				INRGHGLAGEKADAIESAAHDV
		1				IEGRHDDQFPLVIWQTGSGTQS
					į	NMNANESSNDTFPTALHVAAA
						LAVTKQLFSALDRLHAALDAK
						AKEWDSIVKIGRTHLQDATPLT
						LGQEFSGYVQQLANARDRIEGT
27260	57737	1	27532	929	1227	
27369	13/13/	A	21332	727	1227	PENGTFEFSILQVLDNSCHKMG KWS/RGA*RPGILLHIGPSLVSA
						PNVTHPKSFFFLSFLFLRSPPQV
						PSPLNPSFLWTHLTSPLLPRLLL
27270	57720	1	27522	08	412	ARLSQVPILT
27370	57738	A	27533	98	412	LGSGDLPWEINPLSSCSLLCEKH
						PPTTSGPQTDQPKKHLTNFKSG
						ACYMCRK\SGHWA/RANARSPG
		1				FLLSRIPSVWDPT*KFGLVQLTL
27271	57720	1_	27524	14	249	GKPLPEPLELRP\RLSD
27371 27372	57739	A	27534	14	341	
27372	57740 57741	A	27535 27536	392	571	
41313	13//41	I'A	2/330	374	3/1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	ı	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27374	57742	A	27537	<u> </u>	1590	MPNGTNESHRYNASERSQTQK
2/3/4	37742	^	21331		1350	DEQTGKTVGPPEWTPLVRRNG
						GDSGLDFHFFAEKLKIIVDSAG
						i e
	1					RAGTGHMRPPAVHFGHRGQA
ŀ						MITLSPLRAKQKAVLQKPPPLT
						STYSLMLPLFLPDKRPPTTEWF
						LPVMEDAHELTLAWLMLALYR
				:		KPNASVQGSAQEETLCVFRVKE
		1				PLEWQALFADVHSGVNDKGPN
ŀ						INCSLYEHIKNVSEIVLNLAQTQ
	Ì					KNPAHSDPSSTPAGCM\PGTTA
						GGSAVMSACCPSPAAPGPLPGP
						ATGSC/SPSAAPRPPDPPPGHPE
						GIMAIRAAPSCLGACITLQDEET
		Ì			1	CEQTHTHSRIYMIYLFARCLLH
						AIARGRSRKCAASAGGTCPHVR
			,	·		VPGGGSYFRVSLQGQQTHWMR
						PENGFSTCVRTKSRRCPIIREQH
						PTKIPKALTANANQAFFLLVNG
						HSMVASPHQSQRRADLGGFWR
		1				DASSSLLANSQVQVCGSLRKRP
					Ì	HGWVVPFSLRCVAPLTADDSR
						LRTASLEMSTPPMHVQDDWQL
						RRGLPAGNTAVTVSELIYLNAN
						GRLQVEKFLF
27375	57743	Α	27538	279	759	
27376	57744	A	27539	443	696	
27377	57745	Α	27540	1	179	
27378	57746	Α	27541	3	1237	
27379	57747	Α	27542	4	152	
27380	57748	Α	27543	760	908	
27381	57749	Α	27544	203	570	
27382	57750	Α	27545	312	500	
27383	57751	Α	27546	1	441	
27384	57752	Α	27547	1	630	
27385	57753	Α	27548	1	1254	
27386	57754	С	27549	236	408	
27387	57755	С	27550	220	398	
27388	57756	С	27551	254	445	
27389	57757	Α	27552	1	2742	
27390	57758	Α	27553	1	744	
27391	57759	Α	27554	1135	1751	RPGSTLQVRQNYHQGLRRPPIN
		1				R\QINLE\LYAS\YVYLSMSY\YF
						DRD\DVALKNFAKYFLH\QSHE
						E\REHAEKT**KL\QNQRRLAEF
						FLQDYQRNQD\CDDWGRAGLN
		1				\A\MECALAFWKKNVESSHYW
						NLHKL\AT\DKN*PPIWCDFHW
						RHIYLE*AG*KAIKRIWGDHVN
						QTFA/RKMGSAPNLGFGEYLF*
						OSTPWGDSDNESSPWG
			1	L		ZOTI MODODIACOSI WO

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27392	57760	Α	27555	224	547	
27393	57761	В	27556	22	130	
27394	57762	Α	27557	1	408	
27395	57763	Α	27558	1	1011	
27396	57764	Α	27559	56	822	
27397	57765	Α	27560	146	411	
27398	57766	Α	27561	1	885	
27399	57767	Α	27562	115	1200	
27400	57768	Α	27563	791	1114	
27401	57769	A	27564	67	401	RLGSSGREVIHPGERGLENNVC/ H*SSGNQENELEMNKTANGDC RRDPRERSRSPIERAVAPTMSLF GSHLYTSLPSLGLEQPLALTKN SLDASRPAGLSPTL\TPGERQQN
27402	57770	A	27565	109	345	HPLFIFPDPLPPPTFHPLIGPRMC FSPGLALCPHPNLILNCSSHNSY VLWEGPGGK*FESWGRFPHDT VLVIVNKSHKI
27403	57771	С	27566	63	167	
27404	57772	Α	27567	231	314	
27405	57773	С	27568	99	323	
27406	57774	Α	27569	1	1347	
27407	57775	A	27570	192	269	WFYKGEFLCTHS/HCLLPRKTC LLPAAM*YCDSQFSMAGETSQS WQKAKEEQRHILHGGRQKARL TWQQAGECVHRNSPL
27408	57776	A	27571	107	797	AQWRRAAPPAAGVTCPFRLQP GMETPLDVLSRAASLVHADDE KREAALRGEPRMQTLPVAS\AL SSHRTGPPPISPSKRKF\SMEP\G DEDLDCDNDHVSKMS\RIFQPPI LNKTANGRLARRDPRERSRSPI ERAVAPTMSLHGSHL\YTSLPSL GL\EQPLALTKNSLDASRPAGLS PTLTPGERQQNRPSVITCASAG ARNCNLSHCPIAHSGCAAPGPA SYRRPPSATCV
27409	57777	A	27572	l	1686	
27410	57778	A	27573	1	1614	
27411	57779	В	27574	208	366	
27412	57780	A	27575	15	1729	
27413	57781	A	27578	1	1614	WALKER OF THE CHARLES OF THE CHARLES
27414	57782	A	27579	308	464	KAHHHWSLEKCKSEPQ*DTISW TWMKLETIILSKLPQEQKTRNC MFSLISGS
27415	57783	A	27580	291	378	
27416	57784	Α	27581	2	91	
27417	57785	Α	27582	439	519	
27418	57786	Ā	27583	2	91	
27419	57787	A	27584	2	91	
27420	57788	A	27585	2	91	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27421	57789	Α	27586	50	394	
27422	57790	A	27587	1	666	
27423	57791	Α	27588	2	91	
27424	57792	Α	27589	5	91	
27425	57793	Α	27590	884	991	
27426	57794	A	27591	290	460	
27427	57795	Α	27592	86	349	
27428	57796	A	27593	2	89	
27429	57797	Α	27594	723	882	
27430	57798	A	27595	255	352	TGTWMKLETIILSKLTQE\QKTK HCMFSLISGS
27431	57799	A	27596	l	1685	
27432	57800	В	27597	82	263	
27433	57801	A	27598	491	816	RHRGAQRKAFLQRVNCGLCCT WNLCPQKLRGRKWPVQVS\PA AGRDPGGPLL*PEGTLWGAPFC LGAPPPLLTAACAPAAGRAGGT RGAAPACPEDRTNAHSQHHHP HV
27434	57802	A	27599	645	1142	
27435	57803	A	27600	218	326	
27436	57804	A	27601	181	2316	
27437	57805	A	27602	2	238	
27438	57806	A	27603	709	1416	
27439	57807	Α	27604	3	501	SSRALRLLGVVVRIRQAGTMA VTKELLQMDLYALLGIEEKAA DKEVKKAYRQKALSCHPDKNP DNPRAAELFHQLSQALEVLTDA AARAAYDKVRKAKKQAAERT QKLDEKRKKVKLDLEARERQA QGQGE*GGRRESRSTRTLEQEIE RLREKGSRQLEEQQRLI
27440	57808	Α	27605	1	963	
27441	57809	Α	27606	135	384	
27442	57810	A	27607	349	679	SETYWFFPRESQHLDLDVWPPR SEHHSQSTGTHSGVSESLSPRYF QRCNAHSPSQGHEEQYLAPWK HRLYQRMSDLPLNDIR*FQYSK GHHRCQSNEAVQNPKQLQSLL
27443	57811	Α	27608	1590	2758	
27444	57812	Α	27609	123	2312	
27445	57813	Α	27610	1	1809	
27446	57814	C	27611	79	309	
27447	57815	С	27612	77	325	
27448	57816	Α	27613	1	606	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	1	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27449	57817	A	27614	2	686	SQCAELSASPLSPAPGLPRHSRL HALLGLAMPVDLSKWSGPLSL QEVDEQPQHPLHVTYAGAAVD ELGKVLTPTQVKNRPTSISWDG LDSGKLYTLVLTDPDAPSRKDP KYREW\HHFL\VVNMKG\NDISS GTVLSGIVG\SGP\PKGTGLHRY VWLVYEQG\RPLKCDEPIL\SN\ RSGDHRGKIQRWASLPVKK\YE APGPPVAGHRVTPSPKWDEPM CPQTVTKQLSWGK
27450	57818	A	27615	446	1300	
27451	57819	Α	27616	2	346	
27452	57820	A	27617	1	305	MAISTSGSSVPWPSA/PSGPHGR GS\PWGFCLATCWQSIRGQGGD PWSAGSGHPGTKGASAPGPGE GQSGGDSGSA/GR*GSHHLPGP ASFRAGSGQAWDGKGK
27453	57821	A	27618	287	475	
27454	57822	Α	27619	37	314	
27455	57823	Α	27620	1	367	
27456	57824	С	27621	360	610	
27457	57825	Α	27622	604	980	
27458	57826	В	27623	8	442	
27459	57827	Α	27624	1	2268	
27460	57828	A	27625	296	398	APPGPTLPWASTPSRGCT*APPG PTLPWASTPSRGCTSSWFMLPA MRRCGAPC
27461	57829	Α	27626	1	3633	
27462	57830	A	27627	1853	3809	
27463	57831	Α	27628		656	MTHNQEKNKSTNTEMTMMMK LADKDDKTAMINMLQVVKKV EEAMSMMRRNKDVKNIHGRA RWVKPMIPALWEAKEVEGKYS AHNFWGSWKFKSSSRSSSSGPE SPARTHASFCQPDGGPTNKLGT KAFRVSPASSLLVDLNTQEVEII NVRKATPTCSLELGRKRRDGA AERAALDVVVVIYQLAPAAAP NCLNPVTSRR/PPQTPAPEGQGR RQSFEE
27464	57832	Α	27629	127	273	
27465	57833	A	27630	3	405	AAFHARGHRAGLSASSCSWRC CPSSSAPCAPYAAPAARMLQTC LKQSPAGMPPASPSSPAAHSWG STSFSKYSPRSTSTSCCPCISSCW ESWPCPTPSSPL*NKFFPASFPN RQYQLLFTQGSGENKEKDHQL
27466	57834	A	27631	689	987	
27467	57835	A	27632	228	527	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27468	57836	A	27633	108	441	
27469	57837	С	27634	156	287	
27470	57838	A	27635	2	363	RFTKVEMKEK\MLSAAREKGR
						VTHKGKPISLKADLSAETLQAR
						REWGPIFNILKEKNFQPRISYPA
						KLSFISEQEIKYFTDKQMLRDFV
	1					ITRPALKELLKEALNMERNNW
						YQPLQKHAKL
27471	57839	Α	27636	2	367	
27472	57840	A	27637	1	936	
27473	57841	Α	27638	1	865	
27474	57842	Α	27639	11	1287	
27475	57843	Α	27640	1	2565	MGPGARLAALLAVLALGTGDP
	1	-				ERAAARGDTFSALTSVARALAP
						ERRLLGLLRRYLRGEEARLRDL
						TRCNDETITYLLDKRLTVLTAA
						NIPYSSPENGAKRRRQDAFPPIH
						YNTQDALLQYLSGVGWGAPPA
						AQAHRDAPFVDSIAQVLLRTSG
						GSAEASGWSLRSRWAVGGATG
					SWVLSKGDRASLGERVVTGWA	
						TLNVGRSFAYCLTTCVQPPLDV
						GPRKEHAPRPPSLSPTSTRQRGQ
						SERSQDANGRRKQKTKSEPERF
						EDAVLLAGFKVEEEPVQRPRRK
						EWFQGPSPGHCCPAQPQDSAPC
						ILATHAPARAQNAPGTAWAAA
1						LEGTSTVSLDHFHVVGVVVVS
						GGEIILLLSFRFYDKVLSLHEDS
						TTPVANPLLAFTLIKRLQSDWR
		İ				NVVHSLEASENIRALKDGYEKV
						EQDLPAFEDLEGAARALMRLQ
						DVYMLNVKGLARGVFQRVTGS
						AITDLYSPKRLFSLTGDDCFQV
						GKVAYDMGDYYHAIPWLEEA
						VSLFRGSYGEWKTEDEASLED
						ALDHLAFAYFREQSSSPATEQS
						WMENDFDELREEGFRRSNYSE
]						LQEEIRTNGKEVKSFEKKLDEW
						ITRITNAEKSLKDLMELKTKAR
						ELRDECRSLSSRCNQLEERVSV
1						MEDEMNETKRGEKFREKRIKR
						NEQSIQEIWDYVKRPNLRLIGV
						LESDRENGTKLENTLQDIIQENF
27476	57944	-	27641	210	451	<u> </u>
27476	57844	Α	27641	219	451	APAAEGAGRIS/PCSRHSPAGLE/
						WLCPHLCALF*QCPP/PTCHQSA
				1		SPR\WP*G/RPAAGPHPPAATVA
07.477	57045	 	07640	1027	5(1	PKRKGKTKSSTRE
27477	57845	A	27642	237	561	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27478	57846	Α	27643	3	461	TRTRRGSRTAEAR*CTPGWRPA
						GRRSALCSRGHLGP*RPPRTRS
						GAAPGPHSPCGRPDGAPCSRLP
		l				PHRSRSPPHGSHVPAAGWLSAG
		1				PHQRWPAAAAGPGTDQCRVVG
	1					PERASPHIWKGSTVPFLPSWTFL
:	1	1				RVLSVPGCSLPRCCWLGHCQ
27479	57847	Α	27644	2	159	
27480	57848	Α	27645	1	243	
27481	57849	Α	27646	219	462	
27482	57850	Α	27647	256	427	
27483	57851	A	27648	1	954	
27484	57852	A	27649	2	4690	
27485	57853	Α	27650	1	1275	
27486	57854	Α	27651	1	867	
27487	57855	Α	27652	1	472	
27488	57856	A	27653	2	1215	
27489	57857	Α	27654	3	401	
27490	57858	Α	27655	712	1245	
27491	57859	A	27656	2	1178	
27492	57860	Α	27657	278	339	
27493	57861	Α	27658	1	1407	
27494	57862	Α	27659	1	687	
27495	57863	Α	27660	484	776	
27496	57864	Α	27661	299	1318	
27497	57865	Α	27662	1	960	
27498	57866	Λ	27663	122	282	
27499	57867	Α	27664	1	600	
27500	57868	В	27665	1	375	
27501	57869	Α	27667	356	439	
27502	57870	Α	27668	49	360	
27503	57871	Α	27669	2	580	GRVGCGGPWAARVGERIPNMA
						GRKLAS*KPTD*VAFARD/IIPQ
		1				NPKAPLPSFLKS\WNGDPSPSRL\
]				AALP*ESHPAI\DWA*LPRPNVA
						QGLAWVDDFE\KKFNAAERFPC
		1				PEDK\YTAQVDA\EEK\EDVKSL
		1				C/AEWVSLSKA\RIVEYEKEME
						KMKNLIP\FDQMT\IEDLNEAFP
						ETKLDKKKYPYWAHQP\IENL
27504	57872	Α	27670	1	675	
27505	57873	С	27671	137	1357	
27506	57874	Α	27672	1	1032	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
27507	57875	Α	27673	3	938	MANNPGANGQ\PGGPGGPGMG
						KPRCF/RGEVFGIVIRGRGSRP/R
					}	GRGRGR\GRGARGSKGRG*RD
		l				W\VPVHQVGAALVKDH*RSKF
						PWKEIYLFSLPH/IKESEIIDF\FL
						GGLLSKDEGFE*LCPVQEQ\TRA
						GPAATR\FKAFCCYPGTTNG\HV
						G\LGVKCSQE\VAHRPFRGAI\IL
		1				AKL\SIVPVR\RGYWGNKIRKP\
		1				HTVP\CKVT\GRCGSVLVRLIP/S
						QPRGTGIVSAPVPNKL\LMMAG
		i				IDDCYT\SARG\CTATLG\NFAK
	ļ	:				AT\FD\AISKTYSYLTPDLWKET
:						VFTKSPYQEFTDQLVKDHTRVS
						VQRTQAPAVATT
27508	57876	Α	27674	1	864	
27509	57877	A	27675	2	752	RRAHACARRRRKKEMLGVNVL
						TSHSSQERMKLTFKKKAVNFA
						DAAAAQGPLLPAMVNPTMFFH
						IAVDGEPLGCVSFEVRGLESKK
						*LLI*SIKLC*QIG\LFADKVPKT
		l				AENFHALSTGEKGFGYKGSCFH
						RIIPGFMCQGGDCE/RHHNGTG
		1				GKSIYTEKFEDENFILKHTGPGI
						LSMANAGPNTNGSQFFICTAKT
1		1				EWLDGKHVLFGKVKEGTNIVE
1		Ì				AMERFGSRNGKTSKKITIADCG
						QLLISLTCVLS
27510	57878	Α	27676	3	327	AQELHTFEVTGQETVAQIKAHV
		1				ASLEGIAPEDQVVLLAGAPLED
ļ						EATLGQCGVEALTTLEVAGRM
						LGG\AKQEKKKKKTGRAKRRM
						QYNRRFVNVVPTFGKKKGPNA
27511	57879	Α	27677	567	838	

RHHTEEITVDHLLVRRGQAI TLYFRNRSFQPGLDNIIFVVE DAVYLDSEPQRQEYVMND IYQGSKNWIRPCPWNYGQF; KIIDICLKLLDKSLHFQTDPA CALRGSPYVSRVVCAMIN DDNGVLNGNWSENYTDGA AEWTGSVAILKQWNATGCC RYGQCWVFAAVMCTVMRC IPTRVITNFDSGHDTDGNLII YYDNTGRILGNKKKDTIWN VWNECWMARKDLPPAYGC VLDATPQEMSNGVYCCGPA RAIKEGEVDLNYDTPFVFSM ADCMSWLVQGGKEQKLHQ SSVGNFISTKSIQSDERDDIT: YKYEGGSLQERQVFLKALQ KARSFHGSQRGAELQPSRPI SQDSPRSLHTPSLRPSDVVQ KFKLLDPPNMGQDICFVLLA MSSQFKDLKVNLSAQSLLH. SPL.SPFWQDTAFITLSPKEAA PCKISYSQYSQYLSTDKLIRI LGEEKSSPEKILVNKIITLSY TINVLGAAVVNQPLSIQVIFS LSEQVEDCVLTVEGSGLFKI KVFIGVLKPQHQASIILETV. SGQRQIQANMRSNKFKDIKC	SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
TINVLGAAVVNQPLSIQVIFS LSEQVEDCVLTVEGSGLFKF KVFLGVLKPQHQASIILETV SGQRQIQANMRSNKFKDIKO 27513 57881 A 27679 1 756	27512	57880	A	27678	•	1923	ATMAQGLEVALTDLQSSRNNV RHHTEEITVDHLLVRRGQAFNL TLYFRNRSFQPGLDNIIFVVETE DAVYLDSEPQRQEYVMNDYGF IYQGSKNWIRPCPWNYGQFED KIIDICLKLLDKSLHFQTDPATD CALRGSPVYVSRVVCAMINSN DDNGVLNGNWSENYTDGANP AEWTGSVAILKQWNATGCQPV RYGQCWVFAAVMCTVMRCLG IPTRVITNFDSGHDTDGNLIIDE YYDNTGRILGNKKKDTIWNFH VWNECWMARKDLPPAYGGWQ VLDATPQEMSNGVYCCGPASV RAIKEGEVDLNYDTPFVFSMVN ADCMSWLVQGGKEQKLHQDT SSVGNFISTKSIQSDERDDITEN YKYEEGSLQERQVFLKALQKL KARSFHGSQRGAELQPSRPTSL SQDSPRSLHTPSLRPSDVVQVSL KFKLLDPPNMGQDICFVLLALN MSSQFKDLKVNLSAQSLLHDG SPLSPFWQDTAFITLSPKEAKTY PCKISYSQYSQYLSTDKLIRISA
27513 57881 A 27679 1 756							LGEEKSSPEKILVNKIITLSYPSI TINVLGAAVVNQPLSIQVIFSNP\ LSEQVEDCVLTVEGSGLFKKQQ KVFLGVLKPQHQASIILETVPFK
	27513	57881	Δ	27679	1	756	SOUNCIONING TRUIT
27514 57882 A 27680 1 2601		57882	—	<u> </u>	<u> </u>	2601	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
27515	57883	I A	27681	1	1677	MARKDLPPAYGGWQVLDATP
2/313	37863	^	27001	["		QEMSNGVYCCGPASVRAIKEG
1		ļ				EVDLNYDTPFVFSMVNADCMS
		l				WLVQGGKEQKLHQDTSSVGNF
						ISTKSIQSDERDDITENYKYEEE
						HFEAFQSVAQ\LPITRPFSWILRP
		1				F*RP*RKISTSFIRPLFTFL/LRLM
		l				NAHPEFRMAMKDAKTYPGKIS
		l		}		YSQDSQDLSTDKLIRISALGEEK
		l				SSPEKILVNKIITLSYPSITINLLA
		l				RVLSPSLPGPAGLASRSEYGPA
						KPTPTGNSSWPASAARSPGSRP
		1				CLSLHTSPQAEGAGSGLDQPRE
						RLPQCSGELKGSSSAARMGAE
	1	l				NEEAPRASEGCQGCQQAVTSQ
						QDGGPLLQNRFFWDCGDENGA
	1	1				DAVYLDSEPQRQEYVMNDYGF
						IYQGSKNWIRPCPWNYGQAASP
		1				WRYGQWWVFAAVMCTALGIK
		1				SCDFQAARNNEEHHTKALSSRR
		1				LFVRRGQPFTIILYFRAPVRAFL
		l				PALKKANKGKLESFSYICFFSIV
	1	1				FGSKNSYAKVAYLEVAYPATL
		İ				QNGALRKYLVLGAAVVNQPLS
]				IQVIFSNPLSEQVEDCVLTVEGS
						GLFKKQQKVLIP
27516	57884	Α	27682	1	1653	
27517	57885	Α	27683	3	2170	
27518	57886	Α	27684	2	244	ACPSTSTSHCRGATCSCSRTS\C
						SGVLQHSLRHCASGRGFSSRCP
						ACCGSPGLGLPAALPPAAWGL
						QIAPSPQGTPGNSQS
27519	57887	Α	27685	618	851	
27520	57888	Α	27686	78	240	
27521	57889	Α	27687	860	1246	
27522	57890	В	27688	1	2301	

NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27523	57891	A	27689		1719	MHNTDGNRFLSHWGYRQALSI SKPASASLHPSSKTKPLGTQSKT VVAKRNREHGKKERSSSPAME QSWMENDFDELREEGFRRSNY SELREDIQTKGKEVENFEKNLE ECITRITNTEKCLKELMELKTK ARELREECRSLRSRCDQLEERR KQERSKIDTLTSQLKELEKQEQ THSKAGRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTDPTEIQTTIREYYKHLYA NKLENLEEMDTFLDTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL HINRAKDKNHMIISIDAEKAFD KIQQPFMLKTLNKLVLEVLARA IRQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLLS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKHLFKENYKPLLK EIKEDTNKWKNIPCSWV\GRINI VKMAILPKVIYRFNAVPIKLPM TFFTELEKTTLKFIWNQKRACIA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		;		sequence		
27524	57892	A	27690	<u> </u>	1902	MNAKALPTLSPLPQATTESVSL
2732.	0,02	1.	2,020			TQERSSSPATEQSWTENDFDEL
						REEGFRRSNYSELREDIRTKGK
						EVENFEKNLEECITRIINTEKCL
		1				KELMELKTKARELREECRSLRS
						RCDQLEERVSAMEDEMNEMK
						REGKFREKRIKRNEQSLQEIWD
		İ				YVKRPNVRLIGVPESHGENGTK
						LENTLQDIIQENFPNLARQANIQ
						IQEIQRTPQRYSSRRATPRHIIVR
						FTKVEMKERMLRAAREKEIQT
ļ		1				TIREYYKHLYANKLENLEEMD
						KFLDTYTLRRLNQEEVESLNRPI
						TGAGIEAIINSLPTKKIPGPDGFT
						AEFYORYKEELRIKYLGIOFTR
1						DVKDLFKENYKPLLKEIKEDTN
						KWKNIPCSWVGRINIVKMAILP
						KVIYRFNAIPIKLPMTFFTELEK
						TTLKFIWNQKRARIAKSILSQK
ŀ						NKAGGITLPDFKLYYKATVTKT
1						AWYWYQNRDIDQWNRTEPSEI
						MPHIYNYLIFDKPEKNKQRGKD
İ						SLFNKWCWENWLAICRKLKLD
ļ						PFLTPYTKINSRWIKDLNVRPKT
ŀ						IKTLEENLGITIQDIDMGKDFMS
						KTPKAMATKAKIDKWDLIKLK
İ						ELLTAKETTIRVNRQPTKWEKI
						FTTYSSDKGLISRIYNEL/KQIYK
						KKTNNPIKKWAKDM
27525	57893	T _A	27691	11	2781	MGKKONRKTGNSKKOSASPPP
12,323	3,000		2,03,			KERSSSPATEQSWMENDFDEM
1						REEGFRRSNYSELREDIQTKGK
						EVENFEKNLEECITRITNTEKCL
						KELMELKTKARELREECRSLRS
			İ			RCDQLEERVSVMEDEMNEMN
						DGENGTKLENTLQDIIQENFPN
						LARQANVQIQEIQRTPQRYSSR
						RATPRHIIVRFTKVEMKEKMLR
						AAREKDFKPTKIKREKEGHYIM
						VKGSIQQEELTILKIYAPNTGAP
1						RFTKQVLSDLQRDLD
27526	57894	В	27692	1	756	
27527	57895	В	27693	1	1743	
27528	57896	Α	27694	1	1407	
27529	57897	Α	27695	3	391	
27530	57898	Α	27696	604	955	SSVFLGDPPILIGNKEMCLSSVL
						LINGSINFLHPFREDKGAVDVP
						GVATQQLILLNDPVLTASEILG\
						LVSSLSK*TSPPIPGPGGNA*AR
						QPSCP*KGELSWRSAPSLVQFSS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27531	57899	A	27697	1	1783	MGARAGGSCSCLMWLLLASG HFMGCVAAGDTVGPEKFRSCY
			ŀ			TITLLQSKLSYSFGKNNKNFQL
						RKCLQTVDNLFVPNQNGYYCH
•						SQTSLDRAQIDLNGRIRNGSVY
						SAHSTNSLNNPQPYLQPSPMSS
						NPSITGSDVMRPDYLPSHRHSA
						VIPPSYRPTPDYETVMKQLNRG
į						LVHAERQSHSLRNLNIGSSYAY
İ		1				SRPAALVYSQPEIREHAQLPSPA
		1				AAHCPFSLSYSFHSPSPYPYPAE
		ŧ				RRPVVGAVSVPELTNAQLQAQ
						DYPSPNIMRTQVYRPPPPYPPPR
						PANSTPDLSRHLYISSSNPDLITR
						RVHHSVQTFQEDSLPVAHSLQE
						ERSSSPATEQSWTENDFDELRE
				! !		EGFRRSNYSELREDIQTKGKEV
		1				ENFEKSLEECITRITNTEKYLKE
			,			LMELKTKARELCEECRSLRSQC
						DQLEERVSAMEDEMNEMKRE
						GKFREKRIKRNEQSLQEIWDYV
						KRPNLRLIGVPESDGENGTKLE
					1	NTLQDIIQENFPNLAKQANVQI
						QEIQRTPQRYSSRRATPRHIIVR
						FTKVEMKEKMLRAAREKGRVT
						LKG/ITHQT/RQRISRQKLYKPEE
						SGGQYSTFLKKRIFNPEFHIQPN
27532	57900	Α	27698	3	1046	
27533	57901	Α	27699	1	3585	
27534	57902	Α	27700	937	1119	

27535 57903 A 27701 1 2231 MGKKQSRKTGNSKKQSASP KERSSTPATEQSWSENDFDE EEGFRRSNYSKLQEEIQTKG VKHFEKNLDECITRITNREK: KELMELKAKARELREECRSI QCDQVEERTLARLIKKKRE QIDAIKIDKGDITTNPTETQT EYYKHLYTNKLENLEEMDK DTYTLPRLNQDDVESLNRPI SEIEAINHSLPTKKSPGPDRF KFYQSLPSSCDYGHAPAHPL RVSSFWWRGLAGSGVKLQ AVSVTALKAARLELFIPPDSG QLASPSGSLTRTGGGAACQS VCPHSSAFGWSMGLGAMEG AALIGEARASREPMEEVGGS MAACRSQALPRGQLRPSEK: APEHSSSPAMEQSWMENDF LREEGFRRSNYSELREDIQTE KEVENFEKNLEECITRITNTE LKELMELKTKARELREECRE SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEITYVKRPNLHLIGVPESDGENG LENTLQDIIQENFPNLARQAI IQEIQRTPQTYSSRRATPRHII	SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
27535 57903 A 27701 I 2231 MGKKQSRKTGNSKKQSASP KERSSTPATEQSWSENDFDE EEGFRRSNYSKLQEEIQTKG VKHFEKNLDECITRITNREKI KELMELKAKARELREECRS; QCDQVEERTLARLIKKKRE QIDAIKIDKGDITINFTETQT EYYKHLYTNKLENLEEMDK DTYTLPRLNQDDVESLNRPI SEIEAINHSLPTKKSPGPDRF KFYQSLPSSCDYGHAPAHPE RVSSFWWVRGLAGSGVKLC AVSVTALKAARLELFIPPDSI QLASPSGSLTRTGGGAACQS VCPHSSAFGWSMGLGAMEQ AALIGEARASREPMEEVGGS MAACRSQALPRGQLRPSES: APEHSSPSAMEQSWMENDF LREEGFRSNYSELREDIQTI KEVENFEKNLEECITRITNTE LKELMELKTKARELREECRS SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIT YVKRPNLHLIGVPESDGENG LENTLQDIQENFPNLARQAI IQEIQRTPPQTYSSRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLLYFRGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLK, MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAR	NO:	of peptide	hod	in USSN			_ · · · ·
27535 57903 A 27701 I 2231 MGKKQSRKTGNSKKQSASP KERSSTPATEQSWSENDFDE EEGFRSNYSKLQEEIQTKG VKHFEKNLDECITRITNREK KELMELKAKARELREECRSI QCDQVEERTJARLIKKKRE QIDAIKIDKGDITTNPTETQT EYYKHLYTNKLENLEEMDK DTYTLPRLNQDDVESLNRPI SEIEAINHSLPTKKSPGPDFF KFYQSLPSSCDYGHAPAHPI RVSSFWWVRGLAGSGVKLQ AVSVTALKAARLELFIPPDSI QLASPSGLTTRTGGGAACQS VCPHSSAFGWSMGLGAMEC AALIGEARASREPMEEVGGS MAACRSQALPRQQLPSEKS: APPENSSPAMEQSWMENDF LREEGFRSNYSELREDIQTH KEVENFEKNLEECITRITNTE LKELMELKTKARELREECRS SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIV YVKRPNLHLIGVPESDGENC LENTLQDIQENFPNLARQAI IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVT PEQRLENVELAGGHLNTLK, MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAI KKGYLJWMEDEMNEMKQEC REKRLKRNEQSLQEIWDYVI		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
KERSSTPATEQSWSENDFDE EEGFRRSNYSKLQEIQTKG VKHFEKNLDECITRITNREK KELMELKAKARELREECRSI QCDQVEERTLARLIKKKRE QIDAJKIDKGDITTNPTETQT EYYKHLYTNKLENLEEMDK DTYTLPRLNQDDVSSLNRPI SEIEAINHSLPTKKSPGPDRF KFYQSLPSSCDYGHAPAHPE RVSSFWWYRGLAGSGVKLC AVSVTALKAARLELFIPPDSS QLASPSGSLTRTGGGAACQS VCPHSSAFGWSMGLGAMEC AALIGEARASREPMEEVGGS MAACRSQALPRGQLRPSEK: APEHSSSPAMEQSWMENDF LREEGFRRSNYSELREDIQTI KEVENFEKNLEECLTIRITNTE LKELMELKTKARELREECRS SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIPYVKRPNLHLIGVPSDGENG LENTLQDIIQENFPNLARQAI IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVF PEQRLENVELAGGHLNTLK, MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAIR KKGYLVWMEDEMNEMKQEC REKRLKRNEQSLQEIWDYVI					sequence		
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AALIGEARASREPMEEVGGS MAACRSQALPRGQLRPSEKS APEHSSSPAMEQSWMENDF LREEGFRRSNYSELREDIQTE KEVENFEKNLEECITRITNTE LKELMELKTKARELREECRS SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIV YVKRPNLHLIGVPESDGENC LENTLQDIIQENFPNLARQAI IQEIQRTPQTYSSRRATPRHII FTK VEMKEKMLRA AREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 I593 KPRLENYVKNAEASGANARI KKGY/LVMEDEMNEMKQEC REKRLKRNEQSLQEIWDYVI							1
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APEHSSSPAMEQSWMENDF LREEGFRRSNYSELREDIQTE KEVENFEKNLEECITRITNTE LKELMELKTKARELREECRS SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIV YVKRPNLHLIGVPESDGENG LENTLQDIIQENFPNLARQAI IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAII KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							AALIGEARASREPMEEVGGSG
LREEGFRRSNYSELREDIQTE KEVENFEKNLEECITRITNTE LKELMELKTKARELREECRS SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIV YVKRPNLHLIGVPESDGENO LENTLQDIQENFPNLARQAI IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 I593 KPRLENYVKNAEASGANAII KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI					1		MAACRSQALPRGQLRPSEKSRA
KEVENFEKNLEECITRITNTE LKELMELKTKARELREECRS SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIV YVKRPNLHLIGVPESDGENG LENTLQDIIQENFPNLARQAN IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAN KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							APEHSSSPAMEQSWMENDFDE
LKELMELKTKARELRECCES SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIV YVKRPNLHLIGVPESDGENG LENTLQDIIQENFPNLARQAN IQEIQRTPQTYSSRRATPRHIN FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAM KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							LREEGFRRSNYSELREDIQTKG
SRCDQLEERVSAMEDEMNE QEGKFREKRIKRNEQSLQEIV YVKRPNLHLIGVPESDGENG LENTLQDIIQENFPNLARQAI IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLK/ MVAVAGGISFKCGAVLLLG. 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAII KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI	l						KEVENFEKNLEECITRITNTEKC
QEGKFREKRIKRNEQSLQEIV YVKRPNLHLIGVPESDGENG LENTLQDIIQENFPNLARQAN IQEIQRTPQTYSSRRATPRHIN FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG. 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAM KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI	}						LKELMELKTKARELREECRSLR
YVKRPNLHLIGVPESDGENG LENTLQDIIQENFPNLARQAN IQEIQRTPQTYSSRRATPRHIN FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG. 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAM KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI		Ì					SRCDQLEERVSAMEDEMNEMK
LENTLQDIIQENFPNLARQAN IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG. 27536 57904 A 27702 596 I593 KPRLENYVKNAEASGANAN KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							QEGKFREKRIKRNEQSLQEIWD
IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAII KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI			ĺ				YVKRPNLHLIGVPESDGENGTK
IQEIQRTPQTYSSRRATPRHII FTKVEMKEKMLRAAREKGI ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAM KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI		1			<u> </u>		LENTLQDIIQENFPNLARQANIQ
FTK VEMKEKMLRA AREKGI ERSFSNKA ELLFQLHGHQRE SKKEAQV WRDKGLYFRKGI QAQSWSRQVA SILGAQIQVE PEQRLENVELAGGHLNTLK, MVAVAGGISFKCGAVLLLG. 27536 57904 A 27702 596 1593 KPRLENYVKNA EASGANAM KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							IQEIQRTPQTYSSRRATPRHIIVR
ERSFSNKAELLFQLHGHQRE SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLK, MVAVAGGISFKCGAVLLLG. 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAM KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI				İ			FTKVEMKEKMLRAAREKGDSV
SKKEAQVWRDKGLYFRKGI QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 I593 KPRLENYVKNAEASGANAM KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							
QAQSWSRQVASILGAQIQVE PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAM KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							
PEQRLENVELAGGHLNTLKA MVAVAGGISFKCGAVLLLG. 27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAR KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							_
27536 57904 A 27702 596 I593 KPRLENYVKNAEASGANAR KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI							
27536 57904 A 27702 596 1593 KPRLENYVKNAEASGANAM KKGY/LVMEDEMNEMKQEC REKRLKRNEQSLQEIWDYVI							
KKGY/LVMEDEMNEMKQEG REKRLKRNEQSLQEIWDYVI	27536	57904	A	27702	596	1593	
REKRLKRNEQSLQEIWDYVI	27330	37704	``	27702	370	1373	
1 1 1 1 1							1
			1				LQDIIQENFPNLARQATVHIREI
							QRTPQRFSLRRSTPRHIVRFSKV
							1 ` `
							ETKEKMLRAAREKEIQTTIREY
							YKHLYTTKLENLEEMEKFLDT
							YTLPRLNQKEVESMKRPITSSEI
							EAVINILPIKRSPGPDGLTATFY
			1				QRYKEELERSSSPATEQSWMEN
			İ				DFDELREEGFRRSNYSELREDIQ
							TKVKEVENFEKNLEECITRITNT
							EKCLKELMELKTKARELREECR
SLRSRCDQLEERVSAMEDEN		1					

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27537	57905	Α	27703	717	1803	STGRKAPHHTYSKIDHILGSKA
						LPSKCKRT/E/IITNCLSDHSAIKL
						ELRIKKPTQNPSTTWKLNNLLL
						NDYWVNKEMKSEIKMFFETNE
						NKNTTYQNLWDAFKAVCRGK
						FIALNAHKGKQERSKIDTLTSQ
			:			LRELEKQEQTHSKVSRRQEITKI
ļ						RAEPKEIETQKTLQKINESRSWF
						FERINKIDRRLARLIKKKREKNO
						RDAIKNDEGDITTDPTEIQTTIR
			ļ			EYYKHLYANKLENLKEMDKFL
1						NTYTLPRLNQEEAESLNRPIAGS
		l				EIVAIINSLPTKKSPGPDGFTAEF
		ĺ				YQRYKEKLVFGAGYFGMWAL
						AALPSNLLKLSQLCQEAAEVNV
						LVQFVCICPAQEPTEIDVLFSVL
		•				PPLSLILN
27538	57906	Α	27704	407	1696	NILRNAVPHQQQNKA*RRMTL
						TS*EKKASDDQTTPSYRRKFKA
						KAKKLNT/YEKNLDECITRITNR
	1	1				EKCLKELMELKAKARELREEC
		ł				RSLRSQCDRLEERVSVMEDEM
					ļ	NEMKREGKFREKGIKRNEQSL
						QEIWDYVKRPNLHLIGVPESDR
	ļ					ENGTKLENTLQDIIQENFPNLAR
	}					QANIQIQEIQRMPQRYSSRRATP
						RHIIVRYTKVEMKEKMLRAAR
						EKGRVTHKGKPIRLTADLLAET
}						LQARREWGPIFNILKEKNFQPRI
						SYPDKLRFISEGEIKYFTDKQML
						RDFVTTRPALIEALKEVLNMER
		İ				NNRSPSSSPATEQSWMENDFDE
						LREEGFRRSNYSELREDIQTKG
						KEVENFEKNLEECITRITNTEKC
						LKELMELKTKARELREECRSLR
1						SRCDQLEERVSAMEDEMNEMK
						REGKFREKNNKKK
27539	57907	Ā	27705	2597	5904	
27540	57908	A	27706	1	675	
27541	57909	С	27707	137	1357	
27542	57910	Α	27708	1	1032	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27543	57911	A	27709	3	959	MANNPGANGQ\PGGPGGPGMG KPRCF/RGEVFGIVIRGRGSRP/R GRGRGR\GRGARGSKGRG*RE WNAVHQVGAALVKDH*RSKFP WKEIYLFSLPH*RNQRIIDF\FLG GLLSKDEGFE*LCPVQKQTRA\ GQPHPGFKA\FVAIGDY\NGHV
						GLG\VKCSKE\VATGHPVGAII\L AKLSIRPRCAEGYLGNKVLAKP \HTVPLQGDKGRCG\SVLVRLH PLHPRG\TGI\VSAPVA\KKLLM MA\GIDDCYTLS/ARGCTATLG QIWPRAT\FDAISKTYKLP*PPD LWKETVFTKV\PYQ\EFT\DHLV
		ļ				KDPHPESSVQQDSELQLVATT
27544	57912	В	27710	50	1598	
27545 27546	57913 57914	A	27711 27712	334	3916 462	PAFITVNKCSSARKLIQV*GPVA CRVHILPLVVRCPPKPGTTG
27547	57915	A	27713	256	654	
27548	57916	A	27714	1	855	
27549	57917	A	27715	211	436	
27550	57918	A	27716	19	319	
27551	57919	A	27717	987	1392	RHCLCSPSRSSESLQPTASSSSA RSSPSPPASQPVPPGPAGAAAAP HPPCCPPESTCWTWPC*SPLCH WAVA*ARSGPGPLGECFETHGP HGCPPGQSPRPPQ*APSAWWTE VQPR*PRPAPEGSSRRPPPPGAP
27552	57920	A	27718	285	1266	RSQIQRGTDRAPKCTSGPP\HRV AQPQDDAPREEPPYLPNGMPPG RDAPHLPDWAASQRGSSHPRR WPPSQRRSLLPRRVADRPEAAI SALWEAKAGGWETLPEMEITIH NKTRQSKRITHQTNRPNTSSKTI RITKTDLTSWETQSPGSPDRHR KPSTATKHNRFSKIYSRFSIFQC DQGLNGRCGQGKGAGKEQRM QEQGENFQAPPFQSHPALRSLQ MQQVQTEEHFGTLECGKLAQC SFHPTREEDRNQDGKTDMLHF KLELPLQSTEHVLGVQLILTFSY RLHSCGIPSVLSRYPYFSMLAFG ILSRTLRRFVTVSSLLITGI
27553	57921	A	27719	1518	1779	ARSGPGPLGECFETHGPHGCPP GQSPRPPQ*APSAWWTEVQPR* PRPAPEGSSRRPPPPGAPCPAQP PTRRCPGRHQTPPAAGAAVP
27554	57922	A	27720	507	1114	
27555	57923	C	27721	80	223	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	• •
27556	57924	A	27722	11	2373	
27557	57925	A	27723	2	272	RARTPPLWPRARGPGSRVSGAP WFLLDLAGGGFLPPAVLCDLSA ASSTVSGRSNPHC*AWGGLEFF GEVERAESGFPVPEPSLISEMPH
27558	57926	A	27724	195	489	
27559	57927	Α	27725	210	1308	
27560	57928	Α	27726	203	474	
27561	57929	Α	27727	224	892	
27562	57930	Α	27728	l	457	
27563	57931	Α	27729	3	1325	
27564	57932	Α	27730	322	512	
27565	57933	Α	27731	621	737	
27566	57934	Α	27732	441	588	
27567	57935	Α	27733	1	792	
27568	57936	A	27734	8	488	SGCRNSARADADPSLHASPPAP TMATVQLLEGRWRLVDS\KGF DEYMKE\LGVGIALRKMG\AMP KP\DCIITCDGKNLT\IKTESTLK TTQFSCTLGEKFEETTADGRKT QTVCNFTDGALVQHQEWDGK ESTITRKLKDGKLVVECVMNN VTCTRIYEKVE
27569	57937	Α	27735	861	2161	
27570	57938	A	27736	349	625	
27571	57939	Α	27737	1	630	MAQETNHSQVPMLCSTGCGFY GNPRTNGMCSVCYKEHLQRQN SSNGRISPPATSVSSLSESLPVQC TDGSVPEAQSALDSTSSSMQPS PCIK\QSLLSESVASSQLDSTSVD KAVPETEDVQASVSDTAQQPSE EQSKSLEKPKQKKNRCFMCRK KVGLTGFECRCGNVSCES\HRY SDVHNCSYNYKADAAEEN/LE KENPVVVGEKIQKI
27572	57940	Α	27738	1	1089	
27573	57941	A	27739	41	334	AGKMTKLEEHLEGIVNISPQ*S VRKGHFDTLSKG\ELKQLLTKE LANT\IKNIKDKAVIDEIF\QG\LD ANQDE\QVDFQEFIS\LVAIALK AAHYHTHKE
27574	57942	A	27740	1	519	
27575	57943	A	27741	28	314	
27576	57944	A	27742	208	421	
27577	57945	Α	27743	619	890	
27578	57946	A	27744	113	328	LGSGAWGGGDLPWEINPLSSCS LLREKDLLTTSGPQT\TSPRNISP ILNRDPTVQLTWQPLPEPLELW PKAL
27579	57947	A	27745	501	680	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27580	57948	A	27746		405	RPRSERLLWGTSPLS/CALTL*G DPPTTSGPQTNQ\PRNISPISNRD PTGKWTVQLTRQPLPEPLELWP KALRLTPSQIFSA
27581	57949	A	27747	425	484	
27582	57950	A	27748	448	520	
27583	57951	A	27749	3	679	GGGFSDRDRTIALQPGQQIWM WGIGKQVGGCGWLRGKNRVV GAAKDQSGTGEKFYFIPKAMG AMEGSGQRRTLPDPGAHRNPS GGYSATDCEGSRPAPGEINSHA SHTKPVWWFFTQTRMKFGAVT RIGGLPWEVNPLSSCSLLREKD PPTTSGPQT\TSPRNISPILNPELA TLAGNLATGPRNARSPGFLLSR VPSVWDPTENRTVQLTWQPLP
		<u> </u>				EPLELWPKAL
27584	57952	A	27750	3618	3848	NLCKEPSSRRSIHKESLLNFPLM GLDPRPQEGFPRDSPR*REESTS LHDPMASSSSTVFWGLKRQKY FLWPFRAST
27585	57953	A	27751	1	297	
27586	57954	A	27752	244	420	RKETKERSRTPP*SPRTGQMTP CKLQPGVLSFPRTAQSWEPPAV PQSPLKNELRRKYLT
27587	57955	Α	27753	1993	2205	
27588	57956	Α	27754	138	833	
27589	57957	Α	27755	1	875	
27590	57958	Α	27756	1	1041	
27591	57959	Α	27757	3	1447	
27592	57960	Α	27758	23	3257	
27593	57961	A	27759	2	168	GKAGCWPRSRARKCRTSSPSIW AAWRPPTR*LTVTSRPGTSGSE PWAMAAASRWQ
27594	57962	Α	27760	85	1271	
27595	57963	A	27761	5871	6056	TSSAASTAPRWRRKPHGHQKSL PASLRFPGR*TPQPDLPGPPAQP PAQPGPPQAATVPGRW
27596	57964	A	27762	1	280	
27597	57965	Α	27763	1	714	
27598	57966	A	27764	2	558	RRAHACARRRRKKEMLGVNVL TSHSSQERMKLTFKKKAVNFA DAAAAQGPLLPAMVNPTMFFH IAVDGEPLGCVSFEVRGLESKK *LLI*SIKLC*QIG\LFADKVPKT AENFHALSTGEKGFGYKGSCFH RIIPGFTCQSGDFTRHT/GIGGKS ICREKFDDKNFILKHTGPGILSM ANAGPSVNV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27599	57967	Α	27765	1	927	GTRDATAEENRVLLAMVNPTV
						FFDIAVDGEPLGRVSFEVRGLD
						TKK*LLI*SIKLC*QIGGSSIFITS
						D*KNSCLPLIVQQCLLFLRILP\L
						FADKVPKTAENFRALSTGEKGF
						GL*GVPCFHR\IIPGFM\CQG\GD
			1			FTPP*MAPGGKSIYGEK\FEDEN
			:			FI\LKHTGPGILS\MANAGPNTN
						GSQFFICTAKTEWLDGKP\VVF
						GK\VKKGLNIVEAMERFGSRNG
						KTSKKITIADCGQLLISFDLCFIL
						NHQDHSFCALLSGEHPSTPFAR
		1	İ			RILRILWLSLQFLWGSMFSLFPP
		1				MPSWIAAVKFMIIEIKTK
27600	57968	Α	27766	1	798	
27601	57969	Α	27767	1	575	PTRPPTRPPTRPIMAQDQGEKE
		1				NPMRELRIRKLCLNICVGESGD
						RLTRAAKVLEQLTGQTPVFSKA
						\RYTVRSFGIRRNEKIAVHCTVR
]						GAKAEEILEKGLKVREYELRKN
						NFSDTGNFGFGMQDHIDLGIIY
						DPSIGIYGLDFYVVLGRPGFSIA
]			DKKRRTGCIGAKHRISKEEAMR
						WFQQKYDGIILPGK
27602	57970	A	27768	1	1695	,. ====
27603	57971	A	27769	1	228	HUDDAD CANAGES FOR A TUE
27604	579 7 2	Α	27770	1098	1938	IWPRPRDC/RVSYTTVFPPATVT
						APV/VSGGSHDHIQQYSDIEDFR
						QATAASSVMVARAAMWNPSIF
						LKEGLRPLEEVMQKYIRYGGM
						GAALLSDPDKIEKAPSMGTLM
]	GVYLPCLQNIFGVILFLRLTWM
						VGTAGVLQALLIVLICCCCTLL TAISMSAIATNGVVPGYLHTLV
						QNLVNNGYVRDETVRAAPYD
						WRLEPGQQEEYYRKLAGLVEE MHAAYGKPVFLIGHSLGCLHLL
						YFLLRQPQAWKDRFIDGFISLG
27605	57973	A	27771	1	1710	APWGGSIKPMLVLASGSGTRA
27606	57974	A	27772	163	1659	
27607	57975	A	27773	3	297	
27608	57976	A	27774	3	447	SSPHSSRSLSAPPLPGLPLWRHL
			1			RSPSAHRCTVGAPFWAGEGRSP
						LPQLAGRCGGRRASGNRG\ARG
		1				ACGPAGVPGGRGLGGPALGAA
		1				GRPGP*LPSRGAGLGTA/GPPCL
		1				SLPPPPWVPVQPEPPRRAPPPAP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27609	57977	A	27775	3	197	RPDAVPARSLEMKRFPMPPPPP\
27007		'`	21113	ľ		G*FSPGASLDVNPGCYKQAPSC
						SLAQILSNLSNLWSSAVSNF
27610	57978	A	27776	77	379	GRLLDKAGIPH/PPFPSGGLGCQ
27010	31776		2///0	1 ′′	317	H*RRSPLHEHPSSGP\PAGLKPS
						LSCLPAGQGSGPAARY/GLSLPP
						TPWAPVQPEPPRRAPPPAPGRS
						VPSTTQGLRSASA
27611	57979	A	27777	177	444	RGGQGSGPAACYA*/RLPPTPW
27011	31313	^	2////	177		APVRPEPPQRAPPPAPRRPVPST
						TQGLRSASTRRVTGRQLHLQP
						WCGIHWVKPAGLLSLVGRWRV
						LMS
27612	57980	A	27778	165	591	QRAGSPHSPRSLSAPPLPGLPLW
2/012	3/900	^	21110	103	391	RHLRSPSAHRCTVRAPFWAGQ
ŧ						GRSRLPQLAGRCGGRGASGNP
ļ						G\SHGACGPAGVPGGRGLGGPR
}						
						TGSSQLALPAPGNEGLSTPASG
						RRKKLRTHPSIRRNKLQTRYLK
27612	57001	 	07770	1	1605	SCNTHREGPRLH
27613	57981	A	27779	1	1605	
27614	57982	A	27780	2	1970	
27615	57983	A	27781	1	3522 254	
27616	57984	C	27782	183		OVICEI OEL ACTUDOTDATEDALI
27617	57985	Α	27783	39	346	QYISELQFLASTVRQTPATSPAH
						KNFQTPEPQQPGIPPEPPPPGAC
						YKCWKSGHQAKECLQPGIPRK/
						HASHLWQPLPEPPGTLAQGSLT
07(10	57006	 	27704	1	254	DSFPDLLGLAAED
27618	57986	A	27784	72	354	
27619	57987	A_	27785		299	L CCCDI DWCDIDI CCCCI I DEV
27620	57988	Α	27786	273	530	LGSGDLPWGINPLSSCSLLREK
						DPLTISGPQTHQPKEHLTNFKSG
						PH*KSDCSTAPG\ATPRAPGTLA
27(21	57000	+	27700	11	1069	QGALTDSFPDLLSLAAED
27621 27622	57989	A A	27790	148	1068	
27623	57990	A	27791		1910	
	57991	A	27792	2	L	
27624	57992	A	27793	1	1047	WDDMAGGSSNTEGEDDDDI DVD
27625	57993	Α	27794	96	488	WDRMAGGSSNTFGFPPPPLPYR
}						SCER*QRDGGPRSPGSLSVPPW
1						PR/PPILAALEEPFSPPLHRGRPS
				1		LGWPRPELAPSAQRSAAS/RPEA
						SKDHEPTRKKE/PTPDTQP*EL*
25.55	L	1	0.000.5	<u> </u>	0000	HSLPRSSASLALGPHYLYEL
27626	57994	A	27795	3	2086	
27627	57995	A	27796	3	412	
27628	57996	Α	27797	2	390	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27629	57997	A	27798	1	629	MKVGLDQIIEVVPSHSVTSGAA
İ	1					AGECGGVHCDSVCAEGRWGPN
						CSLPCYCKNGASCSPDDGICEC
			1			APGFRGTTCQRICSPGFYGHRC
						SQTCPQCVHSSGPCHHITGLCD
						CLPGFTGALCNE/RLFTVCPSGR
						FGKNCAGICTCTNNGTCNPIDR
						SCQCYPGWIGSDCSQPHCADKC
						VHGRCIAPNTCQCEPGWGGTN
						CSSVKKQSTVCES
27630	57998	A	27799	108	1071	YPLFLSSISACDGDHWGPHCTS
2,030	31770	`	2,777	1.00		RCQCKNGALCNPITGACHCAA
		1				GFRGWRCEDRCEQGTYGNDCH
						ORCOCONGATCDHVTGECRCP
						PGYTGAFCEDLCPPGKHGPQCE
						QRCPCQNGGVCHHVTGECSCP
ł					ļ	SGWMLSFPGWRPI*FSKSL*MQ
				:		GTVCGQPCPEGRFGKNCSQECQ
		İ				CHNGGTCDAATGQCHCSPGYT
		l		ŀ		l .
					•	GERAAVPDVRK\CQDECPVGTY
						GVLCAETCQCVNGGKCYHVSG
		1				ACLCEAGFAGERCEARLCPEGL
		1				YGIKCDKRCPCHLENTHSISLIA
						AKKSNSLHAIALDFRAQCQSVK
27631	57999		27800	243	1296	DRCHASDLPIDIVSTETLR ETQEESSEFLPCGSHQPNG*LLF
2/031	3/999	Α	27800	243	1290	CSTYKRCLCNWGPC*AY*RACP
		Ì				CPALQQCPDI/CPQAQLAIPCAP QQQQLSRCLSFPSSLLQDPNTP
		ļ				G/EYRKDEGRAGSRGAGEKQC
		ŀ				•
		ŀ				THNSPRWLQNTVSNQGSSMPG
						FQSHVPSLLGAFVQCTNCTRVC
						SSPANKIFTTFRLGDPLVSPCHQ
						GFGSNTHCCVESWQSSCSGMH KDLGALHTPAPGSPTNVAATQ
						ARREPRCRLAVLSTLDRSTRQK
						-
						VNKDIQELNSALHQADLTDIYR
						TLHPKSTEYTFFSEPHRTYSKTD
		I		1		HLVGSKGLLSKCKRTEIITNCLS
			Ē.	1		DHSAIKLELRIKKLTQNCSTTW
27632	58000	A	27801	552	827	KLNNLLLNDYWVHNEMKAEID
27633	58000	A	27802	70	200	
27634	58002	A	27802	18	1057	
27635	58002	A	27804	652	960	
27636	58004	A	27805	1	474	
27637	58005	A	27806	1	140	
27638	58005	A	27807	1	1260	
2,050	120000	Τ, ,	12,00,	1*	1.200	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	•	in USSN	location of first	I IV	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27639	58007	I A	27808	126	893	EDGSGGGKFPEGARQGGTGQR
27039	38007	A .	27808	120	093	RRRKAMRRTGAPAQADSRGRG
						RARGGCPGGEATLSQPPPRGGT
		1				RGQEPQ\MKETIMNQEKTRHTC
			ŀ			RHKVRIGGKGTARKKKKVVHI
			}			
			<u> </u>			TATA\DDKK\LQFLLKGS*GVN
						NISGIE\EVNMFTNPRNKLIHF*Q
						PLKVQGISWAANTFHHLQGHA
			ŀ			*DKSSWTEMLPSIFKPSLGAG*V
						*LVLRRLA\EALPQTNLWDGKS
	i					TTLLLGEDDGDDDESSQILWEY
		ļ				FGWRVPRNEANLNLSSTF
27640	58008	Α	27809	180	589	KELPLLIFCRWQFESLHELNVPF
						FKVGSGDTNNFPYLEKTAKKG
						SPNGDLPVGCKSNGHP*SKFIRS
						VKPLNPQLLASLQCTSAYPLQP
	ļ					EDVNLRVISVSRREGVPFLGHL
						LWGRRSLFYNQNSNKHGILYN
27641	58009	Α	27810	623	1082	
27642	58010	Α	27811	548	645	
27643	58011	Α	27812	329	510	
27644	58012	A	27813	3254	3628	
27645	58013	Α	27814	1	960	
27646	58014	Α	27815	349	681	PMASNRAITLTAWPKIPFLGICE
						AKNPRSENMRL/AHHFGSGLPP
						SWELWEQGPPGNSSRYIEFLNK
1						HTYIKGTLRVYTKKFCMLVIKS
						FESKSCVWRYDFDSKSSVNVTV
27647	58015	Α	27816	240	473	
27648	58016	Α	27817	825	1043	
27649	58017	Α	27818	2	418	GKVVCFEAFLQQILGKHQFYW
						CLEGLGHCHHHIGAKYPEDIVD
						EESAQQDAASADIVEVQELYSI
						KGEGQAKKVVGNPVLPQQVPD
						ANDAAQAQAHQVLGVKFIIDD
						L*AERPGKSTP*GRATPPTFLVF
						PRTLCEGI
27650	58018	Α	27819	2	427	
27651	58019	В	27820	51	672	
27652	58020	Α	27821	43	667	
27653	58021	Α	27822	516	1056	WSRAPAPQQCQHWLHPAGRTL
					ĺ	HLRCLLGIWHQCDGDSGQVLR
						GTNENLVFPQDLLEKGLEANNF
1		1	}			AMLGTWEMSSFPGIFIALLLRF
						DISLKKNTHTYFYTSFAAYIFGL
						GLTIFIMHIFKHAQL*GVKS*GS
						SGSDRIQRGNRGISIEGAGEERE
]		1				MMQLVPEPLRARPDRWGLGPH
1						RRA
27654	58022	Α	27823	1	1019	
27655	58023	Α	27824	1061	1258	

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	nea	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27656	58024	Α	27825	44	621	
27657	58025	Α	27826	406	727	
27658	58026	A	27827	2	1337	
27659	58027	Α	27828	1236	1391	
27660	58028	A	27829	228	502	
27661	58029	A	27830	I	1035	
27662	58030	A	27831	146	392	GHRSHQSPEETPNLIPRTPIPPLG TGTSIRSTRIPRTEASGPNGLN\ WYLTPTPPGGQRPSSAASPRGF PPTNNSSRLPAEPE
27663	58031	Α	27832	15	300	
27664	58032	C	27833	289	414	
27665	58033	A	27834	3	576	AALAERWLGEVLVRVGVRVPG GSGGLRHWCPCGLLGRGLGQA PEHKVRLSMEFCSTCTADHISLS SFWRSSFQQPLVPAVSLQSPDR RLSHDPAASSWSGFCGISPAFSA FSECSPSSLRSHPPALLQAAES* FAASSSPSPTWSLSGSGTRKPW S/VACNWLLSDSSSHRRSFWES GIITMVLALTLEELV
27666	58034	A	27835		231	DELLVGGNPRGDAAEEGRCPP GGVGVRYQIQPIWPRRLCSRNP GAAD*GPGS*RWDRCPRDEIWR FLGALVGSVSSG
27667	58035	A	27836	18	398	KVRWERSWSESESESQEGRRR AQALVPSVAS*/SSRPWDRPPST K*GCLWSSAARAQQTIYHSVPS GGHPSSSHWLPAVSLQSPDRRL SHDPAASSWSGFCGISPAFSAFS ECSPSSLRSHPPALGSF
27668	58036	A	27837	1059	1446	AVWSLPAPPAPCLLAGLLCTCC RTP*TASLCARGPVPRPRA*EAT RGTSA*ALHSPPGTLTPTVTRTS PSHLSARAAAPSHPARPTASRSS RLPAWLAVRLSIPPRRGSLGGA GAQAAAASTRFTCCS
27669	58037	A	27838		211	ATALAERWLGEVLVRVGVRVP CGEWRAQALVPIVAS*ATRPSG RGPPTQQT*RTSRIGRS*QTTMR HART
27670	58038	A	27839	316	537	
27671	58039	A	27840	255	475	RPWVRAPYKLLPALLHAPLCAP PSSPWRPV/PASAPSFKLLKS*IF CKQLSLLPTWSLSGSGTRKPWS GPVTGS
27672	58040	Α	27841	622	1127	
27673	58041	A	27842	364	666	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27674	58042	A	27843	37	299	L
						QQSLNIICSPSSLRIPGFLHRNRL
						STPFHVQQPQREHF*YCRSQIH
						GENSAWHIRSHHAEKAHF
27675	58043	Α	27844	84	428	PAEIERSTAKTPGPPGSLEMGLL
						TFRDVAIEFSLEEWQCLDTAQR
					NLYKNVILENYRNLVFLGIAVS	
						KQDLITCLEQEKEPLTVKRHEM
						VNEPTGPRQKRRVTSSR**MKR
		ļ				YVII
27676	58044	A	27845	1	719	CLVONONIECKI CKWECI VKOC
27677	58045	Α	27846	669	830	CLVQNQNIFC*ILS*WSSLV*QS
						ACRQLMPLLHLPNDQQAPVWT ENOPGGHWR
27678	58046	A	27847	223	382	CLVQNQNIFC*ILS*WSSLV*QS
27078	38040	^	27047	223	362	ACRQLMPLLHLPNDQQAPVWT
						ENQPGGHWR
27679	58047	В	27848	1	491	Bright Golf With
27680	58048	A	27849	1	1113	
27681	58049	Α	27850	505	1105	ITCTLYPSLRIVYEAFPATGDNM
						FRRIIKDALFRTIQFCQIMNRSQ
i						YMFTCRCRTEMQVPQHRRKKT
		İ				FKPTVLLNHFVMEIIVLTAGRID
						AAFQDEVAASEGFLKQPVGKD
1						YKFGGPSVKDEKLFGVGTGMG
•						HHN*LSV*TSIQHLLSNTQG/CL
						RVCPALRL/HSRNLSAMVISFSF
27.602	50050	ļ.,	07051	<u> </u>	0.007	SCGARSAISPINARKRWASPVC
27682 27683	58050	A	27851	1	2697 1998	
27684	58051 58052	A	27852 27853	864	1025	CLVQNQNIFC*ILS*WSSLV*QS
2/084	36032		27633	1804	1023	ACRQLMPLLHLPNDQQAPVWT
						ENQPGGHWR
27685	58053	A	27854	1605	1766	CLVQNQNIFC*ILS*WSSLV*QS
2,003	30033	1.	2,05.	1005	1700	ACRQLMPLLHLPNDQQAPVWT
						ENQPGGHWR
27686	58054	Α	27855	677	735	
27687	58055	Α	27856	1126	1568	SSSSTGRSRHKEVSPGCQQDGL
						RCQEWWSVRPG\YEATGGVWG
						KQLGIPASGLPGRRSSESPRKSC
						TPVTSRTGLPVCPWAALSPESR
						SFSLSVRPVCVC\CVGTKMSCA
						PECCFFLVSLSLLSLFLRLLLGL
27/00	50056	<u> </u>	27057	1142	2450	AAHCQFFPAVPLCIL
27688 27689	58056 58057	A	27857 27858	1142	2450 1131	
27690	58058	A	27859	229	402	
27691	58059	A	27860	505	597	
27692	58060	A	27861	1	657	
27693	58061	A	27862	248	382	QPPKITLLYQQWIQTKKKSLKS
						FLP*QEFRKMQKKHSTKSSITL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<u>l</u>			<u></u>	
27694	58062	Α	27863	1	1341	
27695	58063	A	27864	1	739	MGDFNTLLSALDRSTRQKVNK
						DIQELNSALHQADLIDIYRTLHP
	}]		KSTEYTFFSAPHRTYSKIDHLV
				:		GSKALLRKCKRTEIITNCLSDHS
	1					AIKLELRIKKLTQNHSTTWQLN
						NLLLNDYWVHNEMKAEIKMFF
						ETNENKDTTYQNLWYVKDTRI
		1				SGMLWYVKAVCRGKFIALNAH
						KRKQERSKIDTLTSQLKELEKQ
						EQTHSKTSRRQEITKIRAELKEI
						ETQKTLQKINECRSWFFEKINKI
1						DRPLARLIKKKREKNQIDAIKN
						DKGDIITDPTEIQTTIREYYKHL
						YGNKLENL*H*MPTRESRKDLK
						LTP*HHN*KN*RSKSKHIQKLAE
						GKK*LRSEQN*RK*RHKKPFKK
İ					ļ	SMNAGAGFLKRSTKLIDR
27696	58064	Α	27865	1	1920	
27697	58065	A	27866	444	763	
27698	58066	Α	27867	1	651	
27699	58067	A	27868	94	964	VNADWVLQRELEQTSLWSSKQ
						RACCLSHVVGLRMISSCTTRKM
						AEEEQRKIPLVPENLLKKRKAY
						QALKATQAKQALFGKEGAEER
						KRAQ/WFKRLESFLHDSLAAET
						*QG/RISRQLEVQPHALELPDKC
		İ				SLAFVVRIKRIDGGSLLVQRTIA
						RLCLKKIFSGVF\VKAPPRIQKW
						LRIVEPYVTWGFPNLKSVRELIL
					İ	KRGQAKVKNKTIPLT\DITVME
		1				EHLGKFGVICLEDLIHEIAFPGK
		1				HFQEISWVLRPFHLSVAHHATK
						NRVGFLKEMGTLGYRGERINQ
						LIRQLN
27700	58068	A	27869	176	334	
27701	58069	A	27870	3	452	AASTGGGSHLLLSIMAALRPLV
				ľ		KPKIVKKRTKKFIRHQSDRYVK
						IKRNWRKPRGIDNRVRRRFKGQ
						ILMPNIGYGSNKKTKHMLPSGF
						RKFLVHNVKELEVLLMCNKSY
					[CAEIAHNVSSKNRKAIVERA\A
						QLAIRVTNPNARLRSEENE
27702	58070	A	27871	2	423	ATMIKA LIM IAMETORENE
27702	58070	B	27872	193	1698	
21/03	1200/1	l _D	12/0/2	1173	1036	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	tocation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27704	58072	A	27873	263	714	KLNVPIIKATNTIMNMTMNLK
27704	30072	A	2/0/3	203	1/14	MSLTAPPSDICRGPKLSFAGKIQ
	1					1
	1					AIPEKLKTTATAQRPLDTIGLEV
						PVPAAWLLSAVRNCSKLRATS
1					}	GPNLDTMNGSRRQTGSWTEGS
						RSSMKPHLLSDITGALR/SPKVS
07705	50072		07074	2.47	000	*AFCRLATWPFNFLQSGILS
27705	58073 58074	A A	27874 27875	347 17	902 1178	
27706			27876			
27707	58075	A		1	1155	EVETMOSI NIDDI ASVI DIVIDE
27708	58076	Α	27877	3	1109	EKETMQSLNDRLASYLDRVRS
1						LETENRRLESKIREHLEKKGPQ
						VRDWSHYFKIIEDLRAQIFANT
						VDNARIVLQIDNARLAADDFRV
		1			1	KYETELAMRQSVENDIHGLRK
		1				VIDDTNITRLQLETEIEA\LKEEL
		İ				LFMKKNHEE\EVKGLKTPNYA
					Į.	ALG*T\VEVDAP\KSQDLAKI\M
						ADIR\AQ\YDELGSERTERKLDK
						YWSQQIEESTTVFTTQSA\EVGA
						AETNLHRSLKRTV\QSLEDRPW
						TSMRNLKAQLGEQP*GEVEAPL
		l				RPTRWSQLNGILLHLES\ELAQT
		İ				\RAEGQRQA\QEYEALLNIKVKL
1						\EAEIATYRRLLEDGEDFNLGD
						ALDSSNSMQTIQKTTTRRIVDG
						KVVSETNDTKVLEALSQQKAG
27709	58077	Α	27878	1	1305	
27710	58078	A	27879	209	560	
27711	58079	A	27880	219	512	
27712	58080	A	27881	528	803	COROLIE ECTOR (C. A. CL. D. D. A. T. A. D. D.
27713	58081	Α	27882	3	432	SSPCVEFSTSMGACLRPATARSP
						SATCTAWTCTGWRRGRPWWR
	İ				ļ	WTPENSGVAGGDGTSEEDSEE
						VEGAEWWGRRRRQRRGERCG
						GLRRAPCQGAPGKCLCPRPP\GP
						SPC*/CEALGAQRAS*PHRRELK
2771 1	50000	_	07000	117	492	VGGPGPGCELSPMV
27714 27715	58082	A A	27883	117	483 1497	
27716	58083 58084	A A	27884 27885	228	776	
27717	58084	A	27886	1012	1677	
27718	58086	A	27887	194	562	
27719	58087	A	27888	1	423	
27720	58088	A	27889	232	308	
27721	58089	A	27890	1	1692	
27722	58090	A	27891	186	2191	
27723	58091	A	27892	2	141	
27724	58092	Α	27893	1	1692	
L		•				

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ļ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27725	58093	A	27894	186	2192	QRRPRPFPSQGISMTECFLPPTSS
2,723	30073	`	27051		21,52	PSEHRRVEHGSGLTRTPSSEEIS
					:	PTKFPGL\YRTGEPSPPHDILHEP
						PDVVSDDEKDHGKKKGKFKKK
1						EKRTEGYAAFQEDSSGDEAESP
						SKMKRSKGIHVFKKPSFSKKKE
						KDFKIKEKPKEEKHKEEKHKEE
1						KHKEKKSKDLTAADVVKQWK
						EKKKKKKPIQEPEVPQIDVPNL
						KPIFGIPLADAVERTMMYDGIR
						LPAVFRECIDYVEKYGMKCEGI
						YRVSGIKSKVDELKAAYDREES
						TNLEDYEPNTVASLLKQYLRDL
		l				PENLLTKELMPRFEEACGRTTE
		1				TEKVQEFQRLLKELPECNYLLIS
						WLIVHMDHVIAKELETKMNIQ NISIVLSPTVQISNRVLYVFFTH
]			
			ļ			VQELFGNVVLKQVMKPLRWSN MATMPTLPETQAGIKEEIRRQE
			ļ			` `
						FLLNCLHRDLQGGIKDLSKEER
						LWEVQRILTALKRKLREAKRQ
						ECETKIAQEIASLSKEDVSKEEM
		1				NENEEVINILLAQENEILTEQEE
1		l				LLAMEQFLRRQIASEKEEIERLR
1		1				AEIAEIQSRQQHGRSETEEYSSE
		1				SESESEDEELQIILEDLQRQNE
						ELEIKNNHLNQAIHEEREAIIEL
						RVQLRLLQMQRAKAEQQAQE
						DEEPEWRGGAVQPPRDGVLEP
		<u> </u>			410	KAAKEQPKAGKEPAKPSPSRDR
27726	58094	Α	27895	12	413	PSRAPGLQKACTGHEGMAVHP
		ľ				PRIPVQSDHLISIEGLLCKLPCA
						GQVTKESGLVSFSLRPVLPQNT
						LSNSFYLFPFGYASPYVETFLPG
				i		AHSGPAPPGLPVRTPRTAKRL/G
0.000	50005	 	07006	,	261	VAVAPSPTF*ISPRALRSTFVSN
27727	58095	A	27896	1	361	
27728 27729	58096 58097	A	27897 27898	248	162 381	
27730	58097	A	27899	73	254	
27731	58098	A	27899	1	729	
27732	58100	A	27900	1	762	
27733	58101	A	27901	2	334	
27734	58102	A	27903	3	369	
27735	58102	A	27903	669	1006	
27736	58104	A	27904	3	250	
27737	58104	-	27906	721	876	
27738	58105	A A	27906	3887	4013	
27739	58106	A	27907	3423	3627	
21139	120107	ΙΛ.	21300	J423	3021	L

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27740	58108	A	27909	3	226	HETGCCGQAAERDSCWERPPIP LLLPSLSGDYETVRNGGLIFAG
						LAFIVGL\ILLSRRFRCGGTKKR RRINEDEP
27741	58109	Α_	27910	67	264	
27742	58110	A	27911	161	851	
27743	58111	Α	27912	139	351	GGRRIETGGWERPPIPLLLPSLS GDYETVR\NGGL\IFAGLAFIVG\ LLILL\SRRFRCGGNKKRRQINE
27744	58112	Α	27913	2	431	
27745	58113	Α	27914	217	289	
27746	58114	A	27915	255	389	KPNIACSHS*VGTEQ*EHMDTG RGTSHTGACREALDRGPAWEK L
27747	58115	A	27916	14	460	NCLTRRRRRRRRTFLEEERLKP SRKKITKKHTKKRTASLILHAM ICCRSLNSSKTKNTKCLNSINQR LKILSLQKDLMCGTAGRCKTLT EQ*LNTTAITLCLLLREARKTL MTHQSTWTWMKLETIILSKLTQ EQKTKQRMFSLISGS
27748	58116	Α	27917	503	1046	
27749	58117	A	27918	3	198	
27750	58118	A	27919	54	320	
27751	58119	Α	27920	443	477	
27752	58120	Α	27921	l	963	
27753	58121	Α	27922	1	2292	
27754	58122	A	27923	3	736	SCCLHSRLVRARRLRRAVAVM AAQCVRLARRSLPALALSVRPI FPGLLCTATK\QRTSAKNLKGD MGQSEQRADPPATEKTLL\EEK VKL\EEQLKETV\EKYKRALA\D TEELTGRGSQNLLREAKLLRHF KPFCKDLLEVADV\LEKATQCV PK\EEIKDDNPHLKNPLWRGL\V MTEVQIQKVFTKHGLLKLNPV GAKFDPYEHEALFHTPVEGKEP GTVALVSKVG\YKLHG\RTLRP ALVGVVKEA
27755	58123	Α	27924	253	363	
27756	58124	Α	27925	235	318	
27757	58125	A	27926	1	426	
27758	58126	A	27927	146	254	
27759	58127	A	27928	1	1401	
27760	58128	A	27929	61	457	LESTLATAERFLIPSYPSSTGN*L VCFCTT*GQECYSVTRF\SLGYG SPGCLYA*SSLIPCWRWGTPRL CCEKPFTTHFCLRFVSPSKLAVS RWHIPLGSEEKRRSMSAGTISL HFIWMKSPTRTSFQHFCT
27761	58129	A	27930	1	567	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27762	58130	Α	27931	128	586	
27763	58131	Α	27932	271	465	HLTRPGTLLRQNFQRNDQAAT LAVHQYPLLCSNRC/CIPRQT/W VWSGPPANSNRPAAEGPDC*KE N
27764	58132	A	27933		375	MQKSPIFCVAHAGSCRLELFLF GHLGGHHPDTKPGRDTTRKDN FRPISLMNIDAKILNKILANRIQ QHIKKLIHRDQVGFISGVQGWF NIRKSINVIQHINRTKDKNHMII SIDAEKAFDKIQQGFMLKILNK LGIDGMYLKIIRAIYDKPTAKIIL NGQKLEVFPLKTGTRQRCPLSP LLFNIELEVLARAIRQEKEIKGI QLGKEEVKLSLFAHDMIVYLEN PIVSPQNLLKLISNFSKVSGYKI NVQNSQAFLYSNNRQT*AIAGA PPPASLPPCSLISDCCASNE*GSV GIGPSKPGAGYNLLLCHLISPSIS PTSSPKSDTCPIADFSNKSPDRSS AGDILLAMQSLGSMAIFTILILP THEHGMFFHLFVSSFISLSSGL
27765	58133	Α	27934	1	1059	
27766	58134	A	27935	1	533	LSKQGHLNLQRF\LLPFG\C*CLP LRGGV\YRGRQ\ASLSCGGLHP V*AS\RQLCLPTQALA\MAGTPP PASLPPCSLISDCCASNERGSVG MGPSEPRCGNNNLVVC\RFLSL SEKRSSIRVGVTRFS\RCHLSQL CLATKGNSLTPCTSQVRRCLTL LQLTLGAMQPLSCGLPTLSDKP
27767	58135	Α	27936	140	426	
27768	58136	Α	27937	1	918	
27769	58137	Α	27938	54	102	
27770	58138	C	27939	244	462	
27771	58139	Α	27940	234	282	
27772	58140	Α	27941	328	1212	
27773	58141	В	27942	245	338	
27774	58142	Α	27943	483	635	
27775	58143	Α	27944	9882	10134	
27776	58144	Α	27945	2	370	
27777	58145	Α	27946	1682	1945	
27778	58146	A	27947	1172	1732	ESTAAEADTRFGCSWAVWAVE AEGEDCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	,			sequence		
27779	58147	Α	27948	272	393	
27780	58148	Α	27949	333	622	
27781	58149	Α	27950	11	1850	
27782	58150	Α	27951	1	1107	
27783	58151	Α	27952	1	1348	
27784	58152	Α	27953	3	431	KLQNELLLHVSHPGHADAKG
						GFPWP*AAPPLWLCRVQPSFWL
						LSWAGIEGLWLFHTHDTSCQWI
		1				YHSGVALADVLHESPALQQTS
	l					VWTSRSFHTSSEIQAEVPKPQLL
į						TSVHAQAQYSMEAPKAWGLYP
						LKPWPELYLGPF
27785	58153	Α	27954	364	1117	EGHRAEGQCTGSVVLLTSSIGR
		ĺ				SGKQSSGCHFWLLQHQICTCPS
						RVMGPRKKHRPTARGSRPPQPL
						PSGFPSAGAMGQVHCLAAPHS
		1				LERVRNPRQTQ/PPGWEG/PPTR
						ANLALLPTPPAATATNSSIPDSP
						PGSDGSVPAGLTTWLAVLTLD
		1				CPKAFGKVASQACLLWKGEQP
		ŀ				PKTPPVTPSRVSLLASEPNTIRL
1						KNVFPRVFPACTWKSHRHSTPA
						HESSQKGLYPAKPQGWSCPRL
		1				WEPTSCISVTWM
27786	58154	Α	27955	1	224	QWRHCNRSLLPVQGKSGALEG
		1				IGPPRVF\PPE*RAFGGQRAPPDI
		1				P\PPSPRHPTKDRRTAARSGPRR
						KRGQTNE
27787	58155	Α	27956	681	879	LQISHPGHADASGGFPWPWAA
	}					PPLWLCRVQSPS*LLSQPGVECP
		l				QLFQAHSASRHLNSMRPQMNS
						S
27788	58156	Α	27957	835	1482	
27789	58157	Α	27959	1	522	
27790	58158	A.	27960	2	396	
27791	58159	A	27961	1	1501	
27792	58160	A	27962	473	860	
27793	58161	A	27963	370	3675	
27794	58162	A	27964	52	117	DDUTYOEGCTVTEVILLEVVVTC
27795	58163	A	27965	3	290	PRKTVQFGGTVTEVLLKYKTG
						ETNDFELLKNQLLDPAIRDD\QII
					1	NWLLEFRSSVMYLTK\DFE\QLI
						SIILRLPWLNRSQ\TVVEEYLAF
27796	58164	A	27966	1	2988	LGNLVSA
27797	58165	A	27967	1	666	
27798	58166	A	27968	274	930	
27799	58167	C	27969	13	231	
27800	58168	A	27970	46	386	-
27800	58169	A	27971	3	451	
27802	58170	A	27971	160	494	
2/002	130170	ΙΛ_	41314	100	J ⁻ /-	L .,

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27803	58171	A	27973	<u> </u> 1	2406	
27803	58172	A	27974	201	1069	
27804	58173	A	27975	450	647	
27805	58174	A	27976	329	697	
27807	58175	A	27977	141	1506	
27808	58176	A	27978	1	1773	
27809	58177	A	27979	3	460	PHRVMGVPISRGTL*SVFP*PS*
2/007	30177		21717			CTTWPGSLGSCTTACQVRCQPQ
		ł				APHQP*APPERTTSAPAAQSPSR
						SSLWVTAPLVSACPTCSPATHP
						TRSQMPSTHTPCCRGSSPRPRGS
						PSWTRTWTICPKASKADPKAP
						WPCSLMPFYAQTQTLGET
27810	58178	Α	27980	1	1803	MGKDFMSKTPKAMATKAKIDK
						WDLIKLKSFCTAKETTIRVNRE
						PTKWEKIFTTYSSDKGLISRIYN
		1				VLKQIYKKKTNNPIKKWVKDM
						NRHFSKEDIYAAKKHMKKCSP
						SLAIGEMQIKTTKKLMLYYDVI
						RICHDSHKELEQKLAAFLGMED
						AILYSSCFDANGGLFETLLGAE
						DAIISDALNHASIIDGVRLCKAK
						RYRYANNDMQELEAAYRRSTR
						PLSTRLFSFRSRVLTEFRVCPCL
		1				VHTTWGGNLMRLSARSLWQR
		l				AAVNIPKLEGIIEEY/ALLV/WR
						AML/TEVNLSPNPGLVDRINFG
						AHKDMALEDFHRSALAIQGWL
						PRFIEFGACSAEMAPEAVLHGL
						RPIGMACEGDMFRATAGVNTH
						KGSIFSLGLLCAAIGRLLQLNQP
			ľ			VTPTTVCSTAASFCRGLTDREL
						RTNNSQLTAGQRLYQQLGLTG
						ARGEAEAGYPLVINHALPHYLT
						LLDQGLDPELALLDTLLLLMAI
						NGDTNVASRGGEGGLRWLQRE
						AQTLLQKGGIRTPADLDYLRQF
						DRDTSQGSSRVDCSVWELCRA
		1				GRTAGVMAVAAKTKNAGKWH
						NHIIRRFDINPGDRLYDQGGRA
						HHPFAGTHHQKYYRHRSRR
27811	58179	A	27981	1	1974	
27812	58180	Α	27982	344	508	
27813	58181	A	27983	3	492	
27814	58182	Α	27984	65	261	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27815	58183	A	27985	3	529	DAWAFHKMAPKAKNEAPAPP
						KA\EAKAKGF*RAKKGSF*KVS
		1				HSH\KKKKIPHVHPTFRAGRRPL
					R\LRRQP\KYPSGRALPWRNK\L	
					DHLCLSIKFP\LTH*VLPMKKIE	
	ĺ	1				DN\NTLVFIVDVKANKHQIKQA
		ŀ				VKKL\YDI\DVAKVNT/LWIRPD
į						GEKNGICSDLAP\DYDA\LDVA
	1	ļ				NKIGII
27816	58184	Α	27986	105	241	PFFFFEMESPSVAQAVFSLVFRS
						PHCGGIQAHLFNL*RDLFKIWT
27817	58185	С	27987	175	363	
27818	58186	A	27988	724	958	
27819	58187	Α	27989	3	823	
27820	58188	Α	27990	1	877	
27821	58189	Α	27991	487	786	
27822	58190	Α	27992	147	623	RSAVANGLTKRRMGLKLNGRY
		İ				ISLILAVQIAYL\VQAVRAAGKC
						DA\VFKGFSGLFCSSLGDTMAQ
						LPAGPGDDKTNIKTV\CTYWGG
						ISHSCT\VTALTDCQEGAKNMW
		l				DKLRKESKNLNIQGSLFELCGN
						GNGAAGSLLPGFPVLLVSLSAA
						LTTWLSF
27823	58191	A	27993	213	579	ASLLLLAFLAELASLKAGLQKS
						REYSCSSFISSLSSTDAHCVLSE
]						YARPLS/QRPAPNGSSPRCQASE
}						AQSPGHRPPPPLFSSPLAALQLD
						SHRFPSDPNGKDESRPPRLCTKL
						GRGCAGCGK
27824	58192	Α	27994	1	800	
27825	58193	В	27995	54	165	
27826	58194	Α	27996	46	313	
27827	58195	С	27997	30	151	
27828	58196	Α	27998	169	1173	
27829	58197	Α	27999	456	651	
27830	58198	Α	28000	487	833	RNKFCDDQTEGNKIKNRREEK
						HRCRGQSKLNIIIDNVVKAVNG
						GKSQREQAEFADCITFGIRHNTS
						PKMSRVRGGG/TTPWAVLGMA
						EASSSLQSSSQNPGQAGWQTGP
						WVVSLGC
27831	58199	В	28001	1	2268	
27832	58200	Ā	28002	1	639	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27833	58201	A	28003	1913	2388	PIIHNTTAMKKAAKAEPPFTTIV CTE*AILSQRTCSL*FTVINDICP GPRAH/VVQDIHGKLFTGSAIA
			i			NRFQDAMAIPFLGTQGKRVPR
						NGMAIPFPGNRNVIAGAFIPHR QHLGQIQLNPVRQCSNLFAHLL
						AQRSEAIFHMRRHHRIRDTVKK
27834	58202	Α	28004	1	1566	
27835	58203	Α	28005	951	1217	
27836	58204	Α	28006	1294	3108	
27837	58205	A	28007		1896	LFDWLVSQNELKANPAKGVSA PKAPRHLPKNIDVDDMNRLLDI DINDPLAVRDRAMLEVMYGAG LRLSELVGLDIKHLDLESGEVW VMGKGSKERRLPIGRNAVAWI EHWLDLRDLFGSEDDALFLSKL GKRISARNVQKRFAEWGIKQG LNNHVHPHKLRHSFATHMLES SGDLRARGAYLCAKLLSGAAQ VPEWRSAFAWFARCAEQARQN QYLQVSSCVPALEGCDVNGAS FTLEQMLAWRDHPQVTGLAEM MDYPGVISGQNALLDKLDAFR HLTLDGHCPGLGGKELNAYITA GIENCHESYQLEEGRRKLQLGM SLMIREGSAARNLNALAPLINEF NSPQCMLCTDDRNPWEIGHEG HIDALIRRLIEQHNVPLHVAYR VASWSTARHFGLNHLGLLAPG KQADIVLLSDARKVTVQQVLV KG\EPIDAQTLPAEEIGRLAQFA PAYGNTIGRQPLSASDFALQFTP GKRYRVIDVIHNELITHSHSSVY SENGFDRDDVSFIAVLERYGQR LAPACGLLGGSGLNEGALAAT VSHDSHNIVVIGRSAEEMALAV NQVIQDGGGLCVVRNGQVTSE
						GAKERMMGKRYKETSGSIGLK
27838	58206	A	28008	11	3257	VPAPLNLNLSLQPREQLGGQST
27839	58206	A	28008	1	2145	
27840	58207	C	28010	193	363	
27841	58209	A	28011	1	397	
27842	58210	A	28012	2	405	FVSAQGPGGKRFGTAPATPGCL VHDLS*APCLRWYQHPTEEELR ILAGKQQKGKTKKDRKYNGHI ESKPLTIPKDIDLHLETKSVTEV DTLALHYFPEYQWLVDFTVAA TVVYLVTEVYYNFMKPTQEMN ISLV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27843	58211	Α	28013	3	353	GYIEKRISCIALLF/SF*IPVNFLR
						FHDTFI*FCYSS*SIIQLSLWQSQI
						LLCV*LLRSIDFLYLIW*PLTYN
	1					EHASILLSLRAPYQLFDL*NDRS
						HIRYSATLVNNPAVCFAVGHD
27844	58212	Α	28014	106	1814	
27845	58213	Α	28015	37	2847	
27846	58214	Α	28016	1	2430	
27847	58215	A	28017	1	2660	
27848	58216	С	28018	80	328	
27849	58217	В	28019	1	1074	
27850	58218	Α	28020	602	853	
27851	58219	Α	28021	505	649	
27852	58220	Α	28022	672	1903	
27853	58221	A	28023	3	319	
27854	58222	Α	28024	1	219	
27855	58223	Α	28025	2	508	
27856	58224	Α	28026	1	1011	
27857	58225	Α	28027	1	699	
27858	58226	Α	28028	175	351	
27859	58227	Α	28029	1	324	
27860	58228	A	28030	244	1335	
27861	58229	C_	28031	115	231	
27862	58230	Α	28032	2	139	
27863	58231	Α	28033	1	788	
27864	58232	Α	28034	115	358	LIVVRSRRGTSRSGSPRATAMA
						FKDTGKTPVEPEVAIHRIRITLT
	1					SRNVKSLEKVCADLIRGAKEKN
						LKVKGPVRMPTKVK*IVVRSRR
		ļ				GTSRSGSPRATAMAFKDTGKTP
						VEPEVAIHRIRITLTSRNVKSLE
	Ì					KVCADLIRGAKEKNLKVKGPV
				<u> </u>		RMPTKVK
27865	58233	С	28035	179	283	
27866	58234	A	28036	57	431	DUDDI NA COMPUNITO COLLA DICCI.
27867	58235	Α	28037	54	440	RVPELWVGTEVKERKNARSGV
						PSTQRLECGSAESAAGAPASVS
						VQVTAVPAPLFPGWTGGGRAV
		1				NLTEAERMRVVINSVCHWRLY
						E*TANRFS*KQDVGKLTNCVCH
	<u> </u>	<u> </u>			0.600	PEGMLKAVTTQAQVFLVIRHN
27868	58236	A	28038	1	2693	
27869	58237	В	28039	131	350	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27870	58238	A	28040	1	594	MLDITNDQGNASQNHNAIPPYS
						CKNGHNQKIKAGGLWTTVHSL
					1	LLFQLEQRTQQGYGPITHPKTP
						LHPPALLAVDRGSRSSVPATDS
	-					LPSAHDRQQQFHTWVCSRLLA
		1				TVRADPADGQQPQARADVCGC
						RGTGFINLVMIHLMGFEVGRIQ
						QLEQVAPRPQGVSWEVDSSDH
						LQGSPRVEPPGTWDLRVLCSQG
						Q*EAVNCGPQTPGLD/SFDYGH
		}				SCRSKVVSHCGFDLHFPDH**C
						KNGHNQKIKAGGLWTTVHSLL
					•	LFQLEQRTQQGYGPITHPKTPL
						HPPALLAVDRGSRSSVPATDSL
						PSAHDRQQQFHTWVCSRLLAT
						VRADPADGQQPQARADVCGCR
						GTGFINLVMIHLMGFEVGRIQQ
						LEQVAPRPQGVSWEVDSSDHL
						QGSPRVEPPGTWDLRVLCSQG
27871	58239	A	28041	1	285	(33.1.1.2.1.3.1.2.3.(3
27872	58240	Ā	28042	i -	1059	HNLSSSNSFPKMSFPNSSPAANT
	0 02 10	1				FLVDSLISACRSDSFYSSSASMY
		1				MPPPSADMGTYGMQTCGLLPS
						LAKREVNHQNMGMNVHPYIPQ
		l				VDSWTDPNRSCRIEQPVTQQVP
		l				TCSFTTNIKEESNCCMYSDKRN
						KLISAEVPSYQRLVPESCPVENP
						EVPVPRYFRLSQTYATGKTQEY
		ŀ				NNSPEGSSTVMLQLNPRGAAKP
						QLSAAQLQMEKKMNEPVSGQE
		1				PTKVSQVESPEAKGGLPEERSC
		1				LAEVSVSSPEVQEKESKEEIKSD
		1				TPTSNWLTAKSGRKKRCPYTK
į		1				HQTLELEKEFLFNMYLTRER/R
]				ALEISKSVNLTD\RQVKI\WFQN
						RRMKLKKMSRENRIRELTANL
27873	58241	A	28043	358	2292	
27874	58242	A	28044	2	300	HSLS/SFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
_ ,		1				FFFLFFFFFLLLLLFVSFSFSFSFS
						SFSFSSFSSFSFSFFFLLPSSSSS
						SSSFFFFFFLLLLPFFFFFFEMEH
27075	59242		28045	2	241	
27875	58243	A	28045	2	241	
27876	58244	A	28046	1	126	
27877	58245	A	28047	49	183	
27878	58246	A	28048]3	212	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27879	58247	A	28049	13	494	WVVPKNKTTFCSEF/CGAFLWP NNNNNFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
27880	58248	Α	28050	544	729	
27881	58249	Α	28051	1667	1896	
27882	58250	Α	28052	1	477	
27883	58251	A	28053	25	448	RSQFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
27884	58252	Α	28054	47	376	
27885	58253	Α	28055	1	1740	
27886	58254	A	28056	3	1464	
27887	58255	Α	28057	1	394	
27888	58256	A	28058	143	429	STLQKKEARARHLVTPLDILQL FNGFPLLVDCYKLLRYSRVHSF PRFWIFFSIKDHIGFPKENTQRK MRLHPPPQS*TPPRE*VPSFSSG VGKSS
27889	58257	Α	28059	165	408	
27890	58258	В	28060	21	253	
27891	58259	Α	28061	1	150	
27892	58260	Α	28062	1081	1303	
27893	58261	A	28063	147	437	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27904	50262	Ι	28064	107	2499	DIEDDECEDDEMBEEH BEIOCH
27894	58262	Α	28004	107	2499	PIEDPEGRRRMREFILRSIQGVL
						RMAPQIQPKPLLTKSSTSVSQA
						RL/TSKQKALLPRQCSGSAKAQ
						AEREKIEETCQVGMKPPVPGGY
						TLQGKWITTFCNQVQLDTIKIN
				-		GCLKGKLIYLLGDSTLRQWIYY
						FPKVVKTLKFFDLHETGIFKKH
		ŀ				LLLDAERHTQIQWKKHSYPFVT
						FQLYSLIDHDYIPREIDRLSGDK
						NTAIVITFGQHFRPFPIDIFIRRAI
						GVQKAIERLFLRSPATKASVSK
		İ				LKCFWEPTRGTQKYEASQVTG
						AFPLRPKKGAATPSQLVIVNSS
						DAHNKCDEESEVRIKSTLGLKL
ĺ						DCKKGTALTKGTKEDEEDGAM
						SGVDQLCLLSSVDSSGRPQLMT
						DWHGVKGQFSCFKCGEEKELQ
						QKRKLTGKGWNVFFMVLEVG
			,			KTKIKALEVLASGKGTASWFIQ
		1				DFLAVNSSHGRWGKKEEFLFQ
ļ						KWKVDPWLPVRWELVQTGTL
						THLVPEGRSDSVTCAWMPLGS
				ļ		KQVYKEPAGFPDMLRLRGSRV
				1		RMAVVTVHSQLRNLSLGDQHF
						NYPLPLKKKKKKKKKDTLIYPA
·						DWLESCQSDNLSLAERDLVLV
						LRLALCALYGLLAPGNGNTESA
		1				ELHPGDKTEAQRPMALFKVTR
				<u> </u>		PLNERPGDLASHVSRFAKSFLK
						PAMESLECPQSRLVGEARKGHS
						ELVEKIERGCESTVGEGTTRKG
						SKRDHLDSQCKLGQRSQPWGQ
27895	58263	Α	28065	1	1770	SKIDIEDSQCKEGQKSQI WGQ
27896	58264	A	28066	85	204	SPCSTSPFRQLA**RRGPHRSPFP
27690	30204	^	20000	185	204	TVAHLIGEWRLMRNAG
27897	58265	A	28067	1280	1531	I VAHEIGE WREMINIAG
27898	58266	A	28068	1280	882	
27899	58267	В	28069	77	1188	
27900	58268	A	28070	1016	1400	
27900	58269	A	28070	1091	1770	CRGGSGCAVCAELAPGAVHTV
2/701	150203	^	20071	1091	1770	AAERAGAQEAAAGAGPPQLGG
						LIAWATHLOHSAAVPLLSORM
						` `
						CHTCCLSPRKLVIGCRAAKSLSS
						SPCGKWLCAALIRQPSVKGLPS
,	1					CGVPLPLSLSRIQMCSSEATSSW
					}	ELNPDFGEAATSP**ESGF/LQS
	l					VVSTALLPDNTTGETFHHDGRA
						DIGSQFIHRFLVCCHLLVLRWLI
						TLDTKADVVDIGHRLRCFDCRC
						VDSTICD
27902	58270		28072	1568	1819	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27903	58271	A	28073	778	879	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRCANY
27904	58272	A	28074	332	544	CMRRPSCSCPASIRDNTAPHSRT LKVLIIGKLSSGRKLSRILPLLRS SSM*PTRAPN*SSASFTFTSVSG
27905	58273	A	28075	355	614	CMRRPSCSCPASTRDNTAPHSR TLKVLIIGKRSSGRKLSRILPLLR SSSM*PTRAPN*SSASFTFTSVSP L*NFIRLHPVY
27906	58274	Α	28076	1	2226	
27907	58275	Α	28077	31	117	
27908	58276	Α	28078	1	547	
27909	58277	Α	28079	290	730	
27910	58278	A	28080	3	267	TLVKVKDAEDQLGARVGYIEL DLNSGKILESFRPEERFPMMSTF KVLLCGAVLSRIDAGQEQLGRR I\TILRMTWLSTHQSQKSILRMA
27911	58279	Α	28081	1	1785	
27912	58280	Α	28082	551	685	
27913	58281	Α	28083	2	211	
27914	58282	A	28084	1407	1874	PRAAAAPTNLSPELSASPRPRV ACASAWGAGTDVTGWEAAMP RVGRCLPRTGLGSARRLRRPEL GGGAGPAPEAMRGFGADAGST EQPRLPARS*PRLPQRPRRPRKS ERPAGLAPRLRPPQPAEPPGLGS QERGRGTDRAAADPGLPRTSPE SS
27915	58283	Α	28085	1284	1786	
27916	58284	A	28086	1205	1279	LALIVGNRS*MKPYQTTSVTPR CL
27917	58285	Α	28087	423	676	
27918	58286	A	28088	2266	2367	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRCANY
27919	58287	В	28089	743	852	
27920	58288	Α	28090	1	1100	
27921	58289	A	28091	548	652	LALIVGNRS*MKPYQTTSVTPR CLQQWQQRCANY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27922	58290	A	28092	1	2438	MRLFGYARVSTSQQSLDIQVRA
						LKDAGVKANRIFTDKASGSSSD
						RKGLDLLRMKVEEGDVILVKK
						LDRLGRDTADMIQLIKEFDAQG
						VSIRFIDDGISTDGEMGKMVVTI
						LSAVAQAERQRILERTNEGRQE
		İ				AMAKGVVFAENDKKMLSNAFI
						ETADFRTLIETDDRTIVVGRRGT
						GSFNLARAATRLLWRYAMLME
		1				IASYISSHYKLSSQISSETLLNEH
		l				LKKWNSAQGDILRKCRLVAKE
						YLDENNPEESIGDLQFNLNISEI
						ENNIVSLLERSDRKVVILMDKL
						DEAYEPDNIGIG\IIAGLAYASIE
i						LNQKAKCIRPIIFLRDNIFRSLSK
			ļ			1 `
						EDPDYSRNIEGQVIRLHWDWA
						QLLMLSAKRMKVAFKLDIEKD
						QRVWDRCTADDP*KGGNGFKR
					į	CLQFTLYRPRDLLSLLNEAFFSA
1						FRENRETIINTDLEYAAKSISMA
						RLEDLWKEYQKIFPSIQVITSAF
1						RSIEPELTVYTCLKKIEASFELIE
						ENGDPKITSEIQLLKASGILQSL
						YSVGFVGIRDKNTSSYSFCHDG
						RTPDKGFESNEKLLIHPCYWLG
						LNLNRNALAPEEAEEINDEYDI
1						NIISDNSAIRNKTIGQITTHLDQI
						PIGNEGATEFEQWCLDALRIVF
		1				ASHLTDIKSHPNGNAVQRRDII
		1				GTNGGKSDFWKRVLEDYKTRQ
		1				VVFDAKNFEELGPSEYRQLQSY
						LTGPYGKLGFIINRDESEVVRSK
27923	58291	Α	28093	673	916	
27924	58292	В	28094	1	4725	
27925	58293	Α	28095	959	1387	CMRRPSCSCPASIRDNTAPHSRT
1		1				LKVLIIGKRSSGRKLSRILPLLRS
						SSM*PTRAPN*SSASFTFTSVCIS
		1]	RCMSAVMVMAVLTIACRFLKM
		1			1	TVSVGHICSLNFALQTSTTAMA
						VPAAATRASRAQPNGRHPWRI
		<u> </u>				CWKTQKA
27926	58294	С	28096	997	1302	
27927	58295	Α	28097	659	2534	
27928	58296	Α	28098	174	294	
27929	58297	A	28099	31	379	
27930	58298	A	28100	3	518	
27931	58299	A	28101	1	3015	O A A DITTO DIVATIVA DI STATICA D
27932	58300	Α	28102	40	198	QAARTTGFYAHLLRHYKTPVG
						HS*Y*WKLHGENKSSAFAVC*P
0.000		 	20100	200	1106	TCRNPFIDCW
27933	58301	A	28103	390	1186	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27934	58302	A	28104	2	1287	GRVGFASTAQSPRILRSEPVRTP
						PIPAFSPLKTLRIMSLHQFLLEPI
						TCHAWNRDRTRPVCLDYYSLV
}			1			VSFEIKK*IALSPNNHEVHIYKK
ŀ	i					NGSQWVKAHELKEHNGHITGI
						DWAPKSDRIVTCGADRNAYVW
						SQKDGVWKPTLVILRINRAATF
						VKWSPLENKFAVGSGARLISVC
			İ			YFESENDWWVSKHIKKPIRSTV
						LSLDWHPNNVLLAAGSCDFKC
		1				RVFSAYIKEVDEKKASTPWGSK
		1				MPFGQLMSEFGG\SGTGG\WVH
		1				GVSFSASG\SRLGWGSATDSTV
		ł				SVCWMPSKS\LQVSTLKTEFLPL
						LSVSFVSENSVVAAGHDCCPM
						LFNYYDRGCLTFVSKLDIPKQSI
		l				QRNMSAMERFRNMDKRATTE
						DRNTALETLHQNSITQVSIYEV
		l				DKQDCRKFCTTGIDGAMTIWD
						FKTLESSIQGLRIM
27935	58303	С	28105	198	362	
27936	58304	A	28106	1	915	
27937	58305	A	28107	403	519	
27938	58306	Α	28108	88	237	
27939	58307	A	28109	527	1205	
27940	58308	Α	28110	2	272	
27941	58309	Α	28111	39	543	
27942	58310	Α	28112	1	789	
27943	58311	Α	28113	401	912	
27944	58312	В	28114	147	653	
27945	58313	A	28115	586	650	KIQCLCLWLLFLIIFLHAFQETIL
						ALRVLNVFNKRINSLGKNLAFN
						LFVYNKANSMP*RLLWKAPRS
		1				DK*IQ*SLRIQNQCTQISSTAVH
		1				STVTKLRIKSRTQPLLQQL
27946	58314	Α	28116	1	1464	
27947	58315	A	28117	260	462	MLYLSGI*PKAE/TIGAKWTIDL
						KSGSGKVYQGPAKGAADTTIIL
		ŀ				SDEDFHGRWSGASLTLRRHSLV
	<u></u>	L				AG
27948	58316	С	28118	183	254	
27949	58317	Α	28119	98	445	LGSGDLPWEINPLSSCSLLCEKH
]						PPTTSGPQTDQPKKHLTNFKSG
1						ACYMCRKSGHWAEECPQPGIPP
						KPRPICVGPH*KSDCSTHLAATP
						RAPGTPAQGSLTDSFPDLLGLA
						AED
27950	58318	Α	28120	32	143	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
27951	58319	A	28121	39	346	QYISELQFLASTVRQTPATSPAH
						KNFQTPEPQQPGIPPEPPPPGAC
						YKCWKSGHQAKECLQPGIPRK/
	,					HASHLWQPLPEPPGTLAQGSLT
						DSFPDLLGLAAED
27952	58320	Α	28122	159	306	LGSGNLP*EINPLSSCSLFREEDP
						PTTSGPQTNQPKEHLTNFKSAA
						ED
27953	58321	С	28123	80	106	
27954	58322	A	28124	166	423	RPRSERLLWGTSPLS/CALTL*G
						DPPTTSGPQTNQLKEHLTNFKS
		l	<u> </u>			GPHWKMDCPTHPAATPRAPGT
					1	LAQGSLTDSFPDLLGSAAED
27955	58323	A	28125	1	354	
27956	58324	Α	28126	1	702	
27957	58325	Α	28127	317	427	
27958	58326	Α	28128	467	640	SARKRFQLSP**NKITLLKPASS
						AISALAATPRAPGTLAQGSLTD
						SFPDFLSLAAED
27959	58327	В	28129	1	320	
27960	58328	Α	28130	1	605	
27961	58329	Α	28131	273	529	LGSGDLPWGINPLSSCSLLREK
						DPLTISGPQTHQPKEHLTNFKSG
						PH*KSDCSTAPG\ATPRAPGTLA
		ļ <u> </u>				QGALTDSFPDLLSLAAED
27962	58330	Α	28132	459	601	DVDRHVRGSNFHHNEIRSLAAT
]				PRAPGTLAQ/GLTDSFPDLLGLA
		<u> </u>				AED
27963	58331	A	28133	112	331	LGLGDLP\WEINPLSSCSLLHEK
						DPPTTSGPQTDQPKKRLTNFKS
						ATPRAPGTLAQGSLTDSFPDLL
2 - 2 - 1		ļ	22121			GLAAED
27964	58332	A	28134	1	579	
27965	58333	A	28135	72	300	
27966	58334	A	28136	722	820	
27967	58335	A	28137	1	624	
27968	58336	A	28138	348	636	
27969	58337	A	28139	134	1131	
27970	58338	A	28140	1	1209	
27971	58339	A	28141	2	764	
27972	58340	A	28142	3	805	
27973	58341	В	28143	1	861	
27974	58342	A	28144	1	1599	
27975	58343	A	28145	119	593	
27976	58344	Α	28146	[1	573	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
27977	58345	A	28147	163	593	GFLEVQTPHPPNLDGPRRANRN TFLWTCHVGIPDLPALPAPASFL GTQLTLKKASDGPRTEKVTQD LAQPFWTTGRQLRFVLHLSLQQ KDLSKCWRGAEVVLGPTRLFL* GYSEGVKENGTGGVNK*AFSM CDSKWFNPCLTF
27978	58346	A	28148	159	405	PRLRVKYTQLCIL*S/CWRERKK FHLGKRVELRQGTTLGRVGWP KRRLSQGSAGCFPAGLAHSPPH LAEAPGSGFCTALFLWL
27979	58347	В	28149	123	1561	
27980	58348	A	28150	1	1771	
27981	58349	A	28151	68	698	
27982	58350	A	28152	1	1260	
27983	58351	A	28153	57	302	
27984	58352	A	28154	1	245	
27985	58353	A	28155	5	422	
27986	58354	A	28156	3	1372	
27987	58355	A	28157	1	1653	
27988	58356	A	28158	586	867	
27989	58357	A	28159	1	1410	
27990	58358	A	28160		1441	MDIKKGITDISASLRVESGWEA RTRKEKTHINTVIIGHVDSGKST TTGHLIYKCGGVDKRTIEKFEK EAAEMGKCSFKYAWVLDKLK AEREHGITIDISLW\KFETSKYY VTIIGAPGHRDFIKN\MITG\TSQ A\D\CAVLIVAAGVGEFESWYSP RNGQTREHALL\AYTLGC*NKL IVGV\NKMDST\EPPYS\QKRYE EIVKEGSTYIKK\IGYNPSTVAF VP\ISGW\NG*QHCLEAKWLTCP WFQGDGKVTP*GLAIASWEPRL LWRALALQSYPPTRPTDQAPLR PASPRMSYQKLGGIVNVATEV KSVEMHHEALSEVLPGDN/VGA FNVKNVSVKDVRRGNVAGDSK NDPPMEAAGFTAQVIILNHPGQ ISAGYAPVLDCHTAHIACKFAE LKEKIDRRSGKKLEDGPKFLKS GDAAIVDMVPGKPMCVESFSD YPPLGRFAVRDMRQT\VAVGVI K\AVDKK\AAGAGKVTK\SAQK
27991	58359	Α	28161	125	370	
27992	58360	Α	28162	156	547	
27993	58361	A	28163	108	919	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
27994	58362	A	28164	11	712	LNSEGNSGSGDSISYDAPAGNS
						FLEDCELSRQIGAQLKLLPMND
		ŀ				QIRELQTIIRDKTASRGDFMFSA
						DRLITLVVEEGLNQLPYKECMV
	İ					TTPTGYKYEGVKFEKGNCGVSI
]		}				MRSGEAMEQGLRDCCRSIRIGK
•						ILIQSGGETHRAQVYYAQFPPDI
						YRRKVLLMYPILQTG\NTEFEA
		1				VKVL*DHGVHPSVIIQLSPFLIP
		ŀ				HGGQ\SIIQRFPEFPI*PTEVHPV
		1				APTHFGQKYFGTD
27995	58363	A	28165	1	606	GIRSAMONTONLLOMPYGCGE
2,,,,,	30303	l'``	20103	1		ONMVLFAPNIYGLDE\LNETQQ
						LTPEIKSKAIGYLNTGYQRQLN
-					:	YKHYDGSYSTFGERYGRNQGN
						TWLTAFVLKTFAQARAYIFIDE
		ļ				AHITQALIWLSQRQKDNGCFRS
						SGSLLNNAIKVNHSGASFDLSI
						MISARMRIGSDNVKNSKGKPQ
						RKIKPGWHQKRGDRTKVDCDT
						LSYRDGYG
27996	58364	A	28166	1	4626	ESTREGTO
27997	58365	A	28167	15	4479	
27998	58366	A	28168	256	852	
27999	58367	A	28169	319	405	
28000	58368	A	28170	606	896	
28001	58369	Α	28171	1	372	FRRVACVGSAGD\TAGAEP/RG
						ACATAWVCEMAADISESSGAD
						CKGDPRNSAKLDADYPLRVLY
						CGEYCEYMPDVAKCRQWLEK
						NFPNEFAKLTVENSPKQEAGISE
						GQGTAGEEEKKKQKRGKT
28002	58370	Α	28172	1	731	LSRGSAAGGRALGRPWGARRV
						ACVGSAGD\TAGAEP/RGACAT
						AWVCEMAADISESSGADCKGD
		l				PRNSAKLDADYPLRVLYCGVC
1						SLPTEYCEYMPDVAKCRQWLE
						KNFPNEFAKLTVENSPKQEAGI
						SEGQGTAGEEEEKKKQKRGGR
		1				GQIKQKKKTVPQKVTIAKIPRA
		1]	KKKYVTRVCGLATFEIDLKEAQ
						RFFAQKFSCGASVTGEDEIIIQG
						DFTDAII\DVIQEKWPEVG**QPL
						EDLGRK
28003	58371	Α	28173	335	2297	
28004	58372	Α	28174	23	416	
28005	58373	Α	28175	1	681	
28006	58374	A	28176	1	1668	
28007	58375	Α	28177	1	1587	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28008	58376	A	28178	250	687	AATSLPFRASTIASANSILRVGV MTSIHHFVFSKRVCCNFTSKTY FMSQQSSRTCTDGGYQALPFSC SSVSPSQQQTQIKSVRPDYLLVE PPHHMGPSFFASSGLHYDQ*PH HRLHLYWVFSARPWNGDLNPS SAHDI*HE*PLHF
28009	58377	С	28179	45	179	
28010	58378	A	28180	743	1478	
28011	58379	С	28181	151	351	
28012	58380	Α	28182	2	355	
28013	58381	Α	28183	19	428	
28014	58382	В	28184	61	2118	
28015	58383	Α	28185	1	1824	
28016	58384	A	28186	150	1552	KNMETEQPEETFPNTETNGEFG KRPAEDMEEEQAFKRSRNTDE MVELRILLQSKNAGAVIGKGG KNIKALRTDYNASVSVPDSSGP ERILSISADIETIGEILKKIIPTLEE GLQLPSPTATSQLPLESDAVECL NYQHYKGSDFDCELRLLIHQSL AGGIIGVKGAKIKELRENTQTTI KLFQECCPHSTDRVVLIGGKPD RFV\ECIKIILDLISESPIKGR\AQP YDPNFYGWKPMDYG\GFTMMF DDRRGRPVGFPMRGRGGFDRM PPGRGGRPMPPSRRDYDDMSPR RGPPPPPPGRGGRSGSRARNLPL PPPPPPRGGDLMAYDRRGRPGD RYDGMVGFSADETWDSAIDTW SPSEWQMAYEPQGGSGYDYSY AGGRGSYGDLGGPIITTQVTIPK DLAGSIIGKGGQRIKQIRHESGA SIKIDEPLEGSEDRIITITGTQDQI QNAQYLLQNSVKQYSGKFF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	: Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28017	58385	A	28187	221	1634	KNMETEQPEETFPNTETNGEFG
	1					KRPAEDMEEEQAFKRSRNTDE
ŀ						MVELRILLQSKNAGAVIGKGG
						KNIKALRTDYNASVSVPDSSGP
						ERILSISADIETIGEILKKIIPTLEE
						GLQLPSPTATSQLPLESDAVECL
		1				NYQHYKGSDFDCELRLLIHQSL
		1				AGGIIGVKGAKIKELRENTQTTI
						KLFQECCPHSTDRVVLIGGKPD
						RVVECIKIILDLISESPIKGRAQP
		1				YDPNFYDETYDYGGFTMMFDD
			<u> </u>			RRGRPVGFPMRGRGGFDRMPP
						GRGGRPMPPSRRDYDDMSPRR
ļ						GPPPPPGRGG\RGGSRARNLPL
		ı				PPPPPPRGGDLMAYDRRGRPGD
						RYDGMVGFSADETWDSAIDTW
		1				SP\SEWQMAYEPQGG\SG\YDYS
						Y/AQGGRGSYGDLGGPIITTQVT
						IPKDLAG/SLFIGKGGQR\IKQIR
		-				HESGS/SSIKIDEPL\EGSEDRIITI
		ŀ				TG\TQDQIQ\NAQYLLQ\NSVKQ
28018	58386	A	28188	218	497	1G/TQDQIQ/NAQ1LLQ/NSVKQ
28019	58387	C	28189	183	254	
28020	58388	A	28190	1	1056	
28020	58389	A	28191	825	933	
28022	58390	A	28192	1	201	LVGHDRQGEHVCFYENYAEIG
20022	30370	` `		1		NR*GRNLGLTEVTGAVCEALR
						QYSPGNLLSLMGVRVSPSESEE
28023	58391	A	28193	450	509	Q10101122222
28024	58392	A	28194	2	71	SLTIPQPLSPFNLGVTLQSLPSLN
		-				FSSFPFLVENGDAFYLAATLRA
						PGTVAQGSLTPSQIFSA*WRHPS
		i				ISPFS
28025	58393	A	28195	213	350	AVSHLCGTPLEIRLFNSPGSHSQ
						SPWNSGPRLSD*LLPRSSGLSG
28026	58394	A	28196	372	782	LRSADLPWEINPLSSCSLLHEKD
						PPTSSGPQTDQPKEHLTNFKSE
						KKETRFIRGPKTPAPVMD*GRQ
				İ		PSLGV*PLQGCLSDYSPRFQRC
						QTTQGHLPWSFTLSSKSHFSGG
1						RGKSLLQVPEIWPPGQGMPAA
						QDSS
28027	58395	A	28197	189	380	SLCIFSSASALQQQWQHEGWC
20021	30373	_,	2017/	107	300	GQLLPRGHGPNRKLQQQRQWI
,						LL*VPEILPLGQGMPAAQDSS
28028	58396	1	28198	33	302	FRICALSTKLFCLSTPWCQTHIL
28028	ספנפנן	A	20190	33	302	
	1		}			SYPQYLPLLPIYSVLDLRHAFFT
						IALHPSSQPLFAFT*TDPDTH*A
	<u> </u>		L			QQITWAALPQGFTDSPHYVQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28029	58397	A	28199		532	MRVRNREEGNVGKWGERQVD QRDAVMRVRCGIWNNVGDRIE VRAENNGNCGTQQRVGTTEGA GGAESISVRLPRRSGSVSLQLLS REDLGRSQSESLGPEFQGLWK WLPDESSVWPAPGCLLLYCTH VDKEKGRRSLHVEHA*QLKTD AARSPRKPDTYTFCSPGSFSCTH S/SVESHNYHCSRPGLQSGLPHY SRYHT*PS*LH\SLIHLTFTPFPHI SFFPVSHPH
28030	58398	A	28200	266	397	SVHCQRFCRNRVPLVENQILTG ETNILHTCMHTWF*DHVWKVT
28031	58399	A	28201	21	549	LGPLPFSLSPCCLHCQGKRLCG HHEEARRRKNVSIPRKEAGIIHC KGHQK\ASDPIAQDNAYADKL AKKAASVPTSVPHGISQAPPPLP THQARYWQIDFTHMPRVRKLK YLLVWVDTFTGWVEAFPTGSK KATAVISSLLSDIIPQFSLPTSIHS DSRLAFISQITQAVSQALGIK
28032	58400	Α	28202	3	518	KRPHPYLPLLTLFSDSAHLHPG EINNHVAHTRPVWWSLHTDVH EIWCRDSDRGTSLGRSIPCPPVL CSVRKIHLQPQVLRPTSPRNISPI LNQVSGLFLLSSPTSLTVPQPLS PFNLGATLQS/APFS*FQFLSFSG RDKGDTFYPWSQNSGACHRLG KAAFPWCLIIAGTPL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,			
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide			
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)			
				sequence					
28033	58401	A	28203	3	1626	SEGEAKGSITLTVCTALYLKLT			
						LFHKTGVFGPLRFPVVNTLNPS			
						PFHDGTRELGASEAIGQCQSSA			
						AKLRRSGKESESLGPEFQGLWK			
						WLPGSSQCFARESLEEKLSLCF			
						RPSDPGAEPPRTAVRPITERSLL			
						QGDEYCCALGQGVPNPWSTDR			
				1		YWNWATLQEIGPSSCRKTSSGL			
						PLILRYGHVRDLHGSSSHHRPG			
						GPKRNKWFRELGLGSACCMRP			
						RDLVPCVPAAPAVAERGESTA			
						QAVASEGASPKPWQLPGGVGP			
						VGAQKSRIEVWEPLPIFRRMYG			
						KACMSRQKFAAGAGFSWYVPV			
į						AVVGAKVHDVNLHMLSFPSK			
						WKLHTCMKFGAVTQIVTSLGR			
									SSCSLLLEKDPPMVLRPTSPRNI
İ						SPISNLTKETRFIRGPKTPAPVT			
						DWEGSLPLVFNHCRDASLIIHP			
		1				GFRGVRPRRDACLSPSPLANLIN			
						LTFKVYNNRKKLQFLAFTVRQ			
1						TSAMSPAHKNFQ\SLNLSGQAF			
•						LQNLLPQELATSARNPATRPRN			
						ACSPGFLLSHVPSVRDPTGNWT			
						VQLTWHPLPEPLELWPKAL			
28034	58402	A	28204	921	1009				
28035	58403	Α	28205	1	1005				
28036	58404	Α	28206	1	2706				
28037	58405	Α	28207	1336	1490				
28038	58406	Α	28208	466	560				
28039	58407	Α	28209	863	1672				
28040	58408	Α	28210	1	876				
28041	58409	Α	28211	133	746	SVKMVRYSLDPEN\PMKSCK/S			
	İ	1				QRGSNLRVPFKDHS*KLPQAHQ			
		į				RVCHIRKSPTKY\LKDVHLTRN			
		ŀ				QCVPIPDRYNG*QLGQVCRRPK			
						QMGPGTTKGR\WPQKGVLKFL			
		1				PAHALKTAEM*C*TLRVLDVDS			
						LVIEHI\QVNKAP\KM\RRRTYR			
						AHGRINPYMSSPCH\IEM\ILTEK			
		ł				EQIVPKPEEEVAQKKKIS\QKKL			
						KETPTLWHGE			
28042	58410	A	28212	3	466				
28043	58411	Α	28213	1	2772				
28044	58412	Α	28214	11	1353				
28045	58413	A	28215	195	285	DIHLLYPVG/RNRGICRKK*RLR			
			L	<u> </u>	<u> </u>	S*DY*CWR			

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28046	58414	A	28216	23	561	CRPRKFYYEEDWLITKLKGQVS QESLSEKASSQATLPNQPVEKAI IMQLGTLLTFLHELVPTALPSGS CVDTL/SKGLVQNVHHTYSPCQ NFISRCVRAPEEFQKIWNSW*SC LVLI*PPCVILSFLYVQNKSKSL NYTGEKKEKPAAVATAMARVL RETKPIPNLIFAIEQYEKFLHPPV
					0.51	RETRITIVENTALEQ LERI ENTIV
28047	58415	A	28217	2383	2651	
28048	58416	Α	28218	125	1396	
28049	58417	Α	28219	466	643	
28050	58418	Α	28220	73	150	
28051	58419	С	28221	1	240	
28052	58420	Α	28222	2	499	
28053	58421	Α	28223	192	351	
28054	58422	В	28224	1	2103	
28055	58423	Α	28225	247	400	
28056	58424	Α	28226	288	589	WCSRRRGWYLLLGFHNYWRSS TFLVRCTPSCPGGCCPRYGIYPV RSCPRLPGGVSRYGSIHSG/RWC SWSPSWSPWLTSVTPRLYVAL M*AVVCPVVGKQP
28057	58425	Α	28227	319	398	
28058	58426	Α	28228	1299	1506	
28059	58427	Α	28229	1250	1907	
28060	58428	Α	28230	547	638	EKRKSNCPCLQMT*LYI*KTPSS QPKISLS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28061	58429	Α	28231	488	2358	RLSLGHWAAGKQGASDSCEKP
						TQPPSGVLESTTP/CAAPSPPNR
						DSGPCPASSPGLSRPLLSGTAW
						APPPAPPWARVRPPREVWRAD
						LLTPQGGGPATGVSGGEECDSP
	İ					VGGNPGIWKAWGHRRTRVAGI
			ĺ			GRRGGPGEADKQPLLVILRQTG
	i					SGVDLQQTPTDLQLRVLTVRR
						NTNKRKGHPHQNPICTSPSSKT
ŀ						EGRSMRQKVNKDIQELNSALH
	1					QVDLIDIYRTLHPKSTEYTFFSA
					· ·	PHHTYSNIDHIVGSKALLNKCK
						RTEIVANCLSDHSAIKPELRIKK
						LTQNCSTTWKLNNLLLNDYWR
						SKRKTHSKASRRQEITKIRAELK
						EIETQNTLQKINESRSWFFENIN
						KIDRLLERLIKKEREKNQIDAIK
						NDKGDITTDPTKIQTTIREYYKH
						LYKNKLLNLEEMDKFLDTYTL
						PRLNQEEIESLNRPITGYEIEAII
				ļ		NSLPTKKSPGSDGFTAEFYQRY
						KQELVTFLLKLFQSTEKEGILPN
						SFHEASIILIPKPGRDTTKKENFR
		1				PISLMNIDAKILNKILANQIQQHI
		1				KKLIHHDQLGFIPGMQGLFSTC
						KSINVIHHINKTKDKNHMIISID
						AEMASDKIQQPFMLKTLNKLGI
						DGMYLKIIRAIYDKPTANIILNG
28062	58430	В	28232	1	2664	
28063	58431	Α	28233	767	969	KKRVFNPEFHIQPN*AS*VKEK*
						NPLQTSKC*EILSPP\ACPKRAPE
						GSTKHGKEQPVPATAKTGQIV
28064	58432	Α	28234	804	920	RDIYSNKCPQEKPEKI*NGHPNI
		<u> </u>				TIKRIREARAKTFKS
28065	58433	Α	28235	786	935	
28066	58434	В	28236	3	1555	
28067	58435	Α	28237	895	1389	GELLEVVMTLAWSWGLFLARII
						QTQVFKAFNLFVLILRSSWAFC
						WTHGDELWALVSRKPK*HPGF
						CDHAPSTFPPPGLCP/EPTPPPGA
l				ļ		VSQYPCPPPSCPWPRWLVLPLP
						VLAGTSSPWKGFSYPPCCFSPF
						HLPARFLHRGNCLSTFDLVVLP
		L				PLEMPVLALS
28068	58436	Α	28238	704	799	EKRKSNCLCLQMT*LCI*KTPSS
2225	150:25	<u> </u>	100000	1.70	1007	QPKISLGW
28069	58437	C	28239	178	1287	
28070	58438	В	28240	1	1028	
28071	58439	A	28241	476	678	
28072	58440	В	28242	1	1059	
28073	58441	В	28243	1	924	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28074	58442	A	28244	39	200	LPLFLIECPLFPSPA*LPWPGLPT
20071	30112		20211			LC*IGVVREGIPVLCPFSKGMLP
						VFAHSV
28075	58443	Α	28245	225	314	
28076	58444	Α	28246	243	311	
28077	58445	Α	28247	21	1593	RKRTAPAGPRRHPKHCECPNCG
				+		SGKGRPS/CSQTHPPPGKLKSSP
	1			1		*SRKAENSKNQSAFSPPKDHSSS
						PVMEQSWMENDFDELTEVGFR
						SLAETQQQQKEKFRPISLMNID
						VKILNKILANRIQQHIKKLIHHD
						QVGFISGMQGWFNICKSINVIH
						HINRTNDKNHMIISIDAEKAFD
						KIQQPFMLKTLKKLGIDGTYLK
						IIRAIYDKSTASIILNGQKLEAFP
						LKDRTRQGCPLSPLLFNIALEVL
						ARAIRQEKDIKCIQLGKEKVRL
						SLFAEDMIVYLENPIVSAPNLFK
						LISNFSKVSGYKINVQKSQVFL
						YINNRQRESQIMNEFPFTIARRR
						IKYLGIQLTRDVKDLFKENYKP
		1				LLKEIKEDTNKWKNMPCSWIG
						RINIMKMAILAKVIYRFNAIPIK
						LPMTFFTELEKTTLKFIWNQK
28078	58446	Α	28248	129	239	FFLTMSMECSSICLCPPLFR*AV
İ	1					VCRSP*RGPSHPL
28079	58447	Α	28249	3	254	GTAWAPPPAPPWARVRPP\EKC
					GAPTCSHPREEAPRLASPAGKN	
		1				VTVPWGETQGSGRLGVTGEPE
						LLGLGGAGALARLISSLCW
28080	58448	Α	28250	80	517	GHFLGQQPRPQLHSPAPD\PPAP
						TPTDAEGLPQQQQLPQLEPQPE
						CQGPVEAEARQLKSCMKPVRR
ŀ						RPAEEELKTKNMDDNTFAMAE
ŀ						HPDVQESVGPLVAPTPLRPWPQ
						MTLQVCWSLLEFHSRPCLPGY
						HQQRLQNSKDCCLFLP
28081	58449	Α	28251	1	670	
28082	58450	Α	28252	1450	1650	QWISRQKLYKPEESGGQYSTFL
						KKRIFNPEFHIQPN*AS*VKEK*
						NPLQTSKC*EILSPPGLPYKSS
28083	58451	Α	28253	1010	1294	QRFSWQKLYKPEESGGQYSTFL
						KKRIFNPEFHIQPN*AS*VKEK*
						NPLQTSKC*EILSPPGLPYKS\PE
						GSAKHGKEQPIPTTAKTCQIVK
						TIQA
28084	58452	Α	28254	41	812	
28085	58453	В	28255	1	2957	
28086	58454	В	28256	650	3212	
28087	58455	Α	28257	1	556	***

SEQ ID	SEQ ID NO:		SEQ ID NO:		I P	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28088	58456	A	28258	378	566	KHSQGILLQVPEIWPLGQGMPA SRDSS*AVSHLCGTPLEIGWSNL PGSHSQSPWNSGPRLSD
28089	58457	Α	28259	1	253	
28090	58458	Α	28260	409	884	
28091	58459	Α	28261	1	2256	
28092	58460	Α	28262	118	302	
28093	58461	Α	28263	558	659	
28094	58462	Α	28264	1	400	
28095	58463	Α	28265	308	433	
28096	58464	Α	28266	1	711	
28097	58465	Α	28267	559	657	
28098	58466	Α	28268	1	400	
28099	58467	В	28269	232	498	
28100	58468	Α	28270	1	2978	
28101	58469	В	28271	128	290	
28102	58470	A	28272	3	193	DVNIFIRYGLWCFLSPFGLL*QF WRLEVQYQDAADSMSGGDPLS HS
28103	58471	В	28273	125	197	
28104	58472	Α	28274	1	1776	
28105	58473	A	28275	19	223	GFPNRTALPKNGNKNGGEASM VRGCLERAET*GCPNGMPQGE RLSRFGLRTETTGTVTFRLHCL QQSR
28106	58474	A	28276	3	334	
28107	58475	A	28277	2	1698	
28108	58476	В	28278	1	1281	
28109	58477	A	28279	198	532	NSLFLLCLCQALVSG*CWPHK MS*GGFPLFLLTGIVS/GRNGTS SSLYLW*NSAVNPSGPGLFLVS RLLTIASISEPVIGLFRDSTSSWF SLGRVYVSRNLSISSRFSSLFA
28110	58478	A	28280	3	610	TDFCFCFWLPGLSVLFLSFFLSF FLSFFLSFFLSLSFSFSLSLFLFLS VSLSFLPSFLFLSLSLSLFLSLFS LL/YCLSFLSLFSFFFFFLLLSFSLSS SLLFSSLLFSSLLFSS
28111	58479	A	28281	203	470	QAKSVWKKILSFRI*LHRMSDG IFWLCFYISMHLCWLVLYWAV WFKLQTTRLSRWLTDSLPVSY GYCQGMNEGCSSQFKTVFPTLF SAS
28112	58480	A	28282	164	338	GGGGVHVYQTS/GDIRKKEISK EISKG/LTKTPRLLVMSPSSCSR RGIWPNPDTCPLLLL
28113	58481	С	28283	1	603	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28114	58482	Α	28284	179	445	QLSGLASGMRESRDVLGLRFTP LLLWIVHSRAWALVESAVMST WECWVGDERGTGVKLAGAHT ELPTGPGV*YSPPCVHVFSLFNS HL
28115	58483	Α	28285	128	381	
28116	58484	Α	28286	1	1392	
28117	58485	С	28287	1	3169	
28119	58486	Λ	28288	693	905	AQLPTPAPLPFLGRRWGTWGFP GHAFHSWFWYST\GEGAMGSF LALLSFPPLGMKLAILEDFFGIS GTAAPLGSSFGSSLRSSLSVTEA LLARSL/HFLLILLPLLFLLLFLIA FQRTLLVGQCPAKSPLGNALEC NLGAAGSRAHGGEHATGGLQL LALFEAGQSLQPLTACVPGPRP LTCL EESIS*KWPYCPSFHNLHPQAY KAIPHPASLGKT*YNQDNNNAG KLFKANRNPALGCQQPVCSKT DGFRF
28120	58488	Α	28290	3	427	
28121	58489	A	28291	1	1195	
28122	58490	Α	28292	158	779	
28123	58491	Α	28293	227	378	
28124	58492	Α	28294	1	621	
28125	58493	Α	28295	1	351	
28126	58494	Α	28296	1	507	
28127	58495	Α	28297	1	543	
28128	58496	Α	28298	343	428	
28129	58497	Α	28299	785	1178	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	ı	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28130	58498	A	28300	842	2592	 IREEVESLKRPITSSDIEAVINSL
20130	30490	^	28300	042	2392	
						SIKKKVQYQTDSQPNSTRGENL
						GNTIQDTGMGKDFITKTPKAM
						ATKAKIDKWDLIKLKSFCTAKE
				}		TIIRVNRQPTEWEKIFEIYPSNK
		l				GLISRIYKELKQIYKKKTNDPIK
		1				KWAKDMNRHFSKEDIYAAKK
						H/DEKMLIITGTWMKLETIILSK
		1				LTQEQKTKHRMFSLLIPDDGNS
		}				LTRRMLLIGISVKTPVGTGAIPG
					PVGGTTAAGAYGRKEKALSNC	
		ļ				DSILALALAKMSENQMSMESFF
		ŀ				EKGKDPMRRQQKTLTLTKKKN
						AFKRKYQESYLNYGFIATVRAS
						FLVANCIVKAKKPFTIGEELILP
						AAKDICYELLGEAAVQKVPHV
						PLPVSTITRPIDEIAEDIEAQFLE
						RINESLWYTIQIDKSTIADNKAT
	1					MLVFVQYIFQEDVHEDVFFQES
						LRATSQPLKTPQTGKEWVHDPF
	•					VDKPSESTLSMLEEDQLLEIAN
						DGSLKSMFEKTSNLHIVCIKVK
						AEYPEIATKALRRLLAFPWVAA
						VDRECQWGSRDVEMRRLLDPK
						AGFSLLGVGNCHCLRTLEFVGL
						SMSSLCGAMLLCGLRAAPYISL
						RDHKGQGTLL
28131	58499	Α	28301	1	1662	, , , , , , , , , , , , , , , , , , , ,
28132	58500	Α	28302	2	406	CWWDCKLVQPLWKSVWRFLR
						DLELEIPFDPAILLLGIYPKDYKS
		l				CCYKDICT/RVCVPAALFTIANT
						WNQPKCTSMIDWVKKMWHIY
	1					TMEYY\AAIKKDEFMSFAGT*M
						KLETIILSKLTQEQKTKHRMFSL
						ywks
28133	58501	A	28303	1	1404	
28134	58502	Α	28304	68	2269	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	1	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28135	58503	A	28305	189	1890	MKMASSLAFLLLNFHVSLLLV QLLTPCSAQFSVLGPSGPILAM VGEDADLPCHLFPTMSAETME LKWVSSSLRQVVNVYADGKEV EDRQSAPYRGRTSILRDGITAG KAALRIHNVTASDSGKYLCYFQ DGDFYEKALVELKVAALGSNL HVEVKGYEDGGIHLECRSTGW YPQPQIQWSNAKGENIPAVEAP VVADGVGLYEVAASVIMRGGS GEGVSCIIRNSLLGLEKTASISIA DPFFRSAQPWIAALAGTLPILLL LLAGASYFLWRQQKEITALSSEI ESEQEMKEMGYAATEREISLRE RKKIQYLTPDVILYPDMANAIL LVSEDQRSVQRAEEPHDLPDNP ERFEWRYCVLGCESFMSERHY WEVEVGDRKEWHIGVCSKNVE RKKVWVKMTPENGYWTMGLT DGNKYRALTEPRTNLKLPEPPR KVGVILDYETGHISFYNATDGS HIYTFLHASSSEPLYPVFRILTLE PTALTVCPIPK/GREFPRFPTLVP DHSLEIPLTPGLANESGEPQAEV TSLLLPAQPGAKGLTLHNSQSE PYSYRHTLKHFTDIHSIIP

SEQ ID		1	SEQ ID NO:		i e	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
28136	58504	A	28306	172	1905	MKMASSLAFLLLNFHVSLFLVQ
			Ì			LLTPCSAQFSVLGPSGPILAMV
		1				GEDADLPCHLFPTMSAETMELR
						WVSSSLRQVVNVYADGKEVED
						RQSAPYRGRTSILRDGITAGKA
		İ				ALRIHNVTASDSGKYLCYFQDG
						DFYEKALVELKVAALGSDLHIE
	İ					VKGYEDGGIHLECRSTGWYPQ
						PQIKWSDTKGENIPAVEAPVVA
						DGVGLYAVAASVIMRGSSGGG
						VSCIIRNSLLGLEKTASISIADPF :
						FRSAQPWIAALAGTLPISLLLLA
						GASYFLWRQQKEKIALSRETER
						EREMKEMGYAATEQEISLREKL
						QEELKWRKIQYMARGEKSLAY
						HEWKMALFKPADVILDPDTAN
					,	AILLVSEDQRSVQRAEEPRDLP
						DNPERFEWRYCVLGCENFTSGR
						HYWEVEVGDRKEWHIGVCSK
						NVERKKGWVKMTPENGYWTM
						GLTDGNKYRALTEPRTNLKLPE
						PPRKVGIFLDYETGEISFYNATD
						GSHIYTFPHASFSEPLYPVFRILT
						LEPTALTICPIPKEVRRVPPI/AD
1						LVPDHSLETPLDPGA*LMKVGE
20127	60505	<u> </u>	20207	11	2220	PQAGK*HLCFSLPTLGAEGLPF
28137 28138	58505 58506	A	28307 28308	134	2220 509	
28139	58507	A	28309	80	433	VKTELVGWGPSRRGWGAORSP
20135	150507	` `	2030)			AEKMGETPGAAVSRIRLGGRV
						ALRRHVRGEPLRAPDCPLGPDA
		ļ				WVPTRGSHFPGFFPREQSLS/W
						GATPPSYRSSEVRSGAESGRPAP
						DSVGSGVQAH
28140	58508	Α	28310	1	1066	
28141	58509	Α	28311	77	273	
28142	58510	Α	28312	1	415	
28143	58511	Α	28313	11	257	
28144	58512	A	28314	1	654	
28145	58513	Α	28315	2	671	PGEFTRAPRVRRRAMGISRDN
						WHKRRKTGGIRKPYHKKRKYE
						LGRPAANTKIGPRRIHTVRVRG
						GNKK\YRALRLDVGNFSWGSQ
						CCTRKTRIIDVVYNASNNELVR
						TKTLVKNCIVLIDSTPYRQWYE
						SHYALPLGRKKGAKLTPEEEEI
						LNKKRSKKIQKKYDERKKNAK
						ISSLLEEQFQQGKLLACIASRPG
20115	50511	ļ	00015		1050	QCGRADGYVLEGKELEFYLRKI
28146	58514	A	28316	3	1259	
28147	58515	Α	28317	1745	2681	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28148	58516	Ā	28318	1	2502	
28149	58517	Α	28319	1097	1417	
28150	58518	Α	28320	1	398	MTAEERDKFPTDQQAIPSMDPH
					!	WDPDSDHGDWSHKHLLTCVLE
]						GLRRIRKKPMNYSMMSTITQG
ĺ						KEENPSAFLKWLREALRKYTPL
						SPNSLRGQLILKDTFITQSAADI
						RRKLQKQALGPEQNLEALLNQ
						ATSVFYNRDQEEQAQKEKRLSS
						RSVTIRGILGQSVTRPEAHKGL
ŀ						QDIVKHLKAQGLVRKCSSDCN
						TPILGVQKLNGQWRLVQDLGLI
						NKAIIPLYPVVPNPYTLLSQISEE
		İ				AEWFTVLDLKDAFFCIPLHSDS
						QFLFACEDPTDHTSQLTQTILPH
						GFRDSPYLFGQALAQDLGHFSS
						SGTLALQYVDDLPLATSLEASC
		1				QQATLDLLNFLANQGYKASRS
ł		1				KAQLCLQQRDGQTTLYSNQGA
		ł				PEGKYSSSRMRPRVRNSLQNLK
İ						AGPSTTPALSLPTGQNLSLYVT
						ETAGIALGVLTQAHGMNPQPV
						AYLSKKIDVVAKGWPHCLRVV
		ŀ				VAVAILVSEAIKIIQGKDLTVWT
						THDVNGILGAKGSLWLSDNCL
						LRYQALLLEGPVLQIPMCAALN
		l				PATFLPEDGEPIS**PLTLRWPLP
		1				QLPLNSEASLLLLHQFSYLGMP
						LVGGSSHEPA
28151	58519	Α	28321	318	363	
28152	58520	Α	28322	812	910	RAISCCPSHW*KEKPPWRPIRKP
						PLPARWPIH
28153	58521	Α	28323	1638	2180	RSAASLLKSVRPRTHQEEETLD
						TSEHLKEQTADTSSLRTVTLTA
-						RVCGFILEVSETKNSPEGTNSG
						HILTSQMGLSPIAKRRETSASAA
						ALVSATIPICRVQGPLRVLGQE
						VFLLLLRLPTAPLPINDKPP/PN/
						TPLPRRKQAKKSPKDHKNPWAI
		L_				GYVPFKQ*GEGNLA*PGYMSPS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
ļ	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28154	58522	Α	28324	350	1563	FLYIQLYPTPITCSLKYQRKQNG
						SLFWTSRMPSSVFPCTLTPSFSL
		İ				PLRIP/PDHTSQLTWTVLPPGFR
						DSPPLFGQALAQDLGHFSSPGT
						LVLQYVDDLLLATSSEASCQQA
						TLDLLNFLANQGYKVSRSKAQ
						LCLQQVKYLGLILAKGTRALIK
						ERIQPILAYPCPKTLKQLRGFLG
						ITGFCQLWIPGYSEIARPLYTLIK
1						DTQRANTHLVEWESEAETAFK
ŀ						TLKQALVQAPGLSLPTGQNFSL
					,	YVTERAGIALGVLTQTRGTTPQ
						PVAHLSKETDVVAKGWPHCLR
		1				
						VVAAVAVLVSEAIKIIQGKDLIV
						WTTHEVNGILGEKEVYGYQTN
						AYLDTRRSALRDWCFKYARPV
						AAILLLLAFGPCIFNLPVKFVSS
						RIEAIKLQMVLQMDPQISSTNN
20177	50500	ļ.	00005	000	1140	FYRGPLD
28155	58523	Α	28325	830	1143	DWOOLD*VAOKVDVDIDGI DI C
28156	58524	Α	28326	234	510	PWQSLP*VAQKVPKDHRSLPLE
						P*TRSLNNS*QHWWLCPPARAP
						STCSTSCPARDGPPPPSPAPHGP
						RNTSVPG\HSRPGSPPP\PPRTPP
28157	58525	A	28327	2	816	VS
28158	58526	A	28328	1	1311	
28159	58527	A	28329	764	937	
28160	58528	A	28330	1	1389	
28161	58529	A	28331	1	484	
28162	58530	A	28332	72	299	
28163		A	28333	737	847	
28164	58531 58532	A	28334	1	2072	
28165	58533	A	28335	68	223	
28166	58534	A	28336	468	596	
28167	58535	A	28337	358	661	
28168	58536	A	28338	72	300	
28169	58537	A	28339	65	244	
28170	58538	A	28340	2	584	GKSRRMFPAQEEADRTVFVGN
201/0	20236	^	40	_	1007	LEARVREEILYELFLQFLI\AGPL
						TKVTICKDREGKPKSFGFVCFK
						HPESVSYAIALLNGIRLYGRPIN
						1
						VQYRFGSSRSSEPANQSFESCV
					1	KINSHNYRNEEMVVGRSSFPM
						QYFPINNTSLPQEYFLFQKMQR
						HVYNPVLQLPYYEMTAPLPNS
L		L	<u> </u>	<u> </u>	<u> </u>	ASVSSSLNHVPDLEAGPSS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28171	58539	Α	28341	2	367	MTMHYEIPVRTRRSKGTT*LPQ
						NA/SVNNMPH*TGAI*ADISMTN
]						YARIERNHLGRGNSNSKDPKLR
		ł				ESSEHLRKLKTRVVNEQTRLGL
				İ		IMETFVGRGGEAPFYFQCDKHL
						SRSFQGLGLICL
28172	58540	A	28342	98	387	RKQPPKVLQWLLLAF*SHRSW
						LSSPWPSDLWRPWAGGACARL
						LLQQPRDSASLKERQQPQSGAY
l						R*NSHLPGTEHLGEGVAVCAAS
			:			ADLNVTACWL
28173	58541	A	28344	1	269	TIDELLA TILE WE
28174	58542	A	28345	240	483	
28175	58543	A	28346	3	1174	
28176	58544	A	28347	59	310	
28177	58545	A	28348	2423	3104	FFSLFFFISLASGLSILLILSKNQL
						LDSLIF*RVFCVSISFSSALILVIS
1						CLLLAFECVCSCFSSSFNCDVR
						VSILDLSCFLL*AFSAINFPLHTA
						LNASQRFWYVVSLFSLVSKNIFI
1						SAFISLCTQ*SFRSRLFSFHVVER
						L*VRF/CNPEF*FDCTVV/WRDS
						LL*FLFFYIC*GELYFQLCGQFW
		İ				NRCGVVLKKMYILLIWGGEFC
		ł				RCLLGLLGAELSSIPGYSC
28178	58546	A	28349	2006	2830	FFSLFFFISLASGLSILLILSKNQL
20170	30340	1	20347	2000	2030	LDSLIF*RVFCVSISFSSALILVIS
1						CLLLAFECVCSCFSSSFNCDVR
1						VSISDLSCFPLWAFSAINFPLHT
						ALSASQRFWYVVSLFSLVSKNI
						FISAFISLCTQ*SFRSRLFSFHVV
						ERL*VRF/CNPEF*FDCTVV\WR
						*FVIISVLLHLLRRALLPTMWSI
						LE*VWCGAEKNVYSVDLGWR
						VL*MSIRSAWCRAEFNSWVSLL
						TFCLVDLSFSLAALNIFSFISTLV
		1				NLTIMCLGVALLEEYLCGVLCI
28179	58547	В	28350	1	3135	NETIMELO VALLEET LEG VECT
28180	58548	A	28351	3506	4187	FFSLFFFISLASGLSILLILSKNQL
20100	36346	^	26331	3300	14107	LDSLIF*RVFCVSISFSSALILVIS
	}					CLLLAFECVCSCFSSSFNCDVR
						VSILDLSCFLL*AFSAINFPLHTA
						Į.
					1	LNASQRFWYVVSLFSLVSKNIFI
						SAFISLCTQ*SFRSRLFSFHVVER
						L*VRF/CNPEF*FDCTVV/WRDS
						LL*FLFFYIC*GELYFQVCGQFW
						NRCGVVLKKMYILLIWGGEFC
]		<u></u>			RCLLGLLGAELSSIPGYPC

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28181	58549	Α	28352	2150	2831	FFSLFFFISLASGLSILLILSKNQL
						LDSLIF*RVFCVSISFSSALILVIS
						CLLLAFECVCSCFSSSFNCDVR
				İ		VSILDLSCFLL*AFSAINFPLHTA
		}				LNASQRFWYVVSLFSLVSKNIFI
		1				SAFISLCTQ*SFRSRLFSFHVVER
						L*VRF/CNPEF*FDCTVV/WRDS
						LL*FLFFYIC*GELYFPVCGQFW
						NRCGVVLKKMYILLIWGGEFC
						RCLLGLLGAELSSIPGYPC
28182	58550	Α	28353	1	3531	
28183	58551	A	28354	1	3126	
28184	58552	Α	28355	2357	3083	FFSLFFFIILASGLSILLIPSKNQL
			1			LDSLIF*RVFCVSISFSSALILVIS
						CLLLAFECVCSCFSSSFNCDVR
						VSILDLSCFLLWAFSAINFPLHT
İ						ALNASQIFWYVVSLFSLVSKNIF
						ISAFISLCTQ*SFRSRLFSFHVVE
İ						RF*VRF/CNPEF*FDCTVV/WRD
	Ì					SLL*FLFFYIC*GELYFQVCGQF
F						WNRCGVVLKKMYILLIWSGEF
		İ				CRCLLGLLGAELSSIPGYPC*FF
	<u> </u>					VLLICLMLTVGC
28185	58553	Α	28356	6412	7092	FFSLFFFISLASGLSILLILSKNQL
	Į					LDSLSF*RVFCVSISFSSALILVIS
		1				CLLLAFECVCSCFSSSFNCDVR
						VSILDLSCFLLWAFSAINFPLHT
						ALNVSQRFWYVVSLFSLVSKNI
1						FISAFISLCTQ*TFRSRLFSFHVV
						ERL*VRF/CNPEF*FDCTVV/WR
						DSLL*FVFFYIC*GELYFQLCGQ
		1				FWNRCGVVLKKMYILLIWGGE
						FCRCLLGLLGAELSSIPGYPC
28186	58554	A	28357	1	2019	
28187	58555	Α	28358	1	1263	
28188	58556	Α	28359	77	304	
28189	58557	A	28360	1	756	O O D MILL A ON ITA THE O A VICE A CO.
28190	58558	A	28361	1	369	QQRTLLASNEAFKSQAKSASQP
						ASKYMKENDQLKKG\AAVDGG
						KLDVGNAEVKLEEENRSLKAD
			Ì			LQKLKDELASTKQKLEKAENQ
]			VLAMRKQ/SPEGLTKEYDRLLE
	ļ	<u> </u>				EHAKLQAAVDGPMDKKEE
28191	58559	A	28362	879	1156	
28192	58560	Α	28363	54	407	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28193	58561	Α	28364	620	1246	GSTWHGWDGSRCRSQNRWSC
						MTKRSSQPSSLS*SRSRRRWMS
						SSPNW*KTGPESSMSRMSSAG*
					!	SAASSRSCATRWTRRRPAAWR
	1		•			G*GVTPVAWWPPWTCSWSRPR
						EPGSGWPKPSVCWNSSEMRTT
						MSSSGSSTPWPPVSRRRPWTER
		ĺ				RLGSVRGDRLRERSRPAVNRTP
	İ					RMSRVPSGAPRGTPSRRWWM
						MKCWDHQMRGLVEEEVG
28194	58562	Α	28365	86	402	KGWWCRKKGWNWKRSWFLT
						FLQGLLEGPHPPSPTPAPRRTT*
						SLYSAPSRMVQVLLDDLHKWF
						LYSCLVSAISIGIKFPLKIHISPGS
		l				GVLEARETMSHFKEAAL
28195	58563	Α	28366	54	353	
28196	58564	Α	28367	66	352	
28197	58565	Α	28368	442	700	HWNKVPAENPHLPWVRCSPPT
		ļ				PLGKPKPCSSWNRRSGTDVSGT
						GLSESGSSWPSGSCNGVTGTDA
1					-	YGP\GYVKSGSFPGPRVRGTV
28198	58566	Α	28369	1205	1722	WTDFRSIGLMALAGSVLELSAR
						SKDATPDPPRGLGKFPPRLPQA
		i				PRLLGSQRLLSTLCSTLSGRGG
						KNTSRLSFSPSGSVKGRVRDVK
						EPGPIRAHRTAFFPNASS\GSEG
						R*SPSVVAWRGFR/CVGVWRFP
		1				TVGVWHAPPRCTR*SPITGSAP
		ł				LSVWSPPACTGSPTCTAGA
28199	58567	В	28370	163	387	
28200	58568	В	28371	112	419	
28201	58569	Α	28372	1	1902	MSRIAWKLLWKLIQGYLGQPA
						GTARRHPGIGIFKSPPGDFTCNG
						LIAVIKNQSDNQRGMSPGSWSP
						GRENNPTLVEVLEGVVRLPETV
						HTAVRYTSIELVGEMSEVVDRN
2						PQFLDPVLGYLMKGLCEKPLAS
	1					AAAKAIHNICSVCRDHMAQHF
						NGLLEIARSLDSFLLSPEAAVGL
	}					LKGTALVLARLPLDKITECLSEL
						CSVQVMALKKVFVGATSRRVA
						KLFREGLKAHGNSFETSGEAER
						CCTWRPKEMTCVE
28202	58570	Α	28373	1	2019	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28203	58571	A	28374	2	1455	SAAVAARSPQPQRPSATLGPGP QRRPPSAAPTPAWAAAAAPGS RRRRPLPARPLWAPARGAAAA GPAEAPMLARRKPVRAALTINP \TIAEGPSP\TSEGASEANLG\DL QKKLEELE\LDEQ\QKKRLEAFL TQKA/RRVGELKDDDFERISE\L GAGNG\GVVTKSPAQDPSGLIM \ARKLIH\LEIQAGASGNQIIPR/D LQVLHDGTWPTMGG\FYGAFY SDGE\ISICIEHMDGGSL\DQVLK E\AKRIPEEI\LGKVSHRSFSGGL AYLREKHQIMH\RDVKPS\NILV \NSRGEIKLCDFGVSGQLIDSM\ ANSFVG\TRCYM\APERLQG\TH YSVQSDI\WSMGLSLVELAVGR V\PIPPRDAEELEAIFGRPVVDG EEGEPHSISPRPPPGRPVSGHG MDSRPAMAIFELLDYIVNEPP\P KLPNGVFTPDFQE\FVNKCLIKN P\AERADLKMLTNHTFIKRSEG\ EEVDFAGWLCKTPAG*TKPGTP
28204	58572	A	28375	229	257	VTRTAV VSLSASPLVSLAGRSPSRPLGRG CQSLDGYGVGWQAQSPGADE GNRSFT*PELADKNVPNLHVM KAMQSLKSRGYVKERLPSSAP GDCACHPTP
28205	58573	A	28376	3	397	MFNLRGKRLS/GNGRVFSLQAP KQQK*PGGTEDS/YDASGPPPKF LIKEIKLGVPRFFPIRGV*NPGPG KNFGGPFKKT*FCWARVPKM* FFKGGPSSSSPAVSLFNAKESSPI LLRWMTTSTTKSAYKLEFGC
28206	58574	A	28377	1	367	
28207	58575	A	28378		1001	MSWEMEQDEVYKEMSINHKN EGTRVEKPNRYRIIHIQPDAINH VSRKKDVPSASGAGHSRSSTGS RPGVRRLWPLLLRSAPSGPLNN AVPAPGKGPGRWGGSPSLSRSG GKASTRVAPGLSAHSQAASGV PEPAEPQHQRTKASGSRRRSLR VVPEAPKPRTRTAREGKGAGA GHTGGAQEQRRRRWACRGLR GRPGAVSPGGAEAINQLASEHC GNPAAALHRCIASLPRNLLVW AGRMLMPKKNRIAIYELLFKEE VTVVKKDVHMPKHLELADKNS RGYYVKEQFAWRHVYWYLTN ED/MPVSP*LPSSAPGDCACHPT PQPSRDWQASV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28208	58576	A	28379	1	1827	
28209	58577	A	28380	520	680	AEACQSLDGYGVGWQAQSPG ADEGNHGDTGYPHW*GTSRNV SRQTVQTRSLGT
28210	58578	Α	28381	168	378	
28211	58579	A	28382		900	GTRDATAEENRVLLAMVNPTV FFDIAVDGEPLGRVSFEVRGLD TKK*LLI*SIKLC*QIGGSSIFITS D*KNSCLPLIVQQCLLFLRILP\L FADKVPKTAENFRALST\GEKG FGL*GVPCFHRIIPGFMCQGGDF TRHNGT\GGKSI\YGEKFEDENFI LKHTG\PG\ILSMAKCWDPTQN GSQFFNLALAKTEWLGWASHV GVLAK*KKGMNIVEAMERFGS RNGKTSKMITTADCGQLRIKFD LVFYLNHQDHSFWKPQGEHPS NPFARRILRILWLSLAVPFWVPC FPCSLPCLAGLQS
28212	58580	A	28383	393	683	HAKDGMEQRGNNECPKVGKQ VTLQHSDPEDRKTSTRCGENLY MSSDPTSWSSAIQSWYDEILDF VYGVGPKSPNIVLLVII*IIERIPR TNKEHLVPV
28213	58581	A	28384	119	193	
28214	58582	A	28385	1	567	
28215	58583	A	28386	957	1145	EQNLLIYLVSIVQDCMDKGCII* LRHTSGNCMYVSDKFDFKEQCI FSPRSSQKSLSGNDLQK
28216	58584	Α	28387	153	2257	
28217	58585	A	28388	369	539	KKPARRRHLFTLLCCVFSPKLC TAGGPMRRTFKSYDEAGTGLL SVADFRTVLRQYSINLSEEEFFH ILEYYDKTLSSKISYNDFLRAFL Q*TPKL
28218	58586	Α	28389	3	1364	
28219	58587	Α	28390	1	996	
28220	58588	A	28391	296	549	ETSSSVTVSDP\EMENKGGQTL\ NNSSLMAEAPGTMCRFTLAPH V\LAVQGTITDLPDHLLSYDGSE NLSRFWYDFTLENSVLCDS
28221	58589	Α	28392	1	1065	
28222	58590	A	28393	412	428	WILPISEPPSNRIFACWGKPAWT ACCNSLRARR*RAISCCPSHW* KEKPPWRPIRKPPLPARWPDSL MQLARQVSRLESGQ
28223	58591	Α	28394	3	505	
28224	58592	A	28395	1	1201	
28225	58593	В	28396	518	1606	
28226	58594	Α	28397	1	798	
28227	58595	Α_	28398	737	3067	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28228	58596	В	28399	133	239	
28229	58597	A	28400	3	376	
28230	58598	Α	28401	1	1194	
28231	58599	A	28402	405	611	
28232	58600	Α	28403	204	4198	
28233	58601	Α	28404	1	3346	
28234	58602	A	28405	824	1144	KSQSVQKITMFTFITQLLLVVEV KDSLERLAVEVVFILQKAMYE KQAHIYMKSLCPQMVLMLRFI QWVQIMPMLKLENLQHLMAR WNETVKEKK*DTLLFSMHERN
28235	58603	Α	28406	359	517	
28236	58604	Α	28407	68	487	
28237	58605	Α	28408	2	154	
28238	58606	A	28409	3	297	RHKDSPPPHQTQEPSWLHPVDP APGLQVELPASHAPCARTPQPL GGRWDWAPWSRGWCSLGRLG PHRSPWSGWEAQA*QWIPHQG CRWSCLPVTRRVLALLSPWVV DGTGRRGAGGGARWGGSGRT GAHGVGGRLRHSRLQVPSPAL LFKYYYCDIFK
28239	58607	A	28410		609	MVFSNLKGHWLQPIRLDSGSR NTAIGCDNQYKPTGVKLQTFA VSVTALKAARLGLFVPPGGLV VSLGSGVKLQIFASQVVCFDRA LIGAFTIPELDTKVLHVPIRLVR YRVWTQRFSKAPPDSGAQLASP SESHTRAAGGAACQSQCRAPA LLSPWVVDGTGRRGAGGGAHR GGSGCTGTHGVGGRLRHSGLQ VPSSA*VSHPLRGFL/LQPEPPR* APPPAPRRPVPSTTQGLRSAGA RHWDWQAAPPAALVWDSLGE ASWAPESGGALENLCVHTLYL TNLMGTWRTFVSSSGIVNAPIS ALSKQTTWLAKICSFTPEPRETT SPPGGTNNPRRAALRAVTLTAK VCSFTPVGLYWLSQPMAVLRE PESNLIGWSQWPFRLLKT
28240	58608	A	28411	548	753	TLLWE*SRLRKKSHLMMTLNH STHSITFGLDKHCASYLMGFLYI VELLIAQCGSPGATLIQWRMAS MD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		:		sequence		
28241	58609	A	28412		903	MAKKIQLTYKCVQNWWVLGL
202-11	30007	``	20112		703	TDFKNEAADPRRVKLQTFVVS
						VTALKAARLELFIPPGGFVVSL
						ASGVKLQTFAVSVTAHKGSVD
						PKTRHKGSPSPHQTQEPSWLHP
						VDPAPGLQVELPASPAPCARTP
						QPLGGQWDWVPWSRGRCSSG
						RLGPRSSPRWGAGSGMAGCRS
						RALPHGEAAKAQRKVTAAAGP
	1					GAKHLTAWGWQGQLATPSVG
						PAEPTHTQNSHWPASAVCSPSS
						RLRLSLHTYPQAEGAGSGLGQP
		1				RKGLPQCSSRLKGSSSAAKVGA
		l				`
		1				QAEEVPRASEACEG*RAPQVLP
		1				KWEPRQRRCRERARPARAAST
20242	50610	 	20412	1170	1400	LSPLISI
28242	58610	Α	28413	1178	1480	CRHLIQSHSICLHQWDCHTQHL
						YHPQ**WNQQQLHHRCLLQG
			1			SIHLVFGPQWDPRRRRPLRGTR
		1				SAMARMOILRISREYITQEITEA
		<u> </u>				ATKRKVLSVPKE
28243	58611	Α	28414	126	407	WIPHRGCRWSCLPVPCRALALL
						SPWVVDGTGRRGAGGGARQG
		1				GWGSTGAHGVGRRLRHGGLQ
		1				VPSPAPRESS*GPARNRSQRRRS
28244	58612	<u> </u>	28415	27 .	363	DSSLRERK
28244	58613	A	28416	1	576	
28246	58614	A	28417	813	923	YSLIHAAPQQRS*SLSGPHQTY
202.0			-0117			DISSYTCQCLKAVG
28247	58615	A	28418	511	1260	ARHRVLIGVFTIPELDIKVLHVP
						TRLRSPASFTQWIPHWGCRWSC
		1				LPVPRRVPALLSPWVVDGTGG
		1				CGAGGGAHRGGWGCTGAHGG
		1				GGRLRHGGLQVASPAPREGS*G
						PARN*AQSRWAGTAGGPSTPSA
		1				AAGPGAKPLIAPGRQGNEPCH
		1				WCGARQAHAHPELQLATSASW
						TRAFRECVSPAWPSCLGAACFH
		1				CLLIGPFPFSFSSQHLSTSLGHLV
						LLSWHLTSLSVSFRILTRLLRVF
						TGSWGGGAA
28248	58616	A	28419	1	616	100 // 000 // //
28249	58617	A	28420	2879	3022	
28250	58618	A	28421	3	165	
28251	58619	A	28422	340	793	
28252	58620	A	28423	912	3097	
28253	58621	A	28424	1300	1648	
28254	58622	Α	28425	1	599	
		1	1	<u> </u>	1	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28255	58623	Α	28426	2	405	PRVRPLRPPVMVSRDQAHLGPK
						YVGLWDFKSRTDEELSFRAGD
						VFHVARKEEQWWWATLLDEA
						GGAVAQGYVPHNYLAERETVE
						SEP\RDTQAVRHYKIWRRAGGR
						LHLNEAVSFLSLPELVNYHRAQ
						SLSHGLR
28256	58624	Α	28427	3	438	
28257	58625	Α	28428	37	403	
28258	58626	В	28429	1	1176	
28259	58627	Α	28430	2	2150	
28260	58628	Α	28431	1593	3025	
28261	58629	Α	28432	322	2168	
28262	58630	Α	28433	183	591	
28263	58631	Α	28434	2	258	
28264	58632	С	28435	52	363	
28265	58633	Α	28436	1	3363	
28266	58634	Α	28437	1	918	
28267	58635	Α	28438	1	1422	
28268	58636	Α	28439	3	10899	
28269	58637	Α	28440	277	586	
28270	58638	Α	28441	3	3364	
28271	58639	Α	28442	1	1851	
28272	58640	Α	28444	3	253	CGIEDNNFSLALNPDTDILLS/HS
						GGRGAEAPTMCLKLTVSKRAC
						FEGLE\WQFNLWRNKK**C*DK
						KHKTAGCSIS*VMRSVYR
28273	58641	Α	28445	1	950	MGSSAVQSQLAALAPRVLTGG
	1					LADVTALLRAPATPGRLVAGA
ļ						RGGWGYVQSCRGAGAAAVKP
						LGSAETAVPIARLGCRRFSRSRC
						CRRRGRGSLLSFSAAKPIVFKEK
						LTMKTDSLMEEKLECSLWCCL
						SDPSTPGRCCVLERRIVPWMQQ
		l				LLANIKQAEKHEKNHPEVTVA
]		MALTDIDLQLQFSMSQPE/GPPS
		l				PGSRPS*PPPAAALLWTPAGQA
	1			•		CPGPGGAEAADPSRNSTEWLRP
		1		1		PHHSSDCLRGLAHIVSQWVSEC
						LLCSPGSPPRSPLWALCWEHWE
						TWPALPEGNQPSPEGLPPCSRS
		<u></u>				QWPQTPPASDPQ
28274	58642	Α	28446	3	213	LTQHCWTHLVRSSHSRTGSSRL
		1				HNHQLHQPCA*S*LCQKEHASR
		1				GWSEQFNLWRNKK**C*DKKH
						KTAG

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28275	58643	A	28447	142	772	LVNVDVDADLVGLCVSHRHTV EEQYSTLALLNHGPQVALKYV
						HMDEVPMPACCLEGQGCLPAL
						CGECKLQGSFILSAPGRQGSQR
İ						VGPREAQGHIVIGRKLFSTALM
						LIGGQRLEESAAIESGCMEATP
		1				QGMAGSPQVGQAKSPSVPNKE
		1				PIGDF*GGSQDYRGGIQKPID*Q
						CGPVL/SRQSELWCGGRSHSVE
1						FLLGSAASAPPGPGQA
28276	58644	Α	28448	1	1935	
28277	58645	Α	28449	2	1571	
28278	58646	Α	28450	2	301	PRPFYSKNFYKILSLYSSEFNNS
						FVDA\LGSD\QDSGNEDVFDME
						YTEAEAEELKRNAEVIVFIPEYS
						WSNSVSLFPLCPGAKGPTFSVH
20050	50645	 _	20451		1222	CRVHFGPFSSH
28279	58647	A A	28451 28452	240	1329 503	
28280 28281	58648 58649	A	28453	1039	1896	
28282	58650	A	28454	1	2397	
28283	58651	A	28455	1	4011	
28284	58652	A	28456	3	1088	
28285	58653	A	28457	1	4878	
28286	58654	A	28458	1	174	
28287	58655	Α	28459	3	161	
28288	58656	Α	28460	992	1102	
28289	58657	Α	28461	1024	1279	CGHLVSDWSTVVNLAVRRLFV
						GFPQGCQLVHIW*M/PLDAGPE
						HNSLKGFLVPLFPLAATPRAPG
		<u> </u>				TPAQGSLTDSFPDLLGLAAED
28290	58658	A	28462	3	278	HEAAMSMLRLQKRLASSVLRC
		1				GKKKVWVRPL*TNEIANANSR
		i				QQIRKLIKDGLI\IRTPVTAHSWP SCRTNTLSRRMGHS*SLRTLLD
		ł				PVNM*GLLNASWITKC*LLDPV
						NM
28291	58659	A	28463	1	1043	
28292	58660	A	28464	185	804	VTSGCGKKKVWLDPNET\NEI\
						ANANS\RQQIPEASSKMGLIIRK
						P\VTV\HSRA\RCPVKTPLARRG
						RGRATWGIR*GGKGYKPNARN
						AQRKFTW\MRENGGL*TRGCL
						RKIPVNPKKDRIANMY\HSLLPE
					1	G*RGNVFKNKADFSWEHIHKL
					1	EGRQRPRKKAPWLTQA*GPAG
						S*DPRKPRKRR*RAPPRPKKEEI
			<u> </u>			HQRLFSKE\EETKK
28293	58661	Α	28465	221	350	GPSSFRLPTLSSLHVSHGREET*
	l				<u> </u>	HSLET*RDAVSLRIFKSLSV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28294	58662	Α	28466	598	1921	TPIHNCFKENKIPRNPTYKGCEG PLQGELQTTAQGNKRGYKQME EHSMLMGRKNQYRENGHTAQ GNLQI\HAIPIKLPMTFFTELEKT TSKFIWNQKRARITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYLYQNRDIDQWNRTEPSEMT PHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS KTPKAMATKDKIDKWDLIKLK SFCTAKETTIRVNRQPKKWEKI FATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKE DIYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMAIIQKSG NNRCWRGCGEIGTLLHCWWD CKLVPHILTHRWELNNEITWTQ EGEYHTLGTVVGWGEGGGIAL GDIPNAR
28295	58663	Α	28467	1	1863	
28296	58664	Α	28468	2	1308	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	I .	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28297	58665	ĪΑ	28469	1	1901	MPESPTPLLGRDILAKAGAIIHL
						NIGEGTPVCCPLLKEGINPEVW
l						ATEGQYGRAKNAHPVQVKLK
						DSASFPYQRQYPLRPEAQQGLQ
						KIVKDLKVQGLVKTCNSPCDTP
}						ILGVQKPNGQWRLVQDLRIIDE
						AIVPLYPAVPNPYTLLSQIPEEA
						ELFTVLDLKDAFFCIPVHPESQF
						LFAFEDPSIPMSQLTWTVLPQG
						FRDSPHLFHHTLAQDLSQFSYL
	Ì					DTLVLCLPLRNQQECHQATQV
						LLNVLATCGYKVSKQKAQLCS
						QQVKYLGVKLSKGTRALNNEE
					ļ.	QIEHNCQQVIAQTYATRGDLLE
						VPLTDPNLSLYTDGSSFVEKGL
					İ	QKGGYAVVSDNGILERNPLTPG
						TSAQLVELIALPRALELGEGKR
						GSSESICFLSFLVPPMTIYTEQDL
						YNHVVPKPRNKRVPILTFVVGA
						GGLGGLGTGIGGITTSTQFYYK
		İ			1	LSQELNGDMEWVADSLVTLQD
					İ	QLNSLVAVVLQNRRALDLLTA
ļ						KRGGTCLFLGEECCYYVNQSGI
						VTEKVKEIRDQIQRRAEELQNT
		1				GPWGLVSQWMPWILPFLGPLA
						AIILLFLFGPCIFNLLVKFVSSKI
						EAVKLQIILQMEPQMQSMT/KI
						YHGPLDQPASPCSDVNDIKGTP
						PEEISTAQHLLCPNSAGSS
28298	58666	A	28470	1	432	
28299	58667	A	28471	1	4314	
28300	58668	A	28472	1	330	
28301	58669	Α	28473	1	1425	
28302	58670	Α	28474	3	1110	NEEQIEHNCQQVIAQTYATRGD
						LLEVPLTDPNLSLYTDGSSFVE
		1				KGLQKGGYAVVSDNGILERNP
		1				LTPGTSAQLVELIALPRALELGE
						GKRGSSESICFLSFLVPPMTIYT
1						EQDLYNHVVPKPRNKRVPILTF
						VVGAGGLGGLGTGIGGITTSTQ
						FYYKLSQELNGDMEWVADSLV
						TLQDQLNSLVAVVLQNRRALD
						LLTAKRGGTCLFLGEECCYYV
						NQSGIVTEKVKEIRDQIQRRAEE
						LQNTGPWGLVSQWMPWILPFL
						GPLAAIILLFLFGPCIFNLLVKFV
						SSKIEAVKLQIILQMEPQMQSM
						TKIYRGSLDQPASPCSDVNDIEG
						TPPEEISNAQPLLCPN*AGSSWS
						SRRPTSPTALGFSC
28303	58671	В	28475	1	1989	
2000	150071	<u> </u>	120113	<u> </u>	1	L

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28304	58672	A	28476		1280	MGNITADNSSMSCTIDHTIHQT LAPVVYVTVLVVGFPANCLSL YFGYLQIKARNELGVYLCNLTV ADLFYICSLPFWLQYVLQHDN WSHGDLSCQVCGILLYENIYIS VGFLCCISVDRYLAVAHPFRFH QFRTLKAAVGVSVVIWAKELL TSIYFLMHEEVIEDENQHRVCF EHYPIQAWQRAINYYRFLVGFL FPICLLLASYQGILRAVRRSHGT QKSRKDQIQRLVLSTVVIFLACF LPYHVLLLVRRYWEASCDFAK GVFNAYHFSLLLTSFNCVADPV LYCFVSETTHRDLARLRGACLA FLTCSRTGRAREAYPLGAPEAS GKSGAQEEEVTKFEGGRNGHT AKKSPCNSVQDFTGIKAVKLQI VLQMEPQMQS\KLKIYSRPLDR PASPCSDVNDIEGTPPEEISTAQ
28305	58673	A	28477	1	717	PASPCSDVNDIEGTPPEEISTAQ
28305	58674	A	28478	12	409	· · ·
28300	58675	A	28479	1	675	
28307	58676	A	28480	227	399	
28309	58677	A	28481	332	436	
28310	58678	A	28482	980	1399	
28311	58679	A	28483	132	218	RINLMHFRN*TSQQALSLSYNL FLMQRH
28312	58680	Α	28484	1	34	
28313	58681	Α	28485	985	1170	
28314	58682	Α	28486	1	1203	
28315	58683	A	28487	505	716	REPCPVSQREVWRPGCLD/HCP RQSGSLGETLRGTAE\QPWPHS QVLSNLRVLQLPLISLPSLRRRA LFPAA
28316	58684	Α	28488	1	998	
28317	58685	A	28489	477	955	TPIHNGFKENKIPRNPTYKGCE GPLQGELQTTAEGNKRGYKQM EEHSMLMGRKNQYRENGHTA QGNLQVQCHPHQATNDFLHRI GKNYFKVHMEPKKSPHRQVNP KPKEQSWRHHTT*LQ/YYTTRL Q*PK*HGTGTKTEI*INGTEQSP QK*CRISTTI
28318	58686	Α	28490	37	430	
28319	58687	A	28491	507	829	
28320	58688	A	28492	643	945	CALLHSLPQHCVQHPYRSYTHR MASCRWKWGHCHSGIKMYSIP WYSTPMEGKALGDAHPQIAHS H*GAAFL*ALY*EKS*SMANRL WYSRL*PLAGDGRRE
28321	58689	Α	28493	1092	1346	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28322	58690	Α	28494	173	527	
28323	58691	Α	28496	566	895	
28324	58692	A	28497	76	302	KGNLSPSVPSPALPCSLKYPFYD HRTKFTLTTQPFSHTLAQKENQ SPLKHMGKKRLQNIFLPIRP*DQ TPWLERS
28325	58693	Α	28498	921	1008	
28326	58694	В	28499	1	2169	
28327	58695	A	28500	455	523	YPLYHFLLHLFDSSLFSSLLVLL VVY*FC*SFQKTSSWIHYFFEGF FVSLFPSVLL*F*IF
28328	58696	A	28501	876	1061	LLPQFQSLLLVYSEIQLLPGLVL GGCMCRGIYPFLLDFLVYLHRG VYSIL*W*FVFLWDWW
28329	58697	A	28502	74	445	IALIILRYVPSIPRLLRVFSMKSC *ILSKAFSASIEIIMWFLSLVLFIC WITFIDLHMLNQPCIPGMKPT*L WWISFLMCC*IWFASILLRIFTS MFIRDIGLKFSFFVVSLPGFGIK MMLAS
28330	58698	Α	28503	1	957	
28331	58699	Α	28504	41	412	IALIILRYIPSIPSLLRVFSMKGC* ILSEAISASIEIIMWFLSLVLFI*W ITFIDLHVLNKPCIPGMKPS*SW WISFLMCCWIWFASILLRIFASM FIRDIGLKFSFFVVSLPGFGIRM MLAS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28332	58700	A	28505	11	1699	MDEFLDTYTLPRLNQEEIESLN
20332	30,00	ļ · ·	20303	ľ	1077	RPITSSEIEAVINSLPTKKCPGPD
						GFTAEFYQRYKEELVPILLKLIQ
						TIEKEGLLPNSFYEATNILIPKPG
						RDTTKKENFRPISLMNINAKILN
						EILAŢESSIKKLIHHDQDSFIPGM
		ŀ				QGWFNICKSINVIHHINRINNKN
1						HMIISVNAEKAFDKIRHLFMLK
						TLIKLGIDETSLKTVRAIYDKPT
						ANIILNGQKLEAFPLKTGIRQGC
						LLSSLLFNIVLEVLARAIRQEKEI
]			}			KDIQIGREEVKLSLFADDMIVY
						FKNPIVSAQNLLKLIGNFSKVSG
						YKINVQKLQAFLYTNNRQTESQ
						IVSELPFTIAAKRIKYLGIQLTRD
			l			VKYLFKENYKPLHKEIIEDTNK
						WKNIPCSWIGRINIMKMAILPK
						VIYRFNASPIKLLLNFFTELEKN
						CLNFIWNQKRAHIAKTILSKKN
						KAGGITLPDFKLYYKSTVTKTT
						WYWYQNRYIDQWNRTEASEIT
						PHIYNHLIFDESDKNNQWGKDS
						LHNKWYWENWLAICRKLKLD
						SFLTHYTKINSRWIKDLNAGSKI
			·			QY\HADRTKSRERRAIASSYVSS
28333	58701	A	28506	2	1689	WRAWGRGATRRSSCHRQSAPS
		-				LSRVGRSSQIRSALSAASGLWR
						RKPASAKFGRPRTGSLHLPVK*
						KAFVSLQESSA*MNLRQ*PE*D
						WISWIN*QNFGN/CQGSTLKIPV
İ	ĺ					VERKILDLYALSKEHSFSPATEQ
						SWTENDFDELREEGFRRSDFSE
	Ì	İ		1	·	LKEEVRTHRKEAKNLVKRLDK
						WLNRITSVEKSLNDLMELKTM
		Į				AREQLRDECTSFSSQFDHLEER
						KYKLPSENKHLYANKLENLEE
						MDKFLETYTLPRLNQEEVESLN
						RPITGSEIEAIINSLPTKNSPGPD
ł		ĺ				RFTAKFYQMYKEELVPFFLKLF
						QSIEQEGILPNSFYEASIILIPKPG
					•	RDPTKKENFRPISLMNIDAKIFN
						KILANQIQQHIKKLIHHDQMGFI
						PGMQDWFNIRKSINVIQHINRT
						KDKNHTIISIDAEKAFDKIQQCF
				1		MLKTLNKLGIDGTYVKIIRAIY
						DKPTANIILDGQKLEAFPLKTST
						IQGCPLSPLLFNIVLEVLARAVR
						QEKEIKGIQSGKEEVKLSLFAD
						DMTVYLENPIISAQNLLKLKSN
[FSKVSGYKINVQKSQAFLYTNN
28334	58702	Ā	28507	1	1428	, , , , , , , , , , , , , , , , , , , ,
		<u>. </u>	1	<u> </u>	<u> </u>	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28335	58703	ĪA.	28508	211	506	ILSKAISASIEIIMWFLSLVLFIC
						WIMFIDLRMLNQPCTPGMKPT*
						SWWISFLMCCWIRFASILLRIFA
						SMFIRDIGLKFSFFVVSLPGFGIR
						MMLTS
28336	58704	Α	28509	765	950	LLPQFQNLLLVYSEIQLLPGLVL
						GGCMCPGIYPFLLDFLVYLHRG
						VYSIL*W*FVFLWDQW
28337	58705	Α	28510	778	981	SQKEWYQLLFVPLVEFGCESIW
					-	SWAFFGWQAINYCLNFRTCHW
	j					SIQRFNFFLV*SWEGVCVQEFIH
						FF
28338	58706	A	28511	1761	1841	CLQLCSFGLGLSWQCGLFFGSI*
		<u> </u>				TLK
28339	58707	Α	28512	1	1641	
28340	58708	A	28513	1	2307	Nicoto Control of the
28341	58709	A	28514	170	3793	EDDDINGDLAGILLYCOFI CHILVE
28342	58710	Α	28515	178	674	ERPRIMDLAGLLKSQFLCHLVF
		1				CYVFIASGLIINTIQLFTLLLWPI
						NKQLFRKINCRLSYCISSQLVM
						LLEWWSGTECTIFTDPRAY\SS
						MGKENAIVVLNHKFGN/IDFLC
						GWSLSERFGLLGVSQKCIPPCL
						THFFGSAPPLVFLLLVIQNLQKN
20242	50711	 	20516	(00	707	QQSFYLMKWS
28343	58711	A	28516	609	707	CLQLCSFGLGLTWRCGLFFGSI* TLKYFFPIL
28344	58712	Α	28517	1	2167	
28345	58713	В	28518	65	2652	
28346	58714	A	28519	267	703	
28347	58715	A	28520	3	115	
28348	58716	Α	28521	2	317	
28349	58717	A	28522	1	2577	
28350	58718	A	28523	1	669	4.7
28351	58719	Α	28524	1	1089	A CITA CA OD A DVID CA CCCEDTECCO
28352	58720	Α	28525	91	507	AGTASASPAPNRSLSGSEPTSSS
						VTQENGADVQGHERVPWKAR
						SRRFCPMEGTFRKVPSHGSHVP
						EVSMLWKACSGSFRPVEGHSV
		1				RCALTPASGCSP*AGTASASPAP
		1				NRSLSGSEPTSSSVTQENGADV
1						QGHERVPWKARSRRFCPMEGT
1		1				FRKVPSHGSHVPEVSMLWKAC
						SGSFRPVEGHSVRCALTPASGC
						SPSKSKATVGCRCSDFCTVEEF
20252	50721	 	20525		1212	LQKIFLQVESLDRRPRCLPLT
28353	58721	A	28526	120	1213	VDIIVA A LICODETA E*DOCTENDO
28354	58722	Α	28527	130	211	KPHYAAHGQPFTAE*RPGTDNR
		<u> </u>	L	<u> </u>	L	ADNRQ

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28355	58723	A	28528	793	1382	NTTAAGRVIRLTSENGSHTTFR
	1	İ				YDVLDRLIQETGFDGRTQRYH
		1				HDLTGKLIRSEDEGLVTHWHY
						DEADRLTHRTVKGETAERWQY
						DERGWLTDISHISEGHRVAVHY
						RYDEKGRLTGERQTVHHPQTE
						ALLWQHETRHAYNAQGLANR
						CIPDSLPAVEWLTYGSGYLAG
						MKLGDTPLV**ERPADR*ASDG
:						ASPADGSTALAA*DQTCVQRA
						GAGEPLYTGQPARRGMADLRQ
		ļ				RLPGRHETRRHTAGGVHPRPPA
		ŀ				PGNAAQLRPL
28356	58724	Α	28529	1039	1689	
28357	58725	Α	28530	1	2406	
28358	58726	A	28531	1	2928	
28359	58727	A	28532	2	1271	
28360	58728	A	28533	250	929	CKI IAVICDEDTUTCE I I COIC
28361	58729	Α	28534	3	273	GKLIAVIGDEDTVTGF\LLGGIG
						ELNKNRHPNFLVVEKDTTINEIE
						DTFRQFLNRDDIGAFRLLGLCW
28362	58730	A	28535	2	415	LRNRKPDHLPPLPLPCAVTQCH
28363	58731	A	28536	1	690	
28364	58732	A	28537	2551	2651	
28365	58733	A	28538	2	295	
28366	58734	A	28539	1	316	CGHGGRQSWVSRLR*CQEAAG
						MADSCPRSGGAILAFKSAPEVI
		1				RRALSAQSLRATSSSSASGAGA
						FCLSPSKYFPETSASSSATARYV
						LGWAASSGLLTSSQKMG
28367	58735	Α	28540	1	400	
28368	58736	Α	28541	257	516	
28369	58737	A	28542	1	590	EQIASDTCHLQRVVFKNISPAD
						AHRNLCLALRGHKTVTYLTLQ
						GNDQDDMFPALCEVLRHPECN
						LRYLGLVSCSATTQQWADLSL
		1				ALEVNQSLTCVNLSDNELLG*G
						C*VAVHN/S*DTPSAFLQRVVV
					1	GKTGHLTEANLQGTLLLCWVF
						SRELTHLCLAKNPIVNTGVKYL
						CEGLRYPECKLQTLVLWNCDIT
28370	58738	Α	28543	1	2633	
28371	58739	Α	28545	127	2030	
28372	58740	Α	28546	1	3066	
28373	58741	Α	28547	259	3222	
28374	58742	В	28548	1	2640	

SEQ ID NO:	SEQ ID NO: of peptide sequence	ı .	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	T .	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28375	58743	A	28549	2556	3662	RIPLFHYGESWNLLRADQRLIF AKSWPRASRYQQGHQDLFILRS DLPSQVVQTQNISSCRNSC*G*A CMPAGRL*RIPT*K*PANRPVKR PH*GGI*SLPGSKTYAVSVR*PD QK\SDGTLQEHDGICEIHVAKY AEIFGLTSAEPNRFTQFRLSETK EITNPYAMRLYESLCQYRKPDG SGIVSLKIDWIIERYQLPQSYQR TSPCCCHMKKDVFASPSTMISS SRVSNNTSKTTIIKNQCQKDDS RRSLLVKNSRPAKCGSKRSCNT FLAGSLRCRSSPEHTTILRGGVR RCLQQQCEQTVRILHAKVAQK SYGNEKRLIIRPTIRVGPWSQTN NQTDDTSGTVVQSDYQTDDTS GTVVRTNNQTDD
28376	58744	A	28550	2469	2687	ELYH**HTSS*DHRQCRLMDYH CLEDNENRPVCWMALESLVNN EFSSTSDVWGLWSDAVGTHDS GPDALHGH
28377	58745	В	28551	1	1954	

NO: of peptide sequence hod in USSN p0/540,217 soldon for peptide of peptide sequence	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
28378 58746 A 28552 1424 3807 IPLWKWLEGDMNMN QATVLTFTTA/LAGG. KENNQKAYKETYGVS MLQIPKQQNEKYQVI TIKNIESAKGLDVWDS ADGTVAEVNGYHVYE KDADDTSIYMFYQKVI WKNAGRYFKDSDKFD KDQTOEWSGSAFTEST YTDYSGKHYGKQSET SKSDDTLKINGVEDHK GKTYONVQOFIDEGN EAETAVINHKKRKNSP DLITEAAYSLSRDQKR DQIRKSDGTLQEHOGI KYAEIFGLTSAEASKDI FAGKEVYFYRPEEDAG ESPPWIFKRAISPSRGG PYLIPFFIGLQNRFTQFI ITNPYAMRLYESLCQY GIVSLKIDWIERFQLPP PDFRRFLQVCVNEING CVSIRKPDOSGIVSKIA QPPOSYORMPDFRRRE CMHDWLCAEALAWSI VTMQVNLTSLSSDTDE NSGWVSSGSLVRFNTII KRTYPRILPDPDDPRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRPKGAAPGSQT TALQASTLAPANLLPK SKSGVVSSGSLVRRITII KRTYPRILPDPDDRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRPKGAAPGSQT TALQASTLAPANLLPK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDTLKING TIPDGDGKTYQNNQQF TSGDNHTLROPTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDTLKING TIPDGDGKTYQNNQQF TSGDNHTLROPTHYVEEL LVFEANTGTENGYQGI AYYGGGTNFFRKESQ KKRDAELANGALGIIEI LVFEANTGTENGYQGI AYYGGGTNFFRKESQ KKRDAELANGALGIIEI LVFEANTGTENGYQGI AYYGGGTNFFRKESQ KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28381 S8749 B 28555 200 2602 LKKVMKPLITSNTVTD 28381 S8750 B 28556 I 3198 28383 S8751 A 28557 I 2169	1 1	-			I .	1	*=Stop codon, /=possible nucleotide
28378 58746 A 28552 1424 3807		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
QATVLTFTTA/LLAGG KENNQKAYKETYGVS MLQIPRQQQNEKYQV TIKNIESAKGLDVWDS ADGTVAEYNGYHVVF KDADDTSIYMFYQVK WKNAGRVFKDSDKFD KDQTQEWSGSATFTSI YTDYSGKHYGKQXI SKSDDTLKINGVEDHK GKTYQNVQGFIDEGNN EAETAVINHKKRKNSP DLTEAAYSLSRDQKRN DQIRKSDGTLQEHDGI KYAEIFGLTSAEASKD] FAGKEVVFYRPEDAC ESFPWFIKRAHSPSRGI PYLIPFFIGLQNRFTQFI ITINPYAMRLYESLCQY GIVSLKIDWIIERYQLP PDFRRRFLQVCVNEIN CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDR NSGWVSSGSL VRFNTI KRTVPRILPPDDPRSA EMPGHEVPVEEHFPEA PQGARGGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKINV AQVNVSKSDDTLKINV AQVNVSKSDDTLKINV TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEI LVFEANTGTENGYQC AYYGGGTNFFRKESQB KKRDAELANGALGIIEI LLKVMKPLITSNTVTD 28380 58748 B 28554 1 2232 28381 58749 B 28555 200 2602 28382 58750 B 28555 1 3198 28383 58751 A 28557 1 2169					sequence		
QATVLTFTTA/LLAGG KENNQKAYKETYGVS MLQIPRQQQNEKYQV TIKNIESAKGLDVWDS ADGTVAEYNGYHVVF KDADDTSIYMFYQVK WKNAGRVFKDSDKFD KDQTQEWSGSATFTSI YTDYSGKHYGKQXI SKSDDTLKINGVEDHK GKTYQNVQGFIDEGNN EAETAVINHKKRKNSP DLTEAAYSLSRDQKRN DQIRKSDGTLQEHDGI KYAEIFGLTSAEASKD] FAGKEVVFYRPEDAC ESFPWFIKRAHSPSRGI PYLIPFFIGLQNRFTQFI ITINPYAMRLYESLCQY GIVSLKIDWIIERYQLP PDFRRRFLQVCVNEIN CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDR NSGWVSSGSL VRFNTI KRTVPRILPPDDPRSA EMPGHEVPVEEHFPEA PQGARGGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKINV AQVNVSKSDDTLKINV AQVNVSKSDDTLKINV TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEI LVFEANTGTENGYQC AYYGGGTNFFRKESQB KKRDAELANGALGIIEI LLKVMKPLITSNTVTD 28380 58748 B 28554 1 2232 28381 58749 B 28555 200 2602 28382 58750 B 28555 1 3198 28383 58751 A 28557 1 2169	28378	58746	Α	28552	1424	3807	HPLWKWLEGDMNMNIKKIVK
KENNQKAYKETYGVS MLQIFKQQQNEKYQVI TIKNIESAKGLDWSS ADGTVAEYNGYHVVF KDADDTSIYMFYQKV WKNAGRVFKDSDKFP KDQTQEWSGSATFTSI YTDYSGKHYGKQSLT SKSDDTLKINGVEDHE KGKTYQNVQQFIDEGN EAETAVINHKKRKNSP DLTEAAYSLSRDADTLKINGVEDHE KYAEIFGLTSAEASKDI FAGKEVYFYRPEGH KYAEIFGLTSAEASKDI FAGKEVYFYRPEGH FAGKE	20370	30740	1	20332	1,424	3007	
MLQIPKQQQNEKYQV TIKNIESAKGLDVWDS ADGTVAEYNGYHVPK ADADTSIYMFYQKV WKNAGRIVFKDSIKPIS KDQTQEWSGSAFFIS YTDYSGKHYGKQSLT SKSDDTLKINGVEDHK GKTYQNVQQFIDEGN DETEAAYSLSRDQKR DQIRKSDGTLQEHDGII KYAEIFGLTSAEASKDI FAGKEVYFYRPEEDAG ESPPWFIKRAHSPSRGL PYLIPFFIGLQNEFTQFF TITNPYAMRLYESLQQY GIVSLKIDWIIERYQLP PPFRRFLQVCVNEN CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAS VTMQVNLTSLSSDTDR NSGWYSSGSLVRFNTI KRTVPRILIPPPDDFR KRTVPRILIPPPDDFR EMPORENTE CMHDWLCAEALAS SGPPVFIGAAPGSQT TALQASTLAPANLLPK RTVPRILIPPDDFR SGWYSSGSLVRFNTI KRTVPRILIPPDDFR SGWYSSGSLVRFNTI KRTVPRILIPPDDFR SGWYSSGSLVRFNTI KRTVPRILIPPDDFR SGWYSSGSLVRFNTI KRTVPRILIPPDDFR SGWYSSGSLVRFNTI KRTVPRILIPPDDFR SGWYSSGSLVRFNTI KRTVPRILIPPDDFR SGWYSSGSLVRFNTI SGMPHTLAFT SGMPTT SGMP							1 '
TIKNIESAKGLDVWDS ADGTVAEYNGHVVF KDADDTSIYMFVVF KDADDTSIYMFVVF KDADDTSIYMFVVF KDADDTSIYMFVVF KDADDTSIYMFVVF KDADDTSIYMFVVF KDADTSIYMFVVF KDADTSIYMFVVF KDADTSIYMFVVF KDADTSIYMFV KDADTSIYMFV KDADTSIYMFV KDADTSIYMFV KDADTSIYMFV KDADTSIYMFV KDADTSIYMFV KDATTON KDATTON KDATTON KDATTON KDATTON KDATTON KDATTON KTYPEIDAC KDATTON KTYPEIDAC KYAEIFGILTSAEASKDI FAGKEVVFYFYFEIDAC ESFPWFIKRAHSPSRGI PYLIPFFIGLONRFTOFF ITNPYAMRLYESLCOY GIVSLKIDWIERYQLP PDFRRRFLQVCVNEIN CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDR NSGWYSSGSLVRFNTII KRTVPRILPDPDDPRSA EMPGHEVPVEEHFPPA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK SSGPRVPKGAAPGSQT TALQASTLAPANLLPK MYELPSSFAPVLLRLVG DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEE LVFEANTGTENGYQGF AYYGGGTNFFRKESQR KKRDAELANGALGIIE LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LSSSS SSSSS L 28555 L 3198 LSSSSS L 28555 L 3198 LSSSSS L 28555 L 3198 LSSSSSS L 28557 L 2169 LKVMCPLITSNTVTD LONG THE COLUMN LKVMKPLITSNTVTD LKVMKPLITSNTVTD LONG THE COLUMN LKVMKPLITSNTVTD LSSSSSS L 3198 LSSSSS L 3198 LSSSSS L 3198 LSSSSS L 32695 L 3198 LSSSSSS L 3169 LKVMKPLITSNTVTD LONG THE COLUMN LKVMKPLITSNTVTD LONG THE COLUMN LKVMKPLITSNTVTD LONG THE COLUMN LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITSNTVTD LKVMKPLITS							1
ADGTVAEYNGYHVVF KDADDTSIYMFYQKW WKNAGRYFKBODKFD KDQTQEWSGSATFTSI YTDYSGKHYGKQSLTT SKSDDTLKINGVEDHK GKTYQNVQQFIDEGN EAETAVINHKRKNSP DLTEAAYSLSRDQKR DQIRKSDGTLQEHDGI KYAEIFGLTSAEASKD FAGKEVYFYRPEDA FAGKEVYFYRPEDA CSTREPPSFIKRAHSPSRGI ESPPWFIKRAHSPSRGI PYLIPFFIGLQNRFTQFI ITNPYAMRLYESLQQY GIVSLKIDWIERYQLP PDFRRRFLQVCVNEIN CVSIRRPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDB NSGWYSSGSLVRFNTII KRTYPRILPPDDDPRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK PQFSPRAPVLRLVGI DNSIDSWKNAGRVFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNYSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGI AYYGGGTNFFRKESQK KRRDAELANGALGIIE LKKVMKPLITSNTVTD LKKVMKPLITSNTVTD 28380 58748 B 28555 200 2602 28382 58750 B 28555 I 3198 28383 58751 A 28557 I 2169							
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SKSDDTLKINGVEDHK GKTYQNVQQFIDEGM EAETAVINHKKRKNSP DLTEAAYSLSRDQKRN DQIRKSDGTLQEHDGM KYAEJEGLTSAEASKDJ FAGKEVVFYPREDAC ESSPWFIKRAHSPSRGI PYLIPFFIGLQNRFTQFI TINPYAMRLYESLCQY GIVSLKIDWIIERYQLOYEM CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRRE CMHDWLCAEALAWS VTMQVNLTSLSSDTDR NSGWVSSGSLVRFNTI KRTVPRILPDPDDPRSA EMPGHEVPVEEHPAPANLLPK PQGARKGDESMTKAS SSGPRVPKGAAPGSQT TALQASTLAPANLLPK QNOSSFAPVLLRLVG WFLPSSFAPVLLRLVG DNSIDSWKNAGRVFK ANDPILKDQTQEWSGS GKIRLFYTDVSGKHYM AQVNVSKSDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEE LVFEANTGTENGYQGF AYYGGGTNFFKESQF AYYGGGTNFFKESQF AYYGGGTNFFKESQF KKRDAELANGALGIJE LKKVMKPLITSNTVTD 28380							1
GKTYQNVQQFIDEGNY EAETAVINHKKRKNSP DLTEAAYSLSRDQKRN DQIRKSDGTIQEHDGID KYAEIFGLTSAEASKDI FAGKEVVFYRPEEDAC ESFPWFIKRAHSPSRGI PYLLIPFFIGLQNRFTQFP ITNPYAMRLYESLCQY GIVSLKIDWIIERYQLP PDFRRFLQVCVNEING CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDR NSGWVSSGSLVRFNTII KRTVPRILPDPDDPRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGRPVPKGAAPGSQT TALQASTLAPANLLPK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVIVSKSDTLKING TIFDGDGKTYQNVQQ TSGDNHTLRDPHYVEL LVFEANTGTENGYQG AYYGGGTNFFKKSQK KRRDAELANGALGIIE LKKVMKPLITSNTVTD LKKVMK							•
EAETAVINHKKRKNSP DLTEAAYSLSRDQKRN DQIRKSDGTLQEHDGIN KYAEIFGLTSAEASKD FAGKEVVFYRPEEDAG ESFPWFIKRAHSPSRGI PYLIPFFIGLQNRFTQFI ITNPYAMRLYESLCQY GIVSLKIDWIERYQLPP PDFRRFLQVCVNEING CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDR NSGWVSSGSLVRFNTII KRTVPRILPPDPDDPRSA EMPGHEVPVEEHPPEA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG GWFLPSSFAPVLLRUNG DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEE LVFEANTGTENGQYGF AYYGGGTNFFRKESQK KKRDAELANGALGIIE LKKVMKPLITSNTVTD LKVM							
DLTEAAYSLSRDQKRN DQIRKSDGTLQEHDGI KYAEIFGLTSAEASKDI FAGKEVVFYRPEDAG ESFPWFIKRAHSPSRGL ESFPWFIKRAHSPSRGL PYLIPFFIGLQNRFTQFF ITNPYAMRLYESLCQY GIVSLKIDWIIERYQLP PDFRRRFLQVCVNEING CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDR NSGWVSSGSLVRFNTII KRTVPRILPPDDDPRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK SSGPRVPKGAAPGSQT TALQASTLAPANLLPK DNSIDSWKNAGRVFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIEDGDGKTYQNVQQF TSGDNHTLRDPHYVEE LVFEANTGTENGYQGI AYYGGGTNFFRKESQK KRRDAELANGALGIIEL LKKVMKPLITSNTVTD							1
DQIRKSDGTLQEHDGIG KYAEIFGLTSAEASKDI FAGKEVVFYRPEDAC ESFPWFIKRAHSPSRGI PYLIPFFIGLQNRFTQFI ITNPYAMRLYESLCQY GIVSLKIDWIIERYQLP PDFRRRFLQVCVNEING CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTISSDTDR NSGWVSSGSLVRFNTII KRTYPRILPPPDDPRSA EMPGHEVPVEEHFPEA PQGARKGESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK ANDPILKDQTDWSGSGKGV WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEE LVFEANTGTENGYQGF AYYGGGTNFFRKESQB KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							EAETAVINHKKRKNSPRIVQSN
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### FAGKEVVFYRPEEDACE							DQIRKSDGTLQEHDGICEIHVA
ESFPWFIKRAHSPSRGL							KYAEIFGLTSAEASKDIRQALKS
PYLIPFFIGLQNRFTQFF ITNPYAMRLYESLCQY GIVSLKIDWIERYQLP PDFRRRFLQVCVNEIN CVSIRKPDGSGIVSIKIA QPPQSYQRMPDFRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDB NSGWVSSGSLVRFNTII KRTVPRILPDPDDPRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFPDGDGKTYQNVQQE TSGDNHTLRDPHYVEE LVFEANTGTENGYQGI AYYGGGTNFFRKESQE KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28555 10 3198 28382 58750 B 28556 1 3198 28383 58751 A 28557 1 2169							FAGKEVVFYRPEEDAGDEKGY
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GIVSLKIDWIIERYQLPOPDFRRRFLQVCVNEING							PYLIPFFIGLQNRFTQFRLSETKE
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QPPQSYQRMPDFRRRF CMHDWLCAEALAWSI VTMQVNLTSLSSDTDR NSGWVSSGSLVRFNTII KRTVPRILPDPDDPRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK 28379 58747 A 28553 2372 3570 EALLPGDQDSQSGKGV WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYGI AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGF AYYGGGTNFFRKESQF KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							PDFRRRFLQVCVNEINGAVIGIP
CMHDWLCAEALAWSI							CVSIRKPDGSGIVSIKIAWIIERY
VTMQVNLTSLSSDTDR NSGWVSSGSLVRFNTII KRTVPRILPDPDDPRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK 28379 58747 A 28553 2372 3570 EALLPGDQDSQSGKGV WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYGI AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGI AYYGGGTNFFRKESQK KKRDAELANGALGIIEL LKKVMKPLITSNTVTD 28380 58748 B 28554 1 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							QPPQSYQRMPDFRRRFLQSRPA
NSGWYSSGSLVRFNTII KRTVPRILPDPDDPRSA EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK SSGPRVPKGAAPGSQT TALQASTLAPANLLPK ONSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEE LVFEANTGTENGYQGF AYYGGGTNFFRKESQF KKRDAELANGALGIIEI LKKVMKPLITSNTVTD					İ		CMHDWLCAEALAWSIQTASYL
KRTVPRILPDPDDPRSA							VTMQVNLTSLSSDTDRDLSVVS
EMPGHEVPVEEHFPEA PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK 28379 58747 A 28553 2372 3570 EALLPGDQDSQSGKGV WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYGI AQVNVSKSDDTLKINGI TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEE LVFEANTGTENGYQGF AYYGGGTNFFRKESQF KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							NSGWVSSGSLVRFNTIKTSSGEI
PQGARKGDESMTKASI SSGPRVPKGAAPGSQT TALQASTLAPANLLPK 28379 58747 A 28553 2372 3570 EALLPGDQDSQSGKGV WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYGI AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGF AYYGGGTNFFRKESQF KKRDAELANGALGIIEL LKKVMKPLITSNTVTD 28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							KRTVPRILPDPDDPRSAIAEAPS
SSGPRVPKGAAPGSQT TALQASTLAPANLLPK 28379 58747 A 28553 2372 3570 EALLPGDQDSQSGKGV WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYGI AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGE AYYGGGTNFFRKESQE KKRDAELANGALGIIEL LKKVMKPLITSNTVTD 28380 58748 B 28554 L 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 L 3198 28383 58751 A 28557 L 2169							EMPGHEVPVEEHFPEAGTNSGS
TALQASTLAPANLLPK 28379 58747 A 28553 2372 3570 EALLPGDQDSQSGKGV WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYGI AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGF AYYGGGTNFFRKESQF KKRDAELANGALGIIEL LKKVMKPLITSNTVTD 28380 58748 B 28554 1 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 1 3198 28383 58751 A 28557 1 2169							PQGARKGDESMTKASDSSSPSC
28379 58747 A 28553 2372 3570 EALLPGDQDSQSGKGV WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVED LVFEANTGTENGYQGF AYYGGGTNFFRKESQF KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 285851 A 28557 I 2169							SSGPRVPKGAAPGSQTGKKQQS
WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGE AYYGGGTNFFRKESQK KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28555 200 2602 28381 58749 B 28556 I 3198 28383 58751 A 28557 I 2169							TALQASTLAPANLLPKAVHLA
WFLPSSFAPVLLRLVGI DNSIDSWKNAGR/VFK ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGE AYYGGGTNFFRKESQK KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169	28379	58747	Α	28553	2372	3570	EALLPGDQDSQSGKGVAAREV
ANDPILKDQTQEWSGS GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEE LVFEANTGTENGYQGE AYYGGGTNFFRKESQK KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28555 200 2602 28381 58749 B 28556 I 3198 28383 58751 A 28557 I 2169							WFLPSSFAPVLLRLVGNHHVG
GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVED LVFEANTGTENGYQGE AYYGGGTNFFRKESQR KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 l 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 l 3198 28383 58751 A 28557 l 2169							DNSIDSWKNAGR/VFKDSDKFD
GKIRLFYTDYSGKHYG AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVED LVFEANTGTENGYQGE AYYGGGTNFFRKESQR KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 l 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 l 3198 28383 58751 A 28557 l 2169							ANDPILKDQTQEWSGSATFTSD
AQVNVSKSDDTLKING TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVEL LVFEANTGTENGYQGE AYYGGGTNFFRKESQK KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 l 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 l 3198 28383 58751 A 28557 l 2169							GKIRLFYTDYSGKHYGKQSLTT
TIFDGDGKTYQNVQQF TSGDNHTLRDPHYVED LVFEANTGTENGYQGE AYYGGGTNFFRKESQK KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							AQVNVSKSDDTLKINGVEDHK
TSGDNHTLRDPHYVEL LVFEANTGTENGYQGE AYYGGGTNFFRKESQK KKRDAELANGALGIIEL LKKVMKPLITSNTVTD 28380 58748 B 28554 l 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 l 3198 28383 58751 A 28557 l 2169					1		TIFDGDGKTYQNVQQFIDEGNY
LVFEANTGTENGYQGE AYYGGGTNFFRKESQK KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 l 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 l 3198 28383 58751 A 28557 l 2169							TSGDNHTLRDPHYVEDKGHKY
AYYGGGTNFFRKESQK KKRDAELANGALGIIEI LKKVMKPLITSNTVTD 28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							LVFEANTGTENGYQGEESLFNK
KKRDAELANGALGIIE LKKVMKPLITSNTVTD 28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							AYYGGGTNFFRKESQKLQQSA
LKKVMKPLITSNTVTD							KKRDAELANGALGIIELNNDYT
28380 58748 B 28554 I 2232 28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169							LKKVMKPLITSNTVTDEI
28381 58749 B 28555 200 2602 28382 58750 B 28556 I 3198 28383 58751 A 28557 I 2169	28380	58748	В	28554	1	2232	
28383 58751 A 28557 1 2169			В	<u> </u>	200		
	28382	58750	В	28556	1	3198	
28384 58752 A 28558 I 2259			Α	28557	1		
	28384	58752	Α	28558	1	2259	
28385 58753 A 28559 I 2418			A	28559	1		
28386 58754 B 28560 I 1974	28386	58754	В	28560	1	1974	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28387	58755	A	28561	3	2077	
28388	58756	Α	28562	1907	5097	TSKKIVKQAPVLTFTTA/LLAGG
	į]		AIQAFAKENNHKAYKETYGVS
						HITRHDMLQIPKQQQNEKYQVP
						QFDQSTIKNIESAKGLDVWDSW
						PLQNADGTVAEYNGYHVVFAL
				}		AGSPKDADDTSIYMFYQKVGD
						NSIDSWKNAGRVFKDSDKFDA
						NDPILKDQTQEWSGSATFTSDG
						KIRLFYTDYSGKHYGKQSLTTA
						QVNVSKSDDTLKINGVEDHKTI
1		1			-	FDGDGKTYQNVQQFIDEGNEGI
				,		LPISEPPIKQDFRLLG
28389	58757	Α	28563	610	2303	SLPNLDNAAICSSSSSPTRTR*SL
		1				SEGATQ\AFAKEKYPHKHTKKR
					1	SGVFHITRHDMLQIPKQQQNEK
j						YQVPQFDQSTIKNIESAKALDV
		ŀ				WDSWPLQNADGTVAEYNGYH
						VVFALAGSPKDADDTSIYMFY
		İ				QKVGDNSIDSWKNAGRVFKDS
		1				DKFDANDPILKDQTQEWSGSA
		1				TFTSDGKIRLFYTDYSGKHYGK
		1				QSLTTAQVNVSKSDDTLKINGV
		1				EDHKTIFDGDGKTYQNVQQFID
						EGNYTSGDNHTLRDPHYVEDK
						GHKYRGPLESPSTHQAEFNPTS
]				CVSSLGTLQGFPAPAWLALAHP
		1				VHPLKHKSGGSNRLSAAIWGIK
						RKPARVCPGTGIHASSQIQGEW
		1				RTECAVGPKAKAKATAGWRR
		1			•	GNNQHISSTYDINRADTQVRRA
						VNNYDIIVMSNSFNGQSEHQTY
		1				ESIVIDSAPNLGIGTINVVCAAD
		1				VLIVPTPAELFDYTSALQFFDM
						LRDLLKNVDLKGFEPDVRILLT
						KYSNSNGSQSPWMEEQIRDAW
						GSMVLKNVVRETDEVGKGQIR
						MRTVFEQAIDQRSSTGAWRNA
		<u> </u>				LSIWEPVCNEIFDRLIKPRWEIR
28390	58758	Α	28564	1	2079	
28391	58759	A	28565	1	774	<u> </u>

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28392	58760	A	28566		2124	MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKANKETY GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFFKR GAIFRVHKHAVNPMSPKCRRPG GRQAYPLVNWEDRNGRSQKTV HTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFAKENNQK AYKET/YPKQQQNEKYQVPQF DQSTIKNIESAKG\LDVWDSWP LQNADGTVAEYNGYHVVSALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGRVFKDSDKFDAN DPILKDQTQEWSGSATFTSDGR RSLESTTTAARPIWRKDVGGDQ TQEWSGSAPFTSDGKIRLFYTD YSGKHYGKQSLTTAQVNVSKS DDTLKINGVEDHKTIFDGDGKT YQNVQQFIDEGNYTSGDNHTL RDPHYVEDKGHKYLVFEANTG TENGYQGEESLFNKAYYGGGT NFFRKESQKLQQSAKKRDAEL ANGALGIIELNNDYTLKKVMKP LITSNTVTDEIERANVFKMNGK WYLFTDSRGSKMTIDGINSNDI YMLGYVSNSLTGPYKPLNTTG LVLQMGLDPNDVTWASLEPHE SFQWVRGLASSGVKLQTSVVL QLIKAMWTQRVSSSKVYCKEQ
28393	58761	A	28567	1	3987	MNNASTMSKRTSAGCHCWQG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	or peptide sequence	defection,possible nucleotide insertion)
28394	58762	A	28568	1	1950	MNMNIKKIVKQATVLTFTTALL
						AGGATQAFAKENNQKAYKETY
						GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
						DSWPLQNADGTVAEYNGYHV
						VFALAGSPKDADDTSIYMFYQ
						KVGDNSIDSWKNAGRVFKDSD
		1				KFDANDPILKDQTQEWSGSATF
l						TSDGKIRLFYTGSLNSSKTEKY
						QVPHIDQSTIKNIESAKGLDVW
				İ		DSWPLQNADGTVAEYNGYHV
	1				VFALAGSPKDADDTSIYMFYQ	
					KVGDNSIDSWKNAGRVFKDSD	
					KFDANDPILKDQTQEWSGSATF	
		1				TSDGKIRLFYTDYSGKHYGKQS
						LTTAQVNVSKSDDTLKINGVED
						HKTIFDGDGKTYQNVQQFIDEG
						NYTSGDNHTLRDPHYVEDKGH
						KYL/VFEANTGTEEHPQPQ\ERP
		1				RTQSFTSAFAERRECIPNVPADT
						KLSKIKTLRLATSYIAYLMDLL
		1				AKDDQNGEAEAFKAEIKKTDV
	Ì					KEEKRKKELASKCLDLEQLGAS
						VEPTGNLRTKITKEKPRHTGPPE
				ŀ		VVVPGCCPHRSRAYKSDKYAH
				Ì		TLTVTASQHAPPPPTHMEGFEL
						FHLPDLCSPSQDAQTTGRTQMK
						PDHSPRPSHRVPQAKGNNVVIT
						SYMTNRGFFEDKKATFAPSFLM
						NIKGNKTSVVKNSILEQGQLTV
28395	58763	A	28569	2	1778	
28396	58764	Α	28570	1099	2224	DGQQLIALHRLALRELQQAVH
						AGLPQQAKILFDGGSE/TRQNPL
						QQLVHMGLPRPLDKKNFQEP
28397	58765	В	28571	1	1938	
28398	58766	Α	28572	1	2367	
28399	58767	Α	28573	4659	13369	TVFRPFHVGVHVLLIVDSCSKL
		ł				EQHSTLSRAILLIYKGFCRFRNH
		•				HQTGFSPAGANQRGPLAATLSG
						PGGEGQSAVARLTGEKKNHPG
						AQYANRLSPRVGRFINAAGTTG
						FPTGKRAVSATQLMDFADFGT
						TIKQDFRLLGQTSVDRLLQLSQ
						GQAVKGNQLLPVSLVKRKTTL
						APNTQTASPRALADSLMQLAR
						QVSRLESGQGGEDSPNRFFDGG
						RKKQIRTVRQFIDEGNNTPADT
		1		1000		QTLRDPHYVEDKGHKY
28400	58768	A	28574	6803	8521	
28401	58769	В	28575	2010	17745	
28402	58770	Α	28576	1	1060	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			}	sequence		, ,
28403	58771	A	28577	1	3585	
28404	58772	Α	28578	44	317	LKALLLTQSLFGGLLTQTRMKF
						GAVTRIG\DLPWEINPLSSCSLL
						HEKDPPTTSGPQTHQPKEHLTN
						FKSGCSSPCRAKSQFFLSLCSST
28405	58773	Α	28579	98	617	KALLLTQSLFGGLFTRTRMKFG
						AVTQIG\DLPWEINPLSSCSLLR
		İ				EKDPPTTSGPQTHQPKEHLTNF
						KSARFKKIKACYHSPATAWPFK
						AYKLSLQFPHFTCPKTRQALQV
						SSGSVPYQPNCFAYPPHGAKPI
]	İ	YSPILNTSLHNPLFCSGSQTCFL
						YYSFAPFIPASLRFHLD
28406	58774	Α	28580	i i	1500	
28407	58775	Α	28581	42	257	
28408	58776	Α	28582	3	425	KTGKYD/AVIALGTVIRGGTAH
						FEYVAGGAS/NTLAHVA/QDSEI
						PGAFGVLTLKA*TNDERAGTKL
						HGGWGGKCLTACRSALWADL
						QIRPYDHKNRGSNVHNRVPAS
						GAAAMAIHCLECGWAPLAAGD
	ļ					NVGKVCVPDAGLLPA
28409	58777	A	28583	327	1512	SYWTIHIQVSLEINHSYLPGG\IS
						SLKKMAGRNSERKTVLVKSSF
		1				QEVNRGTEALALWENGDFEAP
		ŀ				VLTFTTALLPEGATQAFGKENT
ĺ		ł				QKASKERYGSLNITRNNMLQIL
١.	1					NKQQTEKYQVPQFDQSTIKNIE
`						SAKGLDVWDSWPLQNADGTV
	1					AEYNGYHVVFALAGSPKDADD
,		1				TSIYMFYQKVGDNSIDSWKNA
						GRVFKDSDKFDANDPILKDQTQ
		1	:			EWSGSATFTSDGKIRLFYTDYS
		:		-		GKHYGKQSLTTAQVNVSKSDD
						TLKINGVEDHKTIFDGDGKTYQ
	-					NVQQFIDEGNYTSGDNHTLRDP
						HYVEDKGHKYLVFEANTGTEN
						GYQGGVNADVGDVVVRLPVW
						HRRGGEAVFMQVSRLQILRHLP
						HGVVAVDRDHHIAHDRRRHVA
		İ	ŀ			GDRSGSVRL
28410	58778	Α	28584	845	966	
28411	58779	Α	28585	215	420	NTRRWTEMTFDQVVRIFSIGNL
						QTVLQNRQPGGAIARCTGHIDP
						VTRFRPRAR*GSSHRNKAVDTQ
		1				RH
28412	58780	Α	28586	464	847	

SEQ ID NO:	SEQ ID NO:	Met hod	SEQ ID NO:	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NU:	of peptide sequence	noa	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
28413	58781	A	28587	501	823	PEVQSPDVRHIPGGA*DVLPHQ
						GIKRPDALPGPLLHA*PDNLRCS
	1.					CPRSGTAAGSIHQDARLRYSVW
ļ						RWGLLDRLAAVICRQSTHSRCR
B.						RKQRRALYRRDAGYLRRN
28414	58782	A	28588	335	902	
28415	58783	Α	28589	404	733	
28416	58784	Α	28590	2	246	
28417	58785	Α	28591	466	861	
28418	58786	A	28592	122	926	
28419	58787	A	28593	171	733	
28420	58788	Α	28594	1	774	
28421	58789	A	28595	1	1575	
28422	58790	Α	28596	1	105	SVKLGWNGVSTYVPFCLTICSV SFFQENLHLTTCRA*PSIPPPAA RRSPKKCSP*KLRLP*LSGKSSS YNL
28423	58791	Α	28597	237	461	
28424	58792	A	28598	1	1341	
28425	58793	Α	28599	1	792	
28426	58794	A	28600	16	546	QLNGRSIRHEVMSHRKFSAPRH GSLGFLPRKRSSRHRGKVKSFP KDDPSKPVHLTAFLGYKAGMT HIVREVDRPGSKVNKKEVVEA VTIVETPPMVVVGIVGYVETPR GLRTFKTVFAEHISDE/CRLLPL RQKKAHLMEIHVNGGTVAEKL DWARERLEQQVPVNPVFGQDE
28427	58795	A	28601	1	1251	
28428	58796	A	28602	37	1307	EFGFDGVMSHRKFSAPRHGSLG F\LPRKRSSRHRGKVKSFPKDDP SKPVHLTAFLGYKAGMTHIVRE VDR\PGIHRCNKKERWWRAVT HCIRPPPMVVGGHLVG\YVET\P RG\LRTFKT\VFAEHISDECKRRF YKNWHKA\KKKAFTKYCKKRQ DEDGKKQLEKDFSSMKK\YCQ VI\RVI\AHTQ\MRLLPL\RQK\KA HLMEIQV\NGGTVA\EKL\DWA REKLE\QQ\VPVN\QVFGQDEMI\ DVIGGDQRAKGFKGVTRS\WPT N*LPFKA\HLG\LSRVACFGAW HPARVAFSVARAGQKGYHHRT EINKKIYKIGQGYLIKDGKLIKN NASTDYDLSDKSINPLGGFVHY GEVTNDFVMLKGCVVGTKKR VLTLRKSLLVQTKRRALEKIDL KFIDTTSKFGHGRFQTMEEKKA FMGPLKKDRIAKEEGA
28429	58797	Α	28603	1	2133	
28430	58798	Α	28604	3	245	

NO:				Nucleotide	Tructeonide rotation or mor	Amino acid sequence (X=Unknown,
	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28431	58799	Α	28605	1	1824	
28432	58800	Α	28606	1	1035	
28433	58801	Α	28607	1	496	
28434	58802	Α	28608	1568	1793	1
28435	58803	Α	28609	1	1392	
28436	58804	A	28610	1	1389	
28437	58805	С	28611	104	253	
28438	58806	Α	28612	114	469	VSRPTYAKVFTTSKTAPQKVFP
						TAWCSA/TGHETALSATQVPIQ
						WIATAPNSPAPPSDPRRQSWVS
						QIPSSATSPNFTM*EPRTQEVTE
						PHDSRPAIPSPAVPRRESCTGRP
						HLPATTP
28439	58807	A	28613	3	2196	
28440	58808	Α	28614	237	348	NPVN*SQTT*TSE
28441	58809	Α	28615	950	1094	
28442	58810	A	28616	146	822	LGFLLRLSEMPRKQGVYRTRIW
						KFEDGLSNVLVI/PIEQINHMRD
						VFGSGSERATCLARGRGYINSL
]		ARCQNLVNRDLDHLSLPQDSTL
		İ				VHYIDDIVLHGFSEEEKGQVAQ
						SADLDEGLLKIPGDTFGPEADK
	:					DFLHKDLSTEIVGQSYNTHHM
						AQDSIPWNPSGQEPQVREHEAC
						HHLGSGSPPSWELCEQGPPVTE
						SFQVLVTSGLDKENMAYMHCG
						IICSNKKG
28443	58811	A	28617	1	1791	
28444	58812	Α	28618	244	416	
28445	58813	Α	28619	2	1520	
28446	58814	A	28620	95	421	PVTSTSTKRTPTQKPHPKVISLK
						DQIHHVDKSMMMRKNQCKNV
						EKSKNQNSSSPHDHNSSP\SARA
						ENWTEYESDKLTEVGFRGWVI
						NSSELKEHVLTHCKEAQNLHN
28447	58815	С	28621	46	174	
	58816	Α	28622	425	1291	
	58817	Α	28623	1	1410	
28450	58818	Α	28624	14	348	GLFPNKIPFSVLEIRTWAHLSGR
						HHSAHCTSCAWPQVACLPLAT
						HPSCTCTFCSLQAPGRPGQSPLS
						PRRACGPEDLPPPPYV*DLAPSL
						GPSLGPLMSQSQPRRTPPLRG
28451	58819	Α	28625	96	295	PWKPHPAWRQRWELCHPPFP/I
						RPLTAALREQPGLLGRSTTVFT
						LMAREPPQPAAADSCLCIVQME
	•	I	I	I	1	A

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28452	58820	A	28626	105	389	CQFAHGTASSPRVCLRHRCRS WQKAWAVVCCTFCSLQAPGRP GQSPLSPRRACGPEDLPPPPYV* DLAPSLGPSLGPLMSQSQPRRT PPLAWGS
28453	58821	Α	28627	461	799	
28454	58822	A	28628	1	384	
28455	58823	Α	28629	301	987	
28456	58824	Α	28630	239	384	VLPAGAQAAARSSDTRP*PEPH FS\ESVFPRWIFSAFQSLNNFFQA RF
28457	58825	Α	28631	1	1054	
28458	58826	С	28632	243	392	
28459	58827	Α	28633	1	1104	
28460	58828	Α	28634	194	863	YLLFVKNMSSLEISSSCFSLETK LPLSPPLVEDSAFEPSRKDMDE VEEKSKDVINFTAEKLSVDEVS QLVISPLCGAIS/LNWKGLTENT FEGKKVISL\EYEAYLPMAENE VRKICSDIRQKWPVKHIAVFHR LGLVPVSEAKP*SFAVSS\AHRA AISLKLLSYC/AFDTFKRPRVPI WKK\EIYEESSTWKGNKECFW ASNTLITYVFRACNLNFVKLLL
28461	58829	Α	28635	3	338	SSPPTAPAKLRIVPLVGGLPAR WCLSVCASQCPDTRVHVFLHW WCSSLCPAPVCLSLCRGL*GHF PPDSEDQSSPNCSGYTLEEYKL LRSQTIPSCNGKFPCPPRRAYDG
28462	58830	Α	28636	405	800	
28463	58831	Α	28637	265	539	
28464	58832	Α	28638	3	1116	
28465	58833	A	28640	208	350	VWLKEPSAEPAPCTWSALCGSC LLGGL*NSAFLSHRPHTSGGFFP LN
28466	58834	Α	28641	563	594	
28467	58835	A	28642	245	580	
28468	58836	В	28643	1	435	
28469	58837	Α	28644	673	1012	QPQVSFSSEYAIHIMRCPHSKIS SLYYFNCFRY*DCYCH\TFATTS ISLVRYATGCKLIPRICVRTPRAI PVFSVTYEEKSCPVGKLNTGA WVRAWKATSTSVVHLTKWVL
28470	58838	Α	28645	1171	1328	MVIGGTKNERKHIDSDEPLFPSP NSSARGRAISSTS*ALVPGVRGF LSSIPLSLTTAYPPF*SPFSS
28471	58839	A	28646	34	266	GSCS*DFLVRGAFNVINIKAWA SGPVQGSAVDLSHGLHLGLHL KNDL*FYSFNSGIDKPEIAKLSG CSFGGTFLIWG
1		1	ı			COLOGILPINO

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28473	58841	A	28648	808	926	YCYSSLDPVSLTSLLSLSLPKLK
				·		L*SYKSFFKWSPRCSP
28474	58842	В	28649	107	264	
28475	58843	Α	28650	301	470	EIQLVLSLSGGGYSHAVLMIVS
			<u> </u>			SHKI**FYKGLFPTFALHFSLLLP
						CEEGCICFPF
28476	58844	Α	28651	2	263	WEKKDTEWRKKVILSSV*LRL
			1			VIF*PFSLM\LFSHPVWR*ARSH
						ESHLAITHLWALYF*PPCQICFL
00477	50045	 	200652	62	101	*DRGHQATDGLTNGTPSELN
28477	58845	Α	28652	63	191	DLPWTPGPAC*PMLQC**GGAN
20470	50046	ļ	29652	1	554	IYARRQGADAAGDQGSSCRL MPTYCPGASLLILTYKTPKELLS
28478	58846	A	28653	1	334	IYVSTIRKSRCRERRNRRLGAR
		1				NFRSEEQIYDQWRLDQVGKFFP
						FPRPRENYHFGSEHVGSFSLDK
1						CCNEKLYEVIDLHLKKKFLNTE
i						TLSLVKCEVSRCWVTLNLLLPY
						H/VLFQI*LSWRERQNQSCKTTN
						GSSNGAPDAVHN*NLLWSLGP
						AC*PMLRC
28479	58847	A	28654	3	317	SRRLPFSLICMAKHWLPALPEN
						GYMKQFCVSGLGVLFHGCVFL
			ŀ			CWHHCCFVL*VWSLGSPRSRG
						LHLVKAFFLCYPRSNCFLLNWG
	1					IVGVVQLRFPQEGCLWCH
28480	58848	В	28655	1	400	
28481	58849	В	28656	49	492	
28482	58850	A	28657	1	917	TALETAPTLALPVSSQPFSLHTA
						EVQGCAVGILTQGPGPCPVAFL
						SKQLDLTVLGSPSCLHAVASAA
						LILLEALKITNYAQLTLYSSHNF
						QNLFSFSHLTHILSAPRLLQLYS
						LFVESPTITILPGPDFNLASHIILD
						TTPDPDDCMSLIYLTFTPFPHISF
						FSVPHVDHIWFTDGSSTRPDRH
						SPAKAGYAIESSTSIIEATALPPS TTSQQAELIALTRAFTLAKGLH
						VNIYTDSKYAFHILHHHAVIWA
		1				ERGFLT/IARVLHH*CLFNKNSS
						QGCFTSKGSWSHTLQGPPKGV
						RSHYSRKCLC
28483	58851	A	28658	3737	3886	
28484	58852	A	28659	349	1775	
28485	58853	A	28660	1	1194	
28486	58854	Α	28661	1	704	
28487	58855	Α	28662	41	275	
28488	58856	Α	28663	159	1504	
28489	58857	Α	28664	275	552	
28490	58858	Α	28665	178	619	
28491	58859	Α	28666	3	369	

28492 28493 28494	of peptide sequence 58860 58861	A A	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28493			28667			
,	58861	А		1	340	
28494			28668	516	734	WTGDWRRTCDRENQHVSGAA RTAFIPTNGAISPGINYSPGH*Y* DCHLPQA*P*LCRAAGQNRCH VARTCLG
	58862	A	28669		1163	MHTHARETCLALGKPADDATL TAAIEAVGLENAARVLKLYPFE MSGGMLQRMMIAMAVLCESPF IIADEPTTDLDVVAQARILDLLE SIMQKQAPGMLLVTHDMDKW GRIIADVESQYRYQTTNPKIFAG GDAVRGADLVVTAMAEGRHA AQGIIDWLGLDVDKLGALEERR KVLQVKTENLQAERNSRSKSIG QAKARGEDIEPLRLEVNKLGEE LDAAKAELDALQAEIRDIALTIP NLPADEVPVGKDENDNVEVSR WGTPREFDFEVRDHVTLGEMH SGLDFAAAVKLTGSRFVVMKG QIARMHRALSQFMLDLHTEQH GYSENYVPYLVNQDTLYGVGL YPLGALASGW/WALASGWLPK RRERKD/GDTGAHGVPRGSRKP
28495 28496	58863 58864	A	28670 28671	1069	4770 1398	VIGAQPVLRIRRKQARRQINRL TLILLHYCLTTKLKNGVKPGIV AAFYFLPGAG*IHPAGCHGTQL *SFGKMRVQYTRVTLSQQASG KISAYLIDLGKPLLKLIIHCGVH
28497	58865	A	28672	4246	4453	
28498	58866	A	28673	1	1185	
28499	58867	A	28674	723	878	
28500	58868	Α	28675	1085	1246	
28501	58869	A	28676	1	1254	
28502	58870	Α	28677	1	2175	
28503	58871	Α	28678	340	994	
28504	58872	A	28679	37	261	TITPAGRRMHCKGACMKPLLD VLMILDAVRELE*TITPAGRRM HCKGACMKPLLDVLMILDAVR ELEKQAIKLHEGWENELVIGVD DTFPFSLLAPLIEAFYQHHSVTR
28505 28506	58873	А	28680	410	2298	WAWAASAVQPRSIWQ/GAGVG NLTLLDFDTVSLSNLQRQTLHS DATVGQPKVESARDAPHIAITP VNALLDDAELAALIAEHDLVL D/WYG*RCGT*STERQQR*RG* RSAPAMTAHDRDAIASSSETCA RSRWSVEYASPVCAPPDSRSKR RSASNSAASHVF

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28507	58875	Α	28682	1915	5313	
28508	58876	A	28683	1	4221	
28509	58877	A	28684	1	1007	MAALQMVNGQKWVSSNQKY
						WLVYKTTDPPRLRPIFSGYQPM CPFNGRPFWIHKNPMGVHWAV ATGLALIPIVGIAEFGWFWFGG ETYMAAWNVSGLGTFGAIQST FNVTLWSFIGVESASVAAGVVK NPKRNVPIATIGGVLIAAVCYV LSTTAIMGMIPNAALRVSASPF GDAARMALGDTAGAIVSFCAA AGCLGSLGGWTLLAGQTAKAA ADDGL\FPPIFARVNKAGTPVA
						GLIIVGILMTIFQLSSISPNATKE FGLVSSVSVIFTLVPYLYTCAAL LLLGHGHFGKARPAYLAVTTIA FLYCIWAVYITHIDACVVVYIA GYRAAKLTCA
28510	58878	A	28685	867	1681	
28511	58879	A	28686	865	1290	RWWENRLFRKNPARAQKMVL PERFG*SAYPNGFAGTWRLDKL PIAQIHAHMIGYLAAVDMEKQ QISPAQVVVRHNRCPAIVVHLI GRARELSLKDLVVGIKNQPATV KAFIRPRTAPDVRLAKLLLQAV NRHFGNVMQMVAA
28512	58880	Α	28687	1	709	<u></u>
28513	58881	A	28688	2	657	LMWALPKVTRGPVYMAGSPQT AFIQVGPRVHAHLQPRAAPL*A GEVWKPRLVGRSHWASRPSPA LQKGEPGSPSWENACVPQAPH RLLHQQKAF
28514	58882	A	28689	3	227	NSQDFPACGGLCHAELDRTAA GLVHQH\RHPGHTSVAAEKLCH GDVEGDGCNGPASD/PGYI*GQ AAAPAPLPDLL
28515	58883	A	28690	1227	1719	
28516	58884	Α	28691	1	1701	
28517	58885	Α	28692	15	3298	
28518	58886	A	28693	1767	1998	YCDTTHNSYLLYDSVCRGYAR AVWRYQTDIAANLE*RRLPSGA GKSDWSSGDSEKAKTAAHTIY RDAGRRVRGYRQL
28519	58887	Α	28694	1	370	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28520	150000	<u> </u>	28695	I I	910	MDKERIIQEFVPGKQVTLAHLI
28320	58888	A	28093	1	1910	1 .
						AHPGEELAKKIGVPDAGAIGIM
						TLTPGETAMIAGDLALKAADV
						HIGFLDRFSGALVIYGSGNYTL
				ĺ		ARKTQAVEFNDKGDIDTPGEYF
						NHPRWYHALITTLQDVDMLSP
						LIWGFRNYKDVQVIKATPHKIV
						ILMGILLSPSVFATDINVEFTAT
						VKATTCNITLTGNNVTNDGNN
					•	NYTLRIPKMGLDKIANKTTESQ
	•					ADFKLVA\MGAAVASVGLIPL*
						PEMHHQAHLSLLYRSLVIHLRR
						QVISVWVSKNGLLMMPLSLNL
						TVRKRYAGAQTRCSPIRVLK
28521	58889	Α	28696	605	2021	
28522	58890	Α	28697	2256	2336	CIKCCARRIAREPGYLFS**RCK
1						YPG
28523	58891	Α	28698	1802	4488	TLLRQGSNFLMTRRCATKSWN
						V*SWIKSS/MQMGQKMGVKISD
						EQLDQAIANIAKQNNMTLDQM
						RSRLAYDGLNYNTYRNQIRKE
						MIISEVRNNEVRRRITILPQEVES
l		-				LAQQVGNQNDASTELNLSHILI
						PLPENPTSDQVNEAESQARAIV
						DQARNGADFGKLAIAHSADQQ
						ALNGGQMGWGRIHASLPGIFA
						QALSTAKKGDIVGPISSGGRFD
						GTVEVKDGHLIVNGKKIRVTAE
						RDPANLKWDEVGVDVVAEAT
		1				GLFLTDETARKHITADTPAALR
						WLEENQLEDGHECLLRRVISSD
						GRSRGFINGTAVPLSQLRETSTT
						TGARRVIRAIRRINSSDASTIPTL
					}	MAITISNNTVSDMHSSMTMMS
						TRIRTLITTIYNGDLRMIRQRKL
						CKTAIARTYGNDDTFHPGMRH
						QRMHRVFKNAPHLDQPVVTLN
						IYPKADESSSLKASRGTRGAAY
]	1					RPARQNLYSASSGKKDENPVIE
		1				FKNVSKHFGPTQVLHNIDLNIA
-		Ī				QGEVVVIIGPSGSGKSTLLRCIN
						KLEEITSGDLIVDGLKVNDPKV
		1				
		1				DERLIRQEAGMVFQQFYLFPHL
	1	1				TALENVMFGPLRVRGANKEEA
		1				EKLARELLAKVGLAERAHHYP
						SELSGGQQRVAIARTLAVKH
						KMMLFDETTFDFDPELVHEVL
						KVIHEFAEKGITNDSLTENPAKT
	<u></u>	<u> </u>				QGEGGCLQSQERGPQREPTPRH
28524	58892	Α	28699	1	2307	
28525	58893	A	28700	3	976	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
20506	150004	<u> </u>	0.0701		1126	VI CAVARCODCODECAL I VCCD
28526	58894	Α	28701	2	136	YLSAV*FCSPGQPPSALLVCGR RGYWCLWPLSSCHLTLRLCVS
28527	58895	Α	28702	1	608	
28528	58896	Α	28703	222	329	
28529	58897	A	28704	387	728	
28530	58898	Α	28705	1	1184	
28531	58899	Α	28706	478	627	
28532	58900	Α	28707	33	1072	
28534 28535 28536 28537	58901 58902 58903 58904 58905	A A A	28708 28709 28710 28711 28712	1 531 294 804	777 704 617 1020	RVVEFADEGQGPAALSLWSGS SPETLKLHWPHVQN*IRFSSWK TFRIRSRDFWADRLMRTLLRNF LSKWDHL*GQTLGVSLRRV*NE GSSPCHTPRPSAVLPPVLLDGG R*THMKLHAASSRGWLRTRLT ELEYSLVIRIRRDGGLAGLRGN SGAQGGDA HFLSGGRRQRPPRWTIVA*SPR*
						PRCRCWGSG*RPGTRGALPQPR S*WHPSGSARGRHSGSGLETSG PTVS
28538	58906	A	28713	102	510	PWPHTGGRRQRPPRWTIVA*SP R*PRCRCWGSG*RPGTRGALPV VRKQPGDPKTPLASCPELNQPV PEPAAAPTRQSKRLCYLSHVAD GILQVQARGRHSGSGLRRLLGR PSHEGPWLKGTSCRSGTTCRDR PWV
28539	58907	Α	28714	2	1580	
28540	58908	Α	28715	286	352	
28541	58909	Α	28716	1	531	
28542	58910	Α	28717	1	1440	
28543	58911	Α	28718	238	567	FGDAGKFDGKFSSHSKLLSGFD AWTELALNHRFLLQLVEVLPE ANRQLRQSGAGDGGQQAVF*F HRFLASVHQHKAASASPPYLFR IKCPVPRLRAKPALLLIDNRLYG
28544	58912	Α	28719	1	3534	
28545	58913	Α	28720	1846	2121	
28546	58914	A	28721	176	462	TSRHSVYISDTELKPRKSSKPTF CGCDSLFSPICHFP/HGLSDVALI VQQLRQRG*PLQPARLPVHWR HQNAVVDGVLSGENGGAGWG RAWLRIRRS
28547	58915	Α	28722	225	3465	
28548	58916	Α	28723	937	1770	
28549	58917	Α	28724	142	484	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	3	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28550	58918	Α	28725	1	1521	MIPITWPKFAELHPFCPPEQAEG
						YQQMIAQLADWLVKLTGYDA
		1				VCMQPNSGAQGEYAGLLAIRH
						YHESRNEGHRDICLIPASAHGT
						NPASAHMAGMQVVVVACDKN
		l				GNIDLTDLRAKAEQAGDNLSCI
						MVTYPSTHGVYEETIREVCEVV
						HQFGGQVYLDGANMNAQRRD\
						MAGKPGPLTVRKMRGSRVTVR
						AL*/ASVWIGFDDHRRNLGHTT
						ASGAIKDQISGYEGGAKSAQPA
						WDAYMKAVLEGVPEQPLTPPP
						GIVTVNIDRSTGQLANGGNSRE
						EYFIEVNEIVVNPNATLDWQLA
						LRQAAGKTDLARDMLQMLLDF
						LPEVRNKVEEQLVGENPEGLV
	ļ					DLIHKLHGSCGYSGVPRMKNL
	İ					CQLIEQQLRSGTKEEDLEPELLE
						LLDEMDNVAREASKILGGHDN
						GGNALLHKALPPGNVGKWAM
						APIPPPFPQPGKSVTICWKPASS
						ENRSNLLEIFLRELISNASDAAD
						KLRFRALSNPDLYEGDGELRVR
	-	<u> </u>	2000		1000	VDEVLSPASVPYS
28551	58919	A	28726	1	1279 762	
28552 28553	58920 58921	A	28727 28728	3	1472	MTQDELKKAVGWAALQYVQP
28333	36921	Α	20720	'	1772	GTIVGVGTGSTAAHFIDALGTM
					-	KGQIEGAVSSSDASTEKLKSLGI
						HVFDLNEVDSLGIYVDGADEIW
		1				QTCKAQRCQSPCSKTLGAQPEN
		1				PDLSQISRFPQDERRISNCSSGK
						AANPVLYWSKIEEKIASEPASIY
						SPMTLKDFSKFVKDEIGFSYTG
					·	YSRSGGGTASHGSPKSWAIGSL
						GRFGNEYSGWFDLQLKQRVYN
				1		ENGKRVDAVVMMDGNVGQQ
						YSTGWFGDNAGGENYMQFSD
		1				MYVTTKGFLPFAPEADFWVGK
						HGAPKIEIQMLDWKTQRTDAA
						AGVGLENWKVGPGKIDIALVR
						EDVDDYDRSLQNKQQINTNTID
						LRYKDIPLWDKATLMPRIPTQR
						YGLAKA/SLEAD/VRY/MANAM
						GPEGVRVNAISAGQTRTLAAPG
				1		IK\DSRK\MLAHCEPVTPIRRTVT
]		IEDVGNSAAFLCSDLSAGISGEV
						VHVDGGFSIAAMNERDPFTDL
						HRYRMNLNMMNYGAQRNM
L		1	L		<u> </u>	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28554	58922	A	28729	2	419	RPRPRPRHMLQGTHRQRHLHA GPGVARRRWGGMARRAARGR PRLRLCIFSRSRQLGLRLRFLSST VNEGDQVKTVA\RSGHFCGGLS SFSFSSSFSSGKKRPSNSPGSMR LGSPPSGAGRAGGIVTVAC*AR LSTCNTKQ
28555	58923	Α	28730	725	2804	
28556	58924	A	28731	661	1218	DVREGDRDPFMIKVHSCVFVDF AKTMHDGA/SVSLRGNLISHKG EDRY/VFRDKSGEINVVIPAA/V FDGREVQPDQMINISGIADKLP VIAPTNATSKLKLASQPEDDSEI YDGCNGAQPGDYWFAAFVSG MFSRWLAKTILSRHILSVTIRSC KNGEWLAVGGAENGAYSDSR VAVMLLLSAWGLFDF
28557	58925	Α	28732	1	624	
28558	58926	Α	28733	1	1281	
28559	58927	Α	28734	114	266	
28560	58928	Α	28735	1487	1570	
28561	58929	Α	28736	1	3402	
28562	58930	A	28737	1	2466	
28563	58931	A	28738	372	647	SGWSWNTKFPTGGFRWPAQPG TELESSQPR*LVMPATTSPFRAL DVCEYLPACVAVISGCHPSRFA RSYVSAPD*QNVQLTYPHIVLN RHL
28564	58932	Α	28739	1	2235	
28565	58933	A	28740	3	293	
28566	58934	Α	28741	737	963	
28567	58935	A	28742	3	282	RRLRASGCIDKLPSG**YARPAR *DPAPGFR*STPVRKCDQTRSPA MKVIAAADRKLWCGAICPLSA KPPAGRAPNAPAAPASPNRPMT PSL
28568	58936	A	28743	2	289	
28569	58937	Α	28744	1	1662	
28570	58938	Α	28745	421	2634	
28571	58939	Α	28746	134	954	
28572	58940	Α	28747	1036	1383	
28573	58941	Α	28748	2	589	
28574	58942	Α	28749	1	801	
28575	58943	В	28750	14	499	
28576	58944	Α	28751	3	916	
28577	58945	Α	28752	3	589	
28578	58946	Α	28753	1	1675	
28579	58947	A	28754	1	522	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28580	58948	A	28755	1229	1660	LMVSGFLTSPKDHERIIVAKPEQ FWKLRQVMFMAIVISLPTIGER FSPFLLKSPLIRPSRCGTTDFISG LTARPEFSQSRMVLIAASTITSL MCAGSFLPIRPLASICSLNATTS **LPFSSGRDSSRKRRTQAITCSP RCGS
28581	58949	A	28756	1	230	HAVCLAAVHFSSWALNNSETF NSIWSCASAILGNLGILTGSPPL ALCRTLCLTYPI*CPRDAKALR RPRECVIRHD
28582	58950	A	28757		850	MPVMFLASLSGKHQGHHFPKG ERGKFKIKERGTVATEDRRSGD STFYAIQPTRRQKRVYGLALLL QLHRRRQNLNIDSVSSVGLAAL VTAFIGVDFFANGEQTYSQPLW TWMSVGDFNIGFNLVLDGLSLT MLSVVTEGYSR*EHRPTPSQPR YISSRLSASTRTTM/PGDEQVGV SEEARVALSDHREHGQRQAVQ HQVKTDVKVAYRHPRPQRLAV CLLAVSEEINADKGGYQRRQA HRAY
28583	58951	Α	28758	20	282	
28584	58952	A	28759	38	966	RDGLESRGRVCSLRTAFQRSSS EAFTSDLQAAELQNRASNRPAR IGHAHLVIFPVQSSWM*RKLAS PRNNLVIPQEKALKEYIKIGNLV MSLAAAPLNR*GLL/IEWNDND GGCKGACDRVPHQNVTALNLR DQCINGECYDEVLFHGLEEYIN NLQGDGVIVLHTIGSHGPTYYN RYPPQFRKFTPTCDTNEIQTCTK EQLVNTYDNTLVYVDYIVDKAI NLLKEHQDKFTTSLVYLSDHGE SLGENGIYLHGLPYAIAPDSQK QVPMLLWLSEDYQKRYQVDQ NCLQKQAQTQKDCVLLIFAKQ
28585	58953	A	28760	1120	1335	
28586	58954	A	28761	846	1245	TVRKRGTRHPHGSRRTLSLPLR HSSDRCNRTRSADRSTGPRL/A QPRYISSRLSASTRTTMPVTTES MVSDRPSSTRLKPMLKSPTDIH VHSGWLYVCSPVAKKSTPMKA GTTAGRPTEPTPTIATSGLNALL
28587	58955	A	28762	265	1179	
28588	58956	Α	28763	188	322	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
			:	sequence		
28589	58957	Α	28764	1	3114	MLQQDSNDDTKDVSLFDAEEE
		1				TTNRPRKVKIRHPVASFFHLFFR
						VSAIIVCLLCELLSSSFITCMSKK
						WLAVVIVGVVLQGANLYGYLR
						CKGQEVRETFAEPSLQATQMK
						LKRARLADDLNEKIAQRPGPM
		İ				ELVEKNILPVDSSVKEAIIGKTL
	Ì					KIYYLGAPAEAATKEDERTTSG
		1				PGHHATNYHFLLKFDFYLSWL
						HFVHKDAILSGHPLVRLLSTRV
						LRGPNDVFHGVSSVDSVLAIFV
						LAEPMGSLSASLEN
28590	58958	Α	28765	1	3219	
28591	58959	A	28766	3	245	
28592	58960	Α	28767	2	1193	CANQLRDCLVIPTITGLVRLVV
						AGANGDRLGQPVTGADVRLSR
						CRKVMPSRSVEMGLVPSSSVIV
						TVLPLIGFVLLAFSRGRWSENV
		İ				SAIVGVGSVGLAALVTAFIGVD
						FFANGEQTYSQPLWTWMSVGD
						FNIGFNLVLDGLSLTMLSVVTG
						VGFLIHMYASWYMRGEEGYSR
						FFAYTNLFIASMVVLVLADNLL
						LMYLGWEGVGLCSYLLIGFYY
						TDPKNGAAAMKAFVVTRVGD
						VFLAFALFILYNELGTLNFREM
						VELAPAHFADGNNMLMWATL
		ŀ				MLLGGAVGKSAQLPLQTWLAD
		ļ.				AMAGPTPVSALIHAATMVTAG
		ŀ				VYLIARTHGLFLMTPEVLHLVG
						IVGAVTLLLAGFAAL*Q*K*HP
						RHPKHRNAG**TRVLQRGAGC
29502	58961	_	28768	3	2191	AGAIRVTDHFRG
28593 28594	58962	A B	28769	1	2263	
28595	58963	A	28770	1089	4965	
28596	58964	A	28771	41	249	
28597	58965	A	28772	533	709	VSFLIVSSSLIALWSERQFVIISV
						LLHLLRSALLPTMWSILE*VWC
		1		1		GAEKNVYSVDLG
28598	58966	Α	28773	2714	3599	LGSQWH*IYKLPWAVWSFSQY
28599	58967	Α	28774	45	188	GKVQCHRGLIHVNWLPPVKKF
						*LRQKGKPTSSSQETPKTEPGRL
						LKP
28600	58968	A	28775	722	856	GNDLCPKTIRTGDAWCVPGTT
						RKSAWK*GKISGSLSFLPVRDG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28601	58969	Α	28776	474	1338	PANQKKPRTRWIHSRILPEVRR
		-				GAGTIPSETIPNNRKGGNPP*LIL
		l				*GQHHPDTKTWQRHNKK*KFQ
						ANIPDEH*CENPQ*NNGKPNP\E
		l		1		HSKKLIHHNQVGFISGMQGWF
						NICKSINIIHHINRTNDKNHMIISI
		1				DAEKAFDKIQHPFMLKALNKL
		1				GIDGTHLKIIRAIFDKPTANIILN
		1				GQKLEAFLLKTDTRQGCPLSPL
İ		1				LFNVVLEVLARAIRQEKEITGIQ
		1				IGKEEAPQKQQRLFCRYYHGK
		1				RAPQLLITHLEEDDEWDIIRYY
						NVMSEEEIKRMKEIVKPKII
28602	58970	Α	28777	2289	3225	LTNQNKSRTRWIHSRILPEVQR
						GAGTVSSETIPNNRKRWTPP*LI
						L*GQHHPDTKTWHRHNKKRKF
						QANIPDERQCKNPQ*NTSKPNP
						AAHQKAYP**PSQLHPWDARL
						VQHMQTNKHNPSHKQN\HDKN
						HMIISRDAEKSFNKIQQPFMLKT
						LNKLGISGTYLKIVKMHTMSSS
						HLFYLALCLLTFTSSATAGPETL
						CGAELVDALQFVCGDRGFYFM
		1				EQCTMAVSIRGRELLGPSEQEM
		1				LHKESGKQRQKANTIPVTSKIV
		Ì				HLALYATLLLFVMEQFLGESHK
						SREIFSFEQQISELGKESMKFSEE
		<u> </u>				KEKE
28603	58971	Α	28778	1177	1272	
28604	58972	Α	28779	480	766	SSEIQHWFQGQPRWSRCRVSGR
						RHEASTVLPLCFLLPQNSSSMQ
						LG*NRSMP/HVSESSRTLVL*EV
						TKHQVSSNFKMRDKDRSGRAS
		<u> </u>				SLRKHRRE
28605	58973	A	28780	1	1344	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
20,000	150074		20701	071	2314	DTMOVED TRAVELED II DEVOC
28606	58974	Α	28781	971	2314	PTNQKKSRTRWIHSRILPEVQG
						GAGTIPSETIPINRKRRNPL*LIL*
						GQHHPDTKAWQRHNKKEEL*T
						NSPDEH*CKNPQ*NTGKPNP\EH
						IKKLIHHDQVGFIPGMQGWFNI
		l				HKSINVIQHINRTKDKNHMIISI
		ľ				DAEKAFDKIQQPFMLKTLNKL
						GIDGTYLKIIRAIYDKPTASIILN
						GQKLEAFPLKTGTRQGCSLSLF
						LFNVVLEVLARAVRQEKEIEGI
					:	QLGKDEVKLSLFADNMIVYVE
ŀ						NPIISAQNLLKLISNFSKVSGYKI
						NVQKSQAFLYTNNRQTKSQIM
						SELPFTIASKRIKYLGIQLTRDV
						KDLFKENYKPLLNEIKEDTNK
		l		ł		WKNIPCSWIGRINIVKMAILPKV
						IYRFNAIPIKLPMTFFTELEKTTL
						KFIWNQKRARIAKTILSQKNKT
						GGIMLPDFKLYYKPTVTKTKW
						YWYQNRDIDQWNRIEPPEIISHT
28607	58975	A	28782	148	287	VLHSYAI*IASALKVGISRHHP*
						GSIPSRSLLVATTPTRGVTAALE
28608	58976	Α	28783	1	1938	
28609	58977	Α	28784	1389	1499	
28610	58978	Α	28785	1	351	
28611	58979	A	28786	1	329	KNLDEKLLPASSSSCRIWATSP
						VHHLWQVLKKILF/GLEPYEIST
						LFEQRQAM/LQSIKEGVVAVDD
						RGEVTLINDAAQELLNYHNFIR
						SRSLPVFVLASACGSGTRRRRA
28612	58980	Α	28787	1	419	VRPGHLLDIDDTDMPSLRYSDP
						EAQRIGQPFKGDDILKALNGEE
1						NVAINRGFLAQALRVFTPIYDE
						NHKQIGVVAIGLELSRVTQQIN
						DSRWSIIWSVLFGMLVGLIGTCI
						LVKVLLG/IIFG*TYKSQLFEQR
						QAMGRL
		<u> </u>	L			KVMOKT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28613	58981	Α	28788	1	1795	MWIISCVMKRTAMNCVLWRK
	Į					RRRKVCASIFTGKNRANQKRD
						NVELFDARCRPLNDAADTVRY
						LPVLTVQLLDKQPRLTVLKKIL
		ļ				FGLEPYEISTLFEQRQAMLQSIK
						EGVVAVDDRGEVTLINDAAQE
						LLNYRKSQDDEKLSTLSHSWSQ
						VVDVSEVLRDGTPRRDEEITIK\
						DRLLLITTVPVRSNGVIIGAISTF
]			RDKTEVRKLMQRLDGLVNYA
						DALRERSHEFMNKLHVILGLLH
						LKSYKQLEDYILKTANNYQEEI
						GSLLGKIKSPVI\AGFLISKINRA
						TDLGHTLILNSESQLPDSGTAA
						CGQSLNVLYQRIVGERKLHTGS
						LMSAAGKSNPLAISGLVVLTLI
j						WSYSWIFMKQVTSYIGAFDFTA
						LRCIFGALVLFIVLLLRGRGMRP
						TPFKYTLAIALLQTCGMVGLAQ
						WALVSGGAGKVAILSYTMPFW
1	·					VVIFAALFLGERLRRGQYFAILI
						AAFGICTATQRNRLLPCKNQPC
		İ				KANQYQGTGDVLNQLHIDFRA
		İ				FSGVMVAGSRQIFANEISSGAS
						NVGVVIFSTQDSANTFNVLNAS
						GGSRSVYPVMSDDMNGSSWKF
						STRMQKIDPALSVTSGQLMSHV
28614	58982	Α	28789	190	2058	
28615	58983	Α	28790	199	293	RYPPAETELS*RLCRLLR*STTV
						RL*LCRPL
28616	58984	Α	28791	685	1557	
28617	58985	Α	28792	1	2850	
28618	58986	A	28793	265	535	RIATIRHPSCLHRVGDQYDSLFR
						TATTQRHCRRMHMMTIGYQFQ
						PGALVR*SRANHFPGRGDVNLS
						SRYSNAPGRRHQHQMRRGFVA
						RSQ
28619	58987	Α	28794	409	1305	

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28620	58988	A	28795	379	1703	LKTVLVDGVVKAEKLVEGAKA
20020	30700	^	20193	1379	1703	VLRQAINGDLDWKAKRQPKLE
			1			PLKLSKIEATMSFTIAKGMVAQ
						TAGKHYPAPITAVKTIEAAARF
						GREEALNLENKSFVPLAHTNEA
						RALVGIFLNDQYVKGKAKKLT
						KDVETPKQAAVLGAGIMGGGI
						AYQSAWKGVPVVMKDINDKSL
				1		TLGMTEAAKLLNKQLERGKID
						GLKLAGVISTIHPTLDYAGFDR
						VDIVVEAVVENPKVKKYPSAG
						VFHQLYCRDVVIPMFAIYTFGP
		1				QIVGLLGLGVGKNAALGNVVIS
						LFFMLGCIPPMLWLNTAGRRPL
						LIGSFAMMTLALALLGLIPDMG
						IWLVVMAFAVYAFFSGGPGNG
:						FNRVKEEFDHERFLVALTNYGT
						AMCAFEDAARYAN/LARAVWR
						GYWSFPVDSGKIRPHGDQIKLH
						EKHAV*SSVESRQRHHHLWRC
						SDVQILLRQCGI
28621	58989	A	28796	713	902	CRLARPSPLKRCFQFCSTTHSCI
						PPPLAATRWPVRRRWRPSMCC
						WSRTYR\PG*AKRRYTSPA
28622	58990	В	28797	1	1521	
28623	58991	Α	28798	348	599	RHFQRSLSRSSDSNP*LDPTLFA
						SALASRQRVTESWSERHPDPLQ
						VRRKTEDVKTTPPFLQQSAHRS
						VNIVLWIRGFSPTLLV
28624	58992	A	28799	582	732	
28625	58993	A	28800	1051	1443	DETYINDIA CONCATOCTI DADA
28626	58994	Α	28801	1051	1173	PETYRRIAGRYGATCGTLR*RA
20.627	50005	 . 	20002	1	07.10	SGG*TGETDAAGPGYPPAR
28627	58995	A	28802	1	2742	
28628	58996	A	28803	435	1143	SRPAYHPAPREFQRQWRQDPAP
		l				GLAITPGQQLFITIKLWNDDH\K
						RPREALLDSLKKLQLDYIDLYL
						MHWPVPAIDHYVEAWKGMIEL
		ŀ				QKEGLIKSIGVCNFQIHHLQRLI
						DETGVTPVINQIELHPLMQQRQ
						LHAWNATHKIQTESWSPLAQG
						GKGVFDQKVIRDLADKYGKTP
	}					AQIVIRWHLDSGLVVIPKSVTPS
		l				RIAENFDVWDFRLDKDELGEIA
						KLDQGKRLGPDPDQFGG
28629	58997	A	28804	1040	1079	
28630	58998	Α	28805	300	567	SAGFKKSGTRHCDVRPGACGT
]			1		TLYQRR*VH*\WSTVH\KPETSS
						SKMHGQRGSGLLAKSLVANVI
		1				CSLIRNPLPIMPMPLCAFVSLKM
1	1	1				IKKRPRRH

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28631	58999	A	28806	167	327	KNNSSISGINATER*KTDENNTS VFSSPGKFYRTRTAPLTDRRTN SPAYLSEL
28632	59000	Α	28807	1	1197	
28633	59001	Α	28808	1	4104	
28634	59002	Α	28809	1	1368	
28635	59003	Α	28810	82	1143	
28636	59004	Α	28811	72	212	
28637	59005	Α	28812	1	1078	MKDVTLVRPQDAGANTCAHIL
						SQLPHLQLPTLETLGLINALGY APGDMQPSDSATWGVAELQHE GGDTFMGHQEILGTRPLPPLRM PFRDVIDRVEQALVSAGWQVE RRGDDLQFLWVNQAVAIGDNL EADLGQVYNITANLSVISFDDAI KIGRIVREQVQVGRVITFGGLLT DSQRILDAAESKEGRFIGINAPR SGAYDNGFQVVHMGYGVDEK VQVPQKLYEAGVPTVLVAHHQ RVFAIFAVAIDITQVINIQYCRC QQAACGRRKDQCRNQSKENQY GNITQTDITIRTIAHGV\VIAAMI DNPPRIRKPTKSAS*LWWPLFY LLAVSLFTLWNRYRVFHGLSAS SSPLRPTPY
28638	59006	A	28813	429	611	AAKHPCCGYSFRRRTDVDHNG YSGNACTRLHHAGGIRQ**PNF GYSPPASSCGQVSQNSS
28639	59007	В	28814	1	2703	
28640	59008	Α	28815	1931	2407	HGLRTRQRLSKASRICAALLCR LLTYELSSARWMWTITTAVCV SSCRRWKKPAALVRPLPPASAP GFITTSAKPCCASRNG*KSSFQR TLHVSRHQSRTS*SPQVDTSDN SSEIVNNQAPTARTGSGLRVAV LEQRVQEPLAANAPPQLRVSAI NAAS
28641	59009	В	28816	430	823	
28642	59010	A	28817	1	2667	
28643	59011	В	28818	204	2659	
28644	59012	A	28819	1	2817	
28645	59013	Α	28820	1	1089	
28646	59014	A	28821	1	1891	
28647	59015	Α	28822	2972	3318	KYALTLVRFVTLKVQSVTALK A/CGLYRTEFLFMDRDALPTEE RQFAAYKALAEACGSQAVIVR TMDIGGDYELPYYELPERRDPV SSAGALFVSRWIVERSCADKFR VFCGASGFR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	:	
28648	59016	A	28823	1	1030	MMCIMYRTASSLANQYHIDSE
200.0	33010	1	20023	•		QARRGSQNAFDVNFEAWQLEI
						NHVLEAASAQSQRNYQISALVF
						ISMIIVAAIYISSALWWTRKMIV
		1				QPLAIIGSHFDSIAAGNLARPIA
						VYGRNEITAIFASLKTMQQALR
		i				GTVSDVRKGSQEMHIGIAEIVA
		1				GNNDLSSRTEQQAASLAQTAA
						SMEQLTATVGQNADNARQALG
						TGKNAATTAQAAAVQFIDRCQ
						ADFTRGAYRYRSGTYFICQYLT
						VTVSGIDAHQRGQTDTQRILLQ
						LFLVQFDTHRQTLNDFDPVTGR
						ILRWKQLDRAAGDITGHRTDN
						TSTLQRQPGVTYFGGSLLHGW\
						*SSSLVPRIIA*LALYC
28649	59017	A	28824	1	3087	-SSEVPRIIA LALTC
28650	59017	A	28825	376	1564	
28651	59019	A	28826	1	1174	MVNLALWLKKHRFRLDQVQN
		1				FYPSPLANSTTMYYTGKNPLAK
						IGYKSEDVFVPKGDKQRRLHK
						ALLRYHDPANWPLIRQALEAM
		1				GKKHLIGSRRDCLVPAPTIEEM
	İ	1				REARRONRNTRPALTKHTPMA
		1				TQRQTPATAKKASSTQSRPVNA
		1				GAKKRPKAAELQCPLVMTSGN
						LSGKPPAISNEQALADLQGIAD
						GFLIHNRDIVQRMDDSVVRESG
						EMLRRSRGFLPTGRGLRIDYKQ
						KMRGTRRAGCNFNQSGQGRPS
						LKRGIEQTDIKKAKKQATGLAG
					-	ESMLQDDAFYAVITHAAGPQG
						ALPLTPQMLMESPS\ATCSA*RR
					1	TPGWAGTPTSSPAKRC*LSALRI
						TSSGSTPSCSRRHWRKRARRSD
:						ACHHSRFSPTVWPVTQPKKGR
28652	59020	A	28827	1	1392	Acmiski si i v wi v i Qi kkok
28653	59021	A	28828	1050	1154	-
28654	59022	A	28829	1	2649	
28655	59023	Ā	28830	59	511	
28656	59024	Α	28831	1	2421	
28657	59025	Α	28832	4594	4770	PSTSTIHAYVSGKSRISPHTREA
		1				MI\NDHSKRAWLYALRRAGR
<u></u>						TRHRCPGRTGRQRLL
28658	59026	Α	28833	1	727	
28659	59027	A	28834	1521	3069	EL DICE CDCCCCCDIVIDADA
28660	59028	A	28835	1521	1841	FLPKSLGDSSGESRKHRRRRA
		1			1	FSPDQHPAGNYRTRLSARPFV*
						RCLYYSR*ARRGNYRQH*TTSP
		1				ALYQAASPFQ*SIAG*RAGKTR
	<u></u>	<u>l</u>		<u> </u>		YRSSVYLCVDHFDHSGSW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28661	59029	A	28836	1	1644	
28662	59030	A	28837	1	1245	
28663	59031	A	28838	1	1518	
28664	59032	A	28839	3	491	
28665	59033	A	28840	1092	2827	·
28666	59034	A	28841	162	1760	
28667	59035	В	28842	1	3378	
28668	59036	A	28843	434	763	
28669	59037	Α	28844	1	3066	
28670	59038	A	28845	576	783	PGNVLRLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFAKC ETRMYPEEPVYLPPRYRGSIVIH SIAF
28671	59039	A	28846	855	1134	PGNVLRLENLPAADADQLAGN GGCHS\QVRSIWMIGLHAFAKR ETRMYPEEPVYLPPRYRGRIVL TRDPDGEERCVACNLCAVAWP VGCISLVS
28672	59040	Α	28847	1	890	
28673	59041	A	28848	420	943	CLAADALHLRCLINARHNAQQ EDALVEKAKQ/VTWRLLAAGV CLLTVSS/VARADSLDEQRSRY AQI/KQAWDNRQMDV/VFIHAM PTNTARPTASSTGNIHLVSVLA GAPARWSACWDHCNDQIAPCR ELSRRLLRLHAQYQNTKRVHT QFSGYKTPEMANTAVPTISSQR RALFNPH
28674	59042	Α	28849	1	1247	
28675	59043	Α	28850	533	1029	SKSIMLLCRSVVSMIRRSTVAA FTLAAISVARSVALNLIIRDIGM QAMPLCRSTTGRNRWTSSAKR TILR*RQRILPLTPC*HRMFRSFL KKILSDGKSVTLGALLADVTQS DEPL*GSPAGS/TGQMPAIQPAQ KTHHVKAHSFCS*PAQSSPVNP DDIISFSKSK
28676	59044	Α	28851	749		SPHMPGITAGTPFSVPLAISAPSI SAKSLPGKTA*AWPNIMALTPG ISLR**TEFSAITLYGSADSPECA RTT/INIGTFLAHFRHVFAHGFG NIIHRHFPG
28677	59045 59046	A	28852	776		RQLRTELSAGIAAFRTGNAPAIL RFMKLAPPP*WRRKPLTGV*RV *RGRDSVR*VAFVPTVSAIQQL DPRSLLQQDAFKKAGLDPEQPP KT/WQDLA/VLCRETESLRHEV RLRQRLAGLDPTGKL*AWNGM MPYDADAKDAPQKPLSAEPAC
∠80/8	29040	А	28833	//0	2/30	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28679	59047	Α	28854	383	1367	RPTCWTSIEWVRRVRTAALRSS
				}		GKTWVFCCRRRIAGELMLTNR
				}		HTGGVMVTTFRASEAFAGALE
		1				LTGKATLVALINRCIGAVIRYM
						LIAVIPDIFQRLQVVLNVWILAV
						ANETTVRORRVRRFKVDLVVR
						VHLLLHIEVETVGVVTFIGHAR
						HHAKLSSIETAEAIAQVFTRRA
						VETETITRFFFPLIHCLTQTFNN
						GDTFRAKLLVVVNMLAAEQRV
						NGFVDADVTQRNRRTTVFEDF
		i				RNIIVSIETHATSTRYG*CVGPP
:						AMRACSGAVQPVQWLHPGKL
						RQGEPSRDLVRQRPAALCLPRR
:	1					HRILRGYNGNIQRRLYSTGNGL
28680	59048	Α	28855	1	1477	
28681	59049	A	28856	1	793	
28682	59050	Α	28857	1	1020	
28683	59051	Α	28858	1	613	SAGDGARIEQFDRKGMVNNKF
						NYFIMSKLAEAGIPTQMERLL\S
						DTECLVKKLDMVPVECVVRNR
						AAGSLVKRLGIEEGI\ELNPPLF
						DLFLKNDAMHDPMVNE\SYCE
						TFGWVSKENLARMKELTYKAN
						DVLKKLFDDAGLILVDFKLEFG
						PVQGEVVLGDEF/SPDGSRLWA
						QETLEKMDKDGFRQSL\GGLIG
		<u> </u>				AYEAVARRLGYT
28684	59052	A	28859	1	1002	
28685	59053	A	28860	(05	422	DANGAL OCALICTOCAL TODAY
28686	59054	Α	28861	625	750	RNVQALQGAHGTGGALTDPA*
28687	59055	A	28862	1	1449	QHLGTLCADLL*NGLSPSPRD
28688	59056	A	28863	105	297	
28689	59056	A	28864	55	423	DRPQRNRATLMQLYSRGSPGIR
20009	39037	^	20004		1423	RLEHRFEKVQGKPGFEVFIPGF
						KQGKLGRPLGVKALVFGIDTGL
		1				FQLQAVKNLDGF*FDEASASQP
						GSDNILRELRVRATGRADGSGT
						GFTEDANSFTSYR
28690	59058	Ā	28865	1	2340	of 120/1101 for R
		1	!	314		
28690 28691	59058 59059	A A	28865 28866	314	2340 696	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		<u> </u>				
28692	59060	Α	28867	458	2160	PTLRAFYRVTPHRSLSVMLALK
					<u> </u>	CHGINPLRSWVGTG*VE*EEKY
						NMQT*E/LENWKPISNLHDMSS
						SHSKTLGYKRLTKSNPISCQILL
						YKSRSKGRKNQRSTRTHCHHPS
						PKIYSASAKEPWILATNLPVEIR
						TPKQLVNIYSKRMQIEETFRDL
						KSPAYGLGLRHSRTSSSERFDI
			:			MLLIALMLQLTCWLAGVHAQK
						QGWDKHFQANTVRNRNVLST
						VRLGMEVLRHSGYTITREDSLV
						AATLLTQNLFTHEEAPANSVPA
						AAVIRRVQALIGITGRKAHAGG
		l				SWNGTASSDNFPNIFILPONDF
ŀ						MALAAAVAPPELEALLAAGKV
		ŀ				SVKIQEPCDEILFSRAKVWNGE
						KWACVTIVGGHTNIVHIETHDG
						VVFTQQACVAEGEQESPLTVLS
						RTTLAEILKFVNEVPFAAIRFIL
						DSAKLNCALSQEGLSGKWGLH
						IGATLEKQCERGLLAKDLSSSIV
						IRTSAASDARMGGATLPAMSNS
						GSGNQGIGTELNVSCRFPATNL
						FVHDPTQQAMQRNQRRFAVQT
		l				FPVWRVAQIICAVRPFRQRIGQ
		l				LRDIFHLKGDQFTNRPAKIVAF
28693	59061	A	28868	2095	2722	ERON HERODQI INICIARIVAL
28694	59062	A	28869	789	2509	
28695	59063	Α	28870	57	440	CSWDPQDPHGILQGAGKEDSQ
<u> </u>		l				AQKTTARQKRKTRKTATRQKK
		l				HEKQSEESTNEDT*ARKVEETQ
						HKHDAESTSGSVIQGCVQLFTQ
					:	SFTATPAASATTATRPTILCSSR
						ARAGYPSTTGVSRRESPL
28696	59064	A	28871	3057	3495	MPVRGQRPVSLARHPGTRSDK
		İ				KGHFVVAHPAF/P/DQFLHAAM
						DIKQPVISIDNLLAIHKQAEVTR
						FIGGDMQRADRDHPRIAVALID
						KRIRFGISRRFRAQSIIHRIFAQR
						MHIFRPVIGQHQATGNSRLSAS
		İ				TQRLHHNPAFFGPFH
28697	59065	A	28872	1609	2112	HQPVLTVVMVPVSPLIIRADNP
		` `				FRDEVGFLCQPAVTVIPVKIVR
						VTGDTVIRPHAEGAVRVQLRV
				}		GQAVTCRVCGIRDADIQIRCGG
						VNAGQPAGGAVAVTPGLARAA
				1		DADEFAVVVPGVIAVRQQAVQ
				1		
			 -	1		VLAL*LPGRGISGGEFITAEVRS
28698	59066	A	28873	2	712	VSRCRRSRVYSTRGIL
28699	59067	A	28874	337	383	
20077	137007	I.,	200/4	1001	دودا	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28700	59068	A	28875	65	436	REVWEHAKRMLGDSSLDMGM DDELTYMVAYEYIGRLGKTATI HWKVKSSPSMVWSASVWKKM ALR*LSRTLRPNQEHSLS*ASVP ELKCAASWTKRKKNSTFIASSA IRLTLTWKPKPFLSRL
28701	59069	Α	28876	206	403	
28702	59070	В	28877	1	2046	
28703	59071	Α	28878	1	1335	
28704	59072	A	28879		974	MEAPPIEDVSSRDLNRRRNYGH PADLFWFYSVLRALPEVYASSD AHEKFVKDFVAAWSLNVLYQR IVGERKLHTGSLMSAAGKSNPL AISGLVVLTLIWSYSWIFMKQV TSYIGAFDFTALRCIFGALVLFI VLLLRGRGMRPTPFKYTLAIAL LQTCGMVGLAQWALVSGGAG KVAILSYTMPFWVVIFAALFLG ERLRRGQYFAILIAAFGLFLVLQ PWQLDFSSMKSAMLAILSGVS WGASAIVAKRLYARHPRVDLL\ SLTS\WQMHVCRQLASQLPLSH GAMPRCRRPGHSSNPDRLANVI ARRVLRGMSNRQPVSPCCP
28705	59073	A	28880	1789	2026	CRFFWIN*YCNVSFGANLERA* TSFSALFIDLQPPGYRTTTSKHK VSSSLIKGHVLLDHSFHDLNTQ LWISTNAFRFGN
28706	59074	Α	28881	568	717	
28707	59075	Α	28882	1760	3092	
28708	59076	Ā	28883	1	1206	
28709	59077	A	28884	1	575	MSGSYSSVWAEDDIQFDSRFLE LKGDTKIDLKRFSSQGYVEPGK YNLQVQLNKQPLAEEYDIYWY AGEDDVSKSYACLTPELVAQF GLKEDVAKNLQWSHDGKCLKP GQLEGVEIKADLSQSALVISLPQ AYLEYTWPDWDPPSRWDDGIS GIIADYSITAQTQHAKLNTEDD/ SNESTGSVWQGLWRLQDD
28710	59078	Α	28885	1	718	
28711	59079	A	28886	1326	1953	PARSPEAEAAAACFRSWEWSR YYAWRA\LPSLKAKLALGEDY LNSDIFDGFNYVGGSVSTDDQ MLPPNLRGYAPDISGVAHTTAK VTVSQMGRVIYETQVPAGPFRI QDLGDSVSGTLHIRIEEQNGQV QEYDISTASMPYLTRPGQVRYK IMMGRPQEWGHHVEGGFFSGA EASWGIANGWSLYGGALGDEN YQSAALGVGRDLSTFEA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28712	59080	A	28887	491	681	PTGHRAQKKWNT*TRHSNSY*
		-				KNFAKKLI*GDIREKLOKLEGF
						AGMNATQLIEVATEVYINCDQE
						AKKETEQRLRKKANLLAAALT
						KRKINIVKGRECSHGCGHGRGO
						VEQRAKRWLRLRGGWVKAFP
						VRTEKAREVTKVLLRDIIPGFGL
						PLTLASDNGPAFIAKIVQELTQL
[LKIKWKLHIAYWPQSSEKVEH
						MNQTLKQLLKKFCQETHLRWD
						QVLPMVLLRVRYTPTKQTGYS
						PMRSCSANLK
28713	59081	Ā	28888	1	963	
28714	59082	A	28889	123	593	KRQVLAGFLITPRRLPKNWTHC
						WCWWSM/PAQVKQVLFGETG
						VAQHLKPGTAVMVSSTIASAD
						AQEIATALAGFDLEMLDAPVSG
						GAVKAANGEMTVMASGSDIAF
						ERLAPVLEAVAGKVYRIGAEPG
		1				\QVRP*KLFTSC*RAYILLPEPKR
						WHLQPVR
28715	59083	Α	28890	263	467	
28716	59084	A	28891	1218	1505	AGGDAANRRRLIQHVCSLPLYT
						GLPRGPHGRAAGNPVDQQFAA
	1					GDLGLSPHADAHPGGTDDVRW
	}					CLIST*KRWDSGV*AGAGQYSG
						WRRRSLRWR
28717	59085	В	28892	1	2118	
28718	59086	Α	28893	1084	8334	
28719	59087	Α	28894	2029	3313	
28720	59088	Α	28895	1168	1236	
28721	59089	A	28896	1	284	
28722	59090	A	28897	1	1188	
28723	59091	C	28898	20	878	CO ANA CA LIDENIA MOSTO TOTAL
28724	59092	A	28899	1904	2281	CSAYAGLHPFWLKSTRFCTHIL
						APATAISPNTTIDAPPITAAGMV
						*ISAPNFGEKPNSMAMTAAATN
						TSVE*TLVTAITPIFSA*VVTPLP
						PTEPESIVARPSPTNARPIYGSIL
	<u> </u>	<u> </u>				RPVIPATALR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28725	59093	A	28900	773	6228	MKARLHLLYPMGLRAWCGPV RLCWNLISLGLWSCFSKGWVT TPTTLSCPSPPRRGRMAPWAW GRSRARMCWSWSWSTRPSRPC AVRWSWSSGATGSCWRRPVST APPRPPPWRPAAPTPAPLWART RMPSHWPSTTAPAATAY*/DPD
						AGYQPTPLAAPAEPGSKYSLAS LDRGQGRGGGGGGALEYVPKA VSQPRRHSRPVPSGKYVVDNSR PPTDLEYDPLSNYSARHLSRAS SRDERAAKRPRGSRGSEPYT
28726	59094	A	28901	1116	1497	RGLISDLPSKPSCLMWAASCRN PASLLASE*TVSNA*IPAERAAC KMEQRANSSSVPSGERSVRRLR T*SSAPRAIPIKRSEA*AISTARVI PSGDSIAASRPVLPGSRPQAFSIR
20727	50005	<u> </u>	20002	1	2016	RISFSISRTS
28727	59095	A	28902	1	2916	
28728	59096	A	28903		324	
28729	59097	A	28904	179	1806	
28730	59098	A	28905 28906	1591 531	949	
28731	59099	A_			477	
28732 28733	59100 59101	A	28907 28908	161	333	
28734	59102	Α	28909	1	394	MEGVAFLTFLAARAAVGNRPA SPQIVRKQREGHGGILTRDPVA FDDVAVNFTQEEWALLDISQR KLYKEVMLETFKNLTSVGKSW KDQNIEYEYQNPRRNFRSLIEK KVNEIKDDSHCGETFTQVPDDR LNFQEKKASPEVKSCDSFVCAE VGIGNSSFNMSIRGDTGHKAYE YQEYGPKPYKCQQPKNKKAFR YRPSIRTQERDHTGEKPYACKV CGKTFIFHSSIRRHMNSHWEKP YECSKCDKAFHSSSSYH
28735	59103	В	28910	1	534	
28736	59104	A	28911	238	434	LPCKIHTPNHGPLKNIPSTKN*Q RRRNTSQR*LRHQPFFSSASRPG SRLRFAIGPLQPAEAGMVT
28737	59105	A	28912	358	878	KLCHIACIHSVSFQCESFHVFTG FLSSVCPFMKSKIFDRSEGFPKL LTLIGVLSSVSPFMISKGSEGNK GFPTLLTLIGFLSSVRFFMYLK* LGRIKAPPTYLTFIRSLYRVHYV CLCPFMNSKVLGRSEGFPTFLT CIGLLSIVCRFPTLLTLIGFLSSV SPYMISKGTGMR
28738	59106	Α	28913	1382	1416	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
,	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	:			sequence		
28739	59107	Α	28914	1	333	MFQDPVAFDDVAVNFTQEEWA
						LLDISQRKLYKEVMLETFRNLT
						SVGKSWKDQNIEYEYQNPRRN
						FRSLIEKKVNEIKDDSHCGETFT
		l				QVPDDRLNFQEKKASPEIKSCD
						SFVCGEVGLGNSSFNMNIRGDI
		ŀ	:			GHKAYEYQEYGPKPCKCQQPK
						KAFRYHPSFRTPQRDHTGEKPY
						ACKECGKTFISHSSIQRHVVMH
						SGDGPYKCKFCGKAFHCLSLYL
ļ						IHERIHTGEKPYECKQCGKSFSY
						SATLRIHERTHTGEKPYECQQC
						GKAFHSPRCYRRHERIHTGEKA
						YQCKECGKAFTCPQYVRIHERT
						HSRKKPYECTQCGKAL*YSLKS
						GSLMP*ALFFWLRIVLAMWAL
						LWFHMNFKVVFSNSVKKVIGS
						LMGMAWNLQITLGSMAIFMILI
						LPIHEHGMFFHLFVSSLISLSSGL
28740	59108	Α	28915	1619	2353	
28741	59109	Α	28916	1	1252	MSYSVMFALLLLTPLLFSLLCF
						ACRKRRLSATRTVTVLHSLGIT
						LLLILALWVVQTAADAGEIFAA
		ŀ				GLWLHIDGLGGLFLAILGVIGFL
						TGIYSIGYMRHEVAHGELSPVT
						LCDYYGFFHLFLFTMLLVVTSN
						NLIVMWAAIEATTLSSAFLVGI
		ŀ				YGQRSSLEAAWKYIIICTVGVA
						FGLFGTVLVYANAASVCGTDH
						GGRMMRSWNGGQLISKLLAIT
						P\DKLVLDFGSQAEDNIAVLKA
						QHISIS\AETQGAKVEFTVDQLQ
		ļ				QSEYLQLPAFITVPPPTLWFVQR
						RRYFRISAPLHPPYFCQTKLAD
1						NSTLRFRLYDLSLGGMGALLET
						AKPAELQEGMRFAQIEVNMGQ
	[WGVFHFDAQLISISERKVIDGK
						NETIPTPRLSFRFLNVSPTVERQ
	}			_		LQRIIFSLEREAREKADKVRD
28742	59110	A	28917	2	2282	
28743	59111	Α	28918	518	1046	
28744	59112	Α	28919	8	893	
28745	59113	В	28920	1	3129	
28746	59114	Α	28921	1	1284	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28747	59115	A	28922	3612	5412	 PGLKHQNNGHRGPDAETKGVT
20/4/	39113	^	20922	3012	3412	RDFGPNAKPLAG/VRLN/LERLR
						DTHHIDVAPLVARLDQMMESV
						SQLLQLARAGQSFSSGNYQHV
						KLLEDVILPSYDELSTMLDQRQ
				1		QTLLLPESAADITVQGDATLLR
					,	MLLRNLVENAHRYSPQGSNIMI
						KLQEDDGAVMAVEDEGPGIDE
						SKCGELSKAFVRMDSRYGGIGL
						GLSIVSRITQLHHGQFFLQNRQE
						TSGTRAWVRLKKDQGAYPMSE
						KVVFSQLSRKFIDENDATPAEA
						QQVVYYSLAIGHHLGVIDCLEA
1						ALTCPWDEYLAWIATLEAGSE
						ARRKMEGVPKYGEIVIDINHVP
						MLANAFDKARAAQTSQQQEW
						STMLLSMLHDIHQENAIYLMG
						VFIMLIFFPAPVASEKPLSPDCW
						TTTHTLRMIGENSGLVSYMREK
		į				AVSPNCWNVIHYSGFLHLELLS
						SYDVDVNQIINTICEWISLIKTR
						_
						GVRRPEFQTLLTGSGSEHGERFI
						MNRPTLFFTDLAFHVDRFTQYV
						HDTAQSRFTYRDFNRVFEVFYI
						QTATQTVGGTHCDAPGWWFP
						GAVQSVPAAALIAVAAAPGLA
i						SFLPFARRVPRTVVALLAQAAA
		<u> </u>				YADGMPARADGSFNSP
28748	59116	Α	28923	1	2910	
28749	59117	Α	28924	470	723	PGFGDARKLISLNFFIWV*TA*I
						M*P/LAGSDFVYRNS*RNVFIAQ
						TLQLRSRQPVTMHHATRAFQT
						EHNLILRFECCEYSRYLFT
28750	59118	Α	28925	599	1117	
28751	59119	Α	28926	279	455	SLSHSSGRCSRGGISFWVVWEF
		1				GPVACLAASVV*L*VSVVWLW
						LSPSGQGCLGCRVWL
28752	59120	Α	28927	1	2913	
28753	59121	Α	28928_	1	2328	
28754	59122	В	28929	55	327	
28755	59123	Α	28930	9	107	
28756	59124	Α	28931	1	2106	
28757	59125	Α	28932	1	1123	
28758	59126	Α	28933	260	709	
28759	59127	Α	28934	467	631	LEVIEAPQPNWS*SVQQSACST
						WPGCWVDLEDPQVWVWYEW
						TTKRASLLPIFQD*LKALRKAQ
						VWAFAS*STWPGCWVDLEDPQ
						VWVWYEWTTKRASLLPIFQD
28760	59128	A	28935	989	3010	
	155120	1	1-0755	1. "	1	<u> </u>

SEQ ID NO:	SEQ ID NO: of peptide sequence	l .	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28761	59129	A	28936	3	183	GLYAKSFAQTLYLEQRLAVLR AYFYCALWNHSVSVVAG*CKT DDSANAGDGGSGADRSR
28762	59130	Α	28937	1	1006	
28763	59131	Α	28938	185	384	
28764	59132	Α	28939	2	615	WAFRVIRFIVTANWSLKAVWM RRLIVVAALLTLRTVPMRQLNR LLLITPSLSRHMVSTGPATSCVN RGFLSPTVVSVLSGSPFC/WQDG DQTLTFKVDYIATGKATSEGEE QISLGVRNTSPDVPYLIQSWVM TPDNKKSADFIITPPVFVLNPGN ENLLRIMYIGAPLAKDRETLFFT NVRAVPSTTKRKEGNTLKIAHK RMITN
28765	59133	A	28940	1	1686	
28766	59134	Α	28941	76	981	
28767	59135	Α	28942	1	1998	
28768	59136	A	28943	300	506	DLYWSLNSGKQIQSGRIDDRSA KTVAPHAPAHRQWSASYWRSA *SSSFRLNKKCHTQNHSNCIKM ARE

ence (X=Unknown, spossible nucleotide ble nucleotide insertion) SWQRPFLK WAGG RLIPAGKRLIEPFV DKHERFLLADVSA AVVPDSVIYEAM AENYTLIREAFNAQ AAFLYLNRHCFNG FNVGFGKHKQMT GGLLVIDMTHVLNG
SWQRPFLKWAGG RLIPAGKRLIEPFV DKHERFLLADVSA LAVVPDSVIYEAM AENYTLIREAFNAQ AAFLYLNRHCFNG FNVGFGKHKQMT
RLIPAGKRLIEPFV SDKHERFLLADVSA LAVVPDSVIYEAM AENYTLIREAFNAQ AAFLYLNRHCFNG FNVGFGKHKQMT
RLIPAGKRLIEPFV SDKHERFLLADVSA LAVVPDSVIYEAM AENYTLIREAFNAQ AAFLYLNRHCFNG FNVGFGKHKQMT
SDKHERFLLADVSA LAVVPDSVIYEAM AENYTLIREAFNAQ AAFLYLNRHCFNG FNVGFGKHKQMT
SDKHERFLLADVSA LAVVPDSVIYEAM AENYTLIREAFNAQ AAFLYLNRHCFNG FNVGFGKHKQMT
.AVVPDSVIYEAM AENYTLIREAFNAQ AAFLYLNRHCFNG FNVGFGKHKQMT
AENYTLIREAFNAQ AAFLYLNRHCFNG FNVGFGKHKQMT
AAFLYLNRHCFNG FNVGFGKHKQMT
FNVGFGKHKQMT
`
MGARVIKVEPPGH
YVDGQSLYYSFIN
DLKNDHDKSFGHT
/DTIIQAMSGIMME
RVGTSLADLCGG
ALYGREKSQRGAH
TLSFLEHGLMAYIA
NRHPYMAPFDVF
CCGNDKLFSALCQ
DPRFSSNILRVQN
RTLKTQAAEVWFT
IRIARTDKASMPTV
IIRASTSMTTKQGP
KFCPLSETAATTDS
ASRLPGFSFIRSPK
GPFTRRQAQAFTT
DQGSHFRLVVRDT
TRPPADREAFTRIH
TPAIAAGVFIDGDI
DLAPANQPEFELTV
OFWPQYFGAIPQW
VMDRFCEGYSGGI
GAFMSPEPDNDET
ATMPPYRMTCGTV
TTATLEGQSTAAS
ASSQNHQTKSTETT
QMMTSTLFSSPSV
QETAPPDEMTTSFP
MTSKTITMTTSTDS
TAGTESSTPVTSAV
SRTTSWRTSIQDTS
RSTQTTRESQTSTL
FSPSVHNVTGTVSQ
TSSLCSVTNTSMM
TGSTLGNPGETSS
,

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
28775	59143	A	28950	34	437	CGRLLQKSGFVVSVGIDGIERL
						NTRRARGLPNGTACGQQFSSFR
						GAFCTQVAHIVFCTEGDTDQ/D
						ARKRERFPLRG*SPAEIQSPPAG
						RCCRVHDHRLFRYAGSFFQYPE
						HPERYRFSADAQRPHHRERRLP
28776	59144	Α	28951	1	457	
28777	59145	Α	28952	176	757	KPMKSTAAAADAALLSA\ERQ
]						VIDDAAAHLSEVAQGDDVDAI
						EQAIKNVDKQTQDFAARRMDQ
						SVRRADRSDLIETFDHVCTVIFI
						RDGITSAEVETADTARGNVDVI
						RTGEVGAVCGTEETKSILQYLQ
						YAITKDIFATLCVLLQDGKNNV
						LLTHTSQVFQPHIFAESDQLRN
						RRIFGDRFDSPVSIRMMFGI
28778	59146	Α	28953	1	1503	
28779	59147	Α	28954	425	619	AGWSFLPSPAEQNRWRFPLSRF
		ļ				CQIPAPLQVRS*LACRFFAAYSP
						PLLRKSPAASMAYTTSRLH
28780	59148	Α	28955	55	476	SYHALANVFYQRRMAITQVAG
						RQAQVFKAHLRDDVHHHIDGQ
						VTATESVMEGNRHAVL*TRAT
						NRFFQVGAQFAIARFFSLVGLL
						WRVLESGKIAFSATIPGRYPFLS
						LRLFNFLRHFDCLILRGCRKVL
						HGRAPDGRDR
28781	59149	A	28956	92	3254	
28782	59150	В	28957	12	271	
28783	59151	Α	28958	309	1238	GSGSCYSALVKRKWSARSLRA
		İ				DRNGARRGAYVGRKFGHFGPG
						LAGFFSAHASNLCRRSDRAPAH
						YHQLLNFADPVDMMQ*KRGM
						VFLLLMDQRQQRVDDWRRLPS
		l				LLSVWQSCGDSGRRAPGGR*FH
						WRFQATVFQALAEDLRRNLQI
1			 			VVATVAF/GMGINKPNVRFVVH
						FD/IPRNIESYYQETGRAGR/DGL
						PAEAMLFYDPADMA/WLRRCL
			i			EEKPQGQLQD/IERHKLNAMGA
	-					FAEAQT/CRRLVLLNYFGEGRQ
						EP/CGNCDICLDPPKQYDG/STD
		1				AQIALSTIGRVNQR/FGMGYVV
		<u> </u>				EVIRVAAFLEPDYSHRP
28784	59152	В	28959	1	2123	
28785	59153	A	28960	1	2834	
28786	59154	A	28961	1	2505	
28787	59155	В	28962	145	494	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
	<u> </u>	<u> </u>				
28788	59156	Α	28963	1019	1329	ISGVFFACFTNGSNG*LAHCHA
		ŀ				F*PLLGDFGCRNGVIQGRENAH
		1		:		LMNGGGRRVTALHFQQYRFHH
		ľ				LFNILTARHHLIDNANHAQIDR*
		<u> </u>				RFAFMRLAGGTATHQ
28789	59157	A	28964	1	1423	
28790	59158	Α	28965	1	863	
28791	59159	Α	28966	1	2412	
28792	59160	A	28967	3066	3155	
28793	59161	Α	28968	1	1215	
28794	59162	Α	28969	1	1678	
28795	59163	Α	28970	1	4674	
28796	59164	Α	28971	1	393	
28797	59165	A	28972	2026	2703	NSRCVWNAEFGHQLIAGDHFF
						HHFQAHLVQFGGDFFQLFNLG
						EGQLVVSIFTPVRLAVHGVKIE
						TVFVGFSSLIHGSQTVLVSSASG
						ASVASTRGKCTIVTSGISG/VIA
						KND/GLPRVHGATAPSCASQFL
		ŀ				VFAAPTPRPDRHG*RTDDSTPQ
		ŀ				RLSSPAVEKAPTASSASGNSRN
		l				DKPLREITLITSDRPVPDAAVSP
						TGFWPLTIPFHRCRRMSSLPGIPI
						RQSSA
28798	59166	A	28973	475	661	AYGNPVEYSGRRAPGGR*FHW
20770	37100	[*	20773	173		RFHGHGFPGAGGGSPAKPVNR
						RAAAPIDSAPAPAADGRVSR
28799	59167	A	28974	367	1464	I I I I I I I I I I I I I I I I I I I
28800	59168	A	28975	904	1473	
28801	59169	Α	28976	738	893	
28802	59170	A	28977	1	1108	MADTRYFGMHMSQETPASTTE
						AOIKNERRISPFWLLPFIALMIA
						SWLIWDSYQDRGNTVTIDFMS
						ADGIVPGRTPVRYQGVEVGTV
-						QDISLSDDLRKIEVKVSIKSDMK
						DALREETQFWLVTPKASLAGV
						7
						SGLDALVGGNYIGMMPGKGKE
						QDHFVALDTQPKYRLDNGDLM
						IHLQAPDLGSLNSGSLVYFRKIP
						VGKVYDYAINPNKQGVVIDVLI
						ERRFTDLVKKGSRFWNVSGVD
		<u> </u>				ANVSISGAKVKLESLAA
28803	59171	A	28978	1	861	
28804	59172	A	28979	5	337	
28805	59173	Α_	28980	1	612	
28806	59174	Α	28981	128	1742	
28807	59175	Α	28982	l .	2688	

SEQ ID NO:	of peptide	1	SEQ ID NO: in USSN	location of first	codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28808	59176	Α	28983	361	738	FLQPFPFKREINKFIRDIANNMK
						TDFFSAVTLFTDCVTVMLWII*F
						FQRKFFLKGFI*PPLGSFYRE*IIT
						SLFLYLLCNIFLATHRISCDDFSF
						NIQHVKKFWDSCNLIRFLIRLDL
						SDDQTVHC
28809	59177	В	28984	1	1263	
28810	59178	Α	28985	363	569	KGYSRRSGKHRQGCCNVLRLR
						FPDHQTAPRPMPLKRQTRAPGQ
						SPPGLPADPHPGQF*LPLLRGRF
						AR
28811	59179	Α	28986	1	1035	
28812	59180	Α	28987	275	721	LMVSGFLTSPKDHERIMSGEAR
						AILIASNSSVLVCAFRNFNKSFT
						DLLPSELAQSASERISFNNTLKD
						SGMPGSI*WLPSTMFLYILVRPF
						TSSDLTVSISCRVYAAPYASSA
	1					HTSISPKR*PPNTQRLLTGPVGT
						FWGRKPPLFPTP
28813	59181	В	28988	1	2082	
28814	59182	Α	28989	1	1567	
28815	59183	Α	28990	1	453	
28816	59184	Α	28991	1	777	<u>-</u>
28817	59185	Α	28992	1	1431	
28818	59186	Α	28993	1	561	VDSRGYPYGSRGAGKCRESERL GSESRNPGSIGLENELTAEDVAS
						ADMVILTKDIGIKFEERFAGKTI
						VRVNISDAEFLMTNRISRLKTA
ŀ						LFANTREISLERALLYTASHRQT
						EGEPVILRRAKATAYILEHVEISI
	İ				}	RDEELIAGNRTV/ITARRDYVA
-						GNGPLLAAERAGSIPDASAGPL
						CYQRRRL
28819	59187	В	28994	1	3414	
28820	59188	A	28995	1082	1297	MIMWLAAVAIREINHDSGSATF
						RTPRDPRTVAGKYNLGASLYK
						SELLA*LHSAGAGCLSCQRAKL
			L			GLGRRR
28821	59189	Α	28996	1	2115	
28822	59190	Α	28997	168	317	
28823	59191	A	28998	1331	1471	RWSNGTLENGTL*LLTLPSASLI STNKSPLDDVE*RSLISKAPGDT
28824	59192	Α	28999	147	1456	
28825	59193	Α	29000	1	439	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28826	59194	A	29001	722	2805	TPRAERTASSVALPTSRLLRAR
						AETTTAPSTPMKTHRVISMVFF
						TCSQTGTPSASPVKSSLKVSSLN
						IIIASTTNRPS/VQQF/WPVSPPG
						DGTRRYP\SISLTVLTGNDNVNL
						LRAGIDLAIYFDDAPSAQLTHH
						FLMDEEILPVCSPEYAQRHALT
						DTVINLCHCTLLHDRQAWSND
						SGTDEWHSWAQHYAVNLPTSS
						GIGFDRSDLAVIAAMNHIGVAM
						GRKRLVQKRLASGVYPPRCAY
						PRTHLLETSTTSGVNGVGTYSA
						PFWRMLLNSFVMAFSITLGKIT
						VSMLSAFAIVWFRFPLRNLFFW
						MIFITLMLPVEVRIFPTVEVIAN
						LQMLDSYAGLTLPLMASATAT
						FLFRQFFMTLPDELVEAARIDG
					İ	ASPMRFFCDIVFPLSKTNLAALF
					İ	VITFIYGWNQYLWPLLIITDVDL
						GTTVAGIKGMIATGEGTTEWNS
						VMVAMLLTLIPPVVIVLVMQR
						AFVRGLVDNPAANYIHYGVRE
						SGMTAIANGIAHHGGFVPYTAT
						FLMFVEYARNAARMAALMKA
		-				RQIMVYTHDSIGLGEDGPTHQA
						VEQLASLRLTPNFSTWRPCDQV
						EAAVGWKLAVERHNGPTALIL
		:				SRQNLAQVERTPDQVKEIARGG
						YVLKDSGGKPDIILIATGSEMEI
						TLQAAEKLAGEGRNVRVVSLP
		E	·			STDIFDAQDEEYRESVLPSNVA
						ARVAVEAGIADYWYKYVG
28827	59195	Α	29002	2253	2546	
28828	59196	Α	29003	279	629	NGAGHL*RPPVDGATAAPAGG
						RYAHLRVCPESLPWLHLPAWRI
						YRSGS*SAPCHCRNHRSGSAWQ
						KHYGNRFRFRTVRPYRGRALH
						LRGRNTAITQAADWRLATAQL
						LEIAGVGDE
28829	59197	Α	29004	313	638	RWRQRWFWCLHCLVLFRITPR
						TFALSQCRPWDDSRSQDTSMSH
						SIQWNRMYCNCSMQDEQEADE
						ANGKGPAQVGDRQAWAGR/CR
				:		SHRREGTIPGNPHPRAS*RAGW
				<u> </u>		QR
28830	59198	Α	29005	1	1182	

SEQ ID	SEQ ID NO:	1	_			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28831	59199	Α	29006	1	535	RPYVLP\VAGSNALGA\LGYVES
						ALEI\AQQCEGAVNISSVVVASG
ŀ						SAGTHAGLAVGLEHLMPESELI
						GVTVSRSVADQLPKVVNLQQA
						IAKELELTASAEILLWDDYFAP
						GYGVPNDEGMEAVKLLARLEG
						ILLDPVYTGKAMAGLIDGISQK
						RFKDEGPILFIHTGGAPALFAYH
						PHV
28832	59200	A	29007	1	1953	
28833	59201	Α	29008	1	656	MKLMAIQEQARGEQCFRDSEW
						DLQFHIQVALATQNSALAAIVE
			!			KMWTQRSHNPYWKKLHEHIDS
						RTVDNWCDDHDQILKALIRKD
						PHAAKLAMWQHLENTKIMLFN
						ETSDDFEFNADRYLFAENPVAI
						AKELELTASAEILLWDDYFAPG
	ļ	1				YGVPNDEGMEAVKLLPRLEGIL
		İ				LDPVYTGKAMRGLIDGISQKRF
	:	ŀ				KDEGPILFIHT\GGAPALFAYHP
						HV
28834	59202	Α	29009	1172	1371	
28835	59203	Α	29010	338	528	RHPRCDPYGFCPFTADADDA**
						LGACHHYWRGQRKIYAGSGDS
						RCQPDGRRSAPARRPLRRQR
28836	59204	Α	29011	413	2798	
28837	59205	Α	29012	48	320	LCRPDKAFTPHPA*TKRILSAI*P
						SSFKEGIDHSATFFFAARFALVA
		1				AAIFCVFADGFFAFLASFFAAFG
		1				FVFFSPRKALSGSKFTFLPT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28838	59206	A	29013	767	1428	FTPLSLRAVVIQLANRQYLDEK
				1		SDRAVHQGHIPRQFY*SLRRNL
						TNRHIQLIAIGGAIGTGLFMGSG
						KTISLAGPSIIFVYMIIGFMLFFV
					j	MRAMGELLLSNLEYKSFSDFAS
İ						DLLGPWAGYFTGWTYWFCWV
						VTGMADVVAITAYAQFWFPDL
		1				SDWVASLAVIVLLLTLNLATVK
						NVGEMEFWFAMIKIVRPLSGSR
						TKKMSKSDDNRNNVIGLLEDP
						KSVVKKIKRAVTDSDEPPVVRY
						DVQRPKRSALLERAPERFQEVF
						ILKGREDKRLLPLIHALESQGG
						GYPVGKPPISRREKRPCRASGA
1		ŀ				YSPPVLLILIMDPLGNLPIFMSV
						LKHTEPKRRRAIMVRELLIALL
•						VMLVFLFAGEKILAFLSLRAET
						VSISGGIILFLIAIKMIFPSASGNS
						SGLPAGEEPFIVPLAIPLVAGPTI
		İ				LATLMLLSHQYPNQMGHLVIA
						LLLAWGGTFVILLQSSLFLRLL
						GEKRVNALERLMGLILVMMAP
28839	59207	Α	29014	1	632	
28840	59208	A	29015	1	1215	
28841	59209	Α	29016	38	457	LNRLLKLVHASQSSRAMVFSSI
						RSFMFFSTLFILVRRQFSR*TIML
						SANSDSLTSSLPIWLLFISFSCLT
						ALARTSSTVLKRSGESGHPCLV
						PVFRGNTFNFSPFSIMLAVGGV
		<u> </u>	2224		004	LHCEINCRICSTGRSANPPLDSCI
28842	59210	Α	29017	899	991	
28843	59211	A	29018	1740	1868	MCAFITADUWDI OLDI ETVI VA
28844	59212	Α	29019	1	1084	MSAEITAPWYRLQLDLFTKLVA
						TCMEQFRPKTIPPLAIPERLNAH CEELYELIASLNNILNLYMPAG
1						QEAEHRFAMGELPDEVLEICQR
						LAKLTEMLRGLAELFLNDLSEK
						TGSHDIVRLHRLILQMNRALGM
		l				FEAQSKLWRLASLAQSSGAPVT
						KWATREEREGQLHLWFHCVGI
						RVSDQLERLLWRSIPHIIVTSAT
						LRSLNSFSRLQEMSGLKEKAGD
						RFVALDSPFNHCEQGKIVIPRM
						1
						RVEPSIDNEEQHIAEMAAFFRK QVESKKHLGMLVLFASGRAMQ
						l - 'I
						RFLDYVTDLRLMLLVQGDQPR
						YRLVEL\PANASPTVSAACWW
						AYSHLPKGLI*KVICSARCISTK SLFRPSTARW
28845	59213	Α	29020	1	2022	SEIRISTARW
20043	109213	ΙΔ	27020		4044	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	1	in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28846	59214	A	29021	878	1267	LNSWLPSVPTV*SSVFNAL*TG* ISPAFNPFADM*SASGLP*IKSPL STSTLFFTSLRASLIRLAVRTSPN FSVAVSL**SKSIMLLCRSVVSM IRRSTVAAFTLAAISVARSVALN
						RFLIKSTGNACK
28847	59215	A	29022	294	2305	THE BING FORMER
28848	59216	A	29023	5	337	GAPQHQMMSTYRINGRESPML TYPSTPNFFWLAWQARDFMSK KYG\RRFPIARFLWRSTPAPGVR KTIFIFISLVFVLMCANSWITIW RTSAAAGCHCQVVCAGMNTW RVG
28849	59217	A	29024		1753	MPSTRYQKINAHHYRHIWVVG DIHGEYQLLQSRLHQLSFFPKID LLISVGDNIDRGPESLDVLRLLN QPWFTSVKGNHEAMALEAFET GDGNMWLASGVYRIPLAVIWII GSLTSKAYKAEVQQRREAFNR AKMDYDHLVRQIQQVGGLEGF IAKRTMLEKMKDEILGLPEEEK RALAALHDTARERQKQKFLEG FFIDVASIPGVGPARKAALRSFG IETAADVTRRGVKQVKGFGDH LTQAVIDWKASCERRFVFRPNE AITPADRQAVMAKMTAKRHRL ESALTVGATELQRFRLHAPART MPLMEPLQPTVSVVDKVVEKK GTKEVAEAYLKYLYSPEGQEIA AKNYYRPRDAEVAKKYENAFP KLKLFTIDEEFGGWTKAQKEHF ANGVIAVVAAGIGYWKLTGEE SDTLRKIVLEECLTNQQQNQNP SPCAEVKPNAGYVVLKDLSGPL PYLLMPTYRINGTESPLLTDPST PNFFWLAWQARDFMSKKYG\R RFPIARFLWRSTPAPGVRKTIFIF ISLVFVLMCANSWITIWRTSAA AGCHCQPTGIAQALLSTRQHGG AQCPLLPLSPLLSSSSF
28850	59218	A	29025	865	974	IMPRISGSQSGEHQQPLVATAR WFARA*ILIIPL
28851	59219	Α	29026	1936	2490	
28852	59220	A_	29027	1105	1518	
28853	59221	A	29028	1	975	
28854	59222	A	29029	1	1965	
28855	59223	Α	29030	3338	3553	
28856	59224	Α	29031	95	1289	
28857	59225	Α	29032	1	732	
28858	59226	Α	29033	1	672	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		,
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28859	59227	A	29034	2	265	ARNEVAQPGVHETLDELTTRL
	·					AEGLLEAAEEAGIPLVVNHVGG
						MFGIFFTDAESVTCYQDVMAC
						D/GGTL*AFLPYDAGRRCLQHG
						RYQ
28860	59228	Α	29035	852	933	PAPYALLLLPMHPHGLRRRDR
						QGRIHNLNDRRRHWHRVRVCH
		l				LLRRERSRKDAPADGHPPL\RA
			ŀ			VGGRNQN*FGELRTTTCFTQTD
						FLTFNLTSVTSNEASFTQFRTQG
:						LVVFHQSAGDTVTDRTSLTRDT
						TTFNGDVQVQFLNHVDQFQRL
						TNYHAGSFTTEVLFQRTLVDYD
						FTVARFDENASCGTFAATSAVV
						LIFSHCLRLLCRVVVLVTRVNF
						QFTEHSTTQRAFWQHAFNRDF
						NHTLRTASNHLFKGRLFDTTDV
		1				AGVVIVHFVSTLVAGYSNFVSV
						QNDDVITGIYVRSVFRFVLTAQ
						ATSQFSSQTAQSFTGRVNNIPV
						AFYGFWFSCAKYYRHGARWCS
						NGRKIDQRHTHCFFCPCIRTDFA
						VEIGKEEFIT
28861	59229	Α	29036	1	797	MIVFIENFKTSSPKYADILLPDL
						MTVEQEDIIPNDYAGNMGYLIF
						LQPVTSEKFERKPIYWILSEVAK
				•		RLGPDVYQKFTEGRTQEQWLQ
						HLYAKMLAKDPALPSYDELKK
						MGIYKRKDPNGHFVAYKAFRD
						DPEANPLKTPSGKIEIYSSRLAEI
						ARTWELEKDEVISPLPVYASTF
						EGWNSPERRTFPLQLFGFHYKS
		1				RTHSTYGNIDLLKAACRQEVWI
						NPIDAQKRGIANGDMVRVFNH
						RGEVR\LPAKVTPHPVGTWTAE
28862	59230	Α	29037	1	1019	
28863	59231	В	29038	1	2727	
28864	59232	Α	29039	1	2250	
28865	59233	A	29040	1	2850	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	i e	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28866	59234	Α	29041	1	1339	MTGKCGKFGNFLESWRAQKTG
				ŀ		ICGKVWNFLENLLNGFGQNAY
						SDTDNEVQAEVVSDKDKELVG
						NWSKGHSCYAKRLAAFCPCLR
						DLWNFELERDDLGYLVEEISKQ
						QTIQEEADHKNLESLQTEDAIE
						KKTPFSGEKFKLAAEICISNKDP
		1				NINSQDDGENVPRVAVHPNGC
						FAWKLPVLSRKFERKPIYWILS
		l				EVAKRLGPDVYQKFTEGRTQE
						QWLQHLYAKMLAKDPALPSY
						DELKKMGIYKRKDPNGHFVAY
						KAFRDDPEANPLKTPSGKIEIYS
						SRLAEIARTWELEKDEVISPLPV
		İ				YASTFEGWNSPERRTFPLQLFG
						FHDKSRTHSTYGNIDLLKAACR
						QEVWINPIDAQKRGIANGDMP
		l				YVFSSQMAKFTPRT\GLSSLIWK
						AHKCGEALETLQKQ*C*QSGAT
						LPAGPRARAWPPYPRLFPTGLA
	1					CVDLHGNARKAT
28867	59235	Α	29042	378	530	AFLPYDAGRRCLPGTVSV*SGL
		1				YVRGAQHGRYQ*HHRCCTSDK
						IWRADKG
28868	59236	В	29043	1	1617	
28869	59237	Α	29044	417	607	
28870	59238	A	29045	954	1163	
28871	59239	Α	29046	444	3793	
28872	59240	Α	29047	475	732	
28873	59241	Α	29048	1	219	
28874	59242	Α	29049	1	2438	
28875	59243	A	29050	2	175	
28876	59244	A	29051	1	411	
28877	59245	Α	29052	172	378	LSLLRELGPVVAALLFAGRAGS
						ALT/VRNRPDARYRATLQYGD
						DGGGSAASGYFSPFLGWGYFIT
						TVDG
28878	59246	В	29053	1	1641	
28879	59247	Α	29054	1	3036	
28880	59248	Α	29055	1	1419	
28881	59249	Α	29056	1	1500	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28882	59250	I A	29057	2	1760	 KSQLHDPCCAPIQQEAVRAVV
20002	37230	 	2,057		1700	GQPPQQHLGFPVERGVCQREC
						DFEKELEARIASLSDSVSNAREE
						RMALRQEQEQLQSRIQSLMQR
						APVWLAAQNSLNQLSEQCGEE
						FTSSQRTHGHSEGNITKRGLLG
						ELRFENGDPSNDQSYGRHKDG
						MAEIGTFHGGDLRGLTNKLDY
						LQQLGVNALWISAPFEQIHGW
						VGGGTKGDFPHYAYHGYYTQ
						DWTNLDANMGNEADLRTLVD
		l				SAHQRGIRILFDVVMNHTGYAT
		l				LADMQEYQFGALYLSGDEVKK
						SLGERWSDWKPAAGQTWHSFN
i						DYINFSDKTGWDKWWGKNWI
						RTDIGDYDNPGFDDLTMSLAFL
		l		ļ		PDIKTESTTASGLPVFYKNKMD
		l				THAKAIDGYTPRDYLTHWLNO
						WVRDYGID/GFRVDTPKCLRCN
						PSITIGTNYSAS*PQWSSIPGAL*
						G*/PAWAG/GLPWAPSVLLLDH
						LRQGFTMLEENLGNTIQDIGMG
						KDFMSKTPKATVTKAKIEKWN
1						LIKLKSFCTAKETTIRVNRQPTE
						WEKIFAIYSSDKGLISRIYKELK
						QIYKEKNKQPHQQVGEGHEQT
						LLKRRHGCSQQTHEKMLNHQ
28883	59251	Α	29058	1	1119	
28884	59252	A	29059	3	2599	DOGEC A LIDDO A CIVINA A VEGA C
28885	59253	Α	29060	225	1245	RGSTGAHPRSAGKHYAKTSAG
						NAAGDP*YGQMGPHHRGCGKP
						VPLPDHQSENLRWW*RRAWCG
						SGGYR\MAEGRHAAQGIIDWLG
						LDVDKLGALEERRKVLQVKTE NLQAERNSRSKSIGQAKARGED
						IEPLRLEVNKLGEELDAAKAEL
						DALQAEIRDIALTIPNLPADEVP
						VGKDENDNVEVSRWGTPREFD
						FEVRDHVTLGEMHSGLDFAAA
						VKLTGSRFVVMKGQIARMHRA
						LSQFMLDLHTEQHGYSENYVP
						YLVNQDTLYGVGLYPLGALAS
		ŀ				GWLPKRRERKDATPGPTGYPG
						AHGNLELPERSEGPRAGGEPRR
						RTGHTQKGSPDRGQTPPKGP
28886	59254	С	29061	201	1244	RIGHT QUOSI ENGQITT NOT
28887	59255	A	29062	1	2530	
28888	59256	Α	29063	675	920	RTYRLAGRQKQRRGGGTDSRS
]	QNPWRSHRRHLP*RSSGAGKR
						GGKRFAGGAERRNPRLCRKPEP
						PAGGDGRRRRLAAAGAD

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		U7/34U,21/	sequence	or behave sequence	deterion, -possible flucteofide insertion)
28889	59257	A	29064	498	707	
28890	59258	Α	29065	510	554	
28891	59259	Α	29066	600	734	PECLSAPDH*YKHCCSTGTQAR QPDADCPLLPPRLAAHNERQTR
28892	59260	A	29067	1	1295	MCCNRCRNYAPGKGFSDVSFD
20092	39200	^	29007	1	1293	LWPGEVLGIVGESGSGKTTLLK
						SISARLTPQQGEIHYENRSLYA
		İ				MSEADRRRLLRTEWGVVHQHP
						LDGLRRQVSAGGNIGERLMAT
Ì						GARHYGDIRATAQKWLEEVEIP
			:			ANRIDDLPTTFSGGMQQRLQIA
						RNLVTHPKLVFMDEPTGGLDV
						SVQARLLDLLRGLVVELNLAV
						VIVTSSPDQDWGFTPEPRLAAR
						FPGSTHSSRSRRNRGRRHPRPRS
						LPTPSAPHSRAPGDGVKLVPPP
						ARVTRNEPAPSDSVTLGVPHEP
]						GACIGTPILTFVRPSTSAINAAA
						EESTGTILFGAGGFKRTDLNDT
						ESDSTTLVASRYWDLSSGWQR
1						AINLRWSLDHFTQGEITNTTML
						FYPGVMISRTRSRGGLMPTWG
						DSQRYSIDYSNTAWGSDVDFSV
						FQAQNVWIRTLYDRHRFVTRG
						TLGWIETGDFDKVPPDL*LKSR
						VGQRSELGSQYTPRARVEPPKL
						LSRKVRAHFGSRAPGAGRA*RH
						LRAPDCGVRWVWAGSGAGDG GGRGCGGSGTSEWILGSGRRGE
28893	59261	A	29068	84	128	OGROCOGSOTSE WILDSORROE
28894	59262	A	29069	1547	1822	CSRCSIPAFRVKPAPLKPRVFSP
						AWNVPERLWHLAPSTFSGGEQ
						QRVNIAR/ELYRRLPHSAA*RN
						YRLP*RQNSAALSRLYAAFLPR
						РОУНН
28895	59263	A	29070	1520	1656	
28896	59264	A	29071	563	976	
28897	59265	A	29072	1	1011	
28898	59266	A	29073	1	1097	
28899	59267	Α_	29074	1	2490 879	
28900 28901	59268 59269	A	29075 29076	1	1317	
28901	59270	A	29076	1428	1619	YAARRALCGSPCPFPGGCNGE
20902	372/0	^	270//	1440	1017	NCRLPPQLHADLTARIFYETRG
						WWWWSPRRWILNE*LPGWQ
28903	59271	A	29078	468	638	AQTSPDCGRCPWLSDYAKSG*
20,03	3,2,1	 	270,0	100	050	HQLWARWQNNGLAHTPRADS
				1		-
		<u>L_</u>		<u> </u>		THQQSALDGRISSLT

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28904	59272	A	29079	1886	2329	PLLVWINTRPSLTTGRESASPAT LVCHATVPSLVIASHVLSFL*W SFTVLVISRIGVAFAHAIFWSIT ASLAIRMAPAGKRAQALSLIAT GTALAMVLGLPLGRIVGQYFG WRMTFFAIGIGALITLLCLIKLL PLLRRTVKYTSGC
28905	59273	Α	29080	1	2319	
28906	59274	A	29081	3	194	STSSLAAQSLRFGYETSQTGLA TYCGEKIQ*FFADLQQPVCADS YPLLVQMKKLGPIVFFFDI
28907	59275	Α	29082	3109	3384	
28908	59276	Α	29083	703	1000	DCFLRRLIKRPFGTSMKDQAVR FEEGFMAMGALGLAMVGMTA LAPVLAHVLGPVIIPVYEMLGA NPSMFAGTLLA\WIWAAVFLAK ELAGGVRLLVLIF
28909	59277	Α	29084	2040	4603	
28910	59278	Α	29085	3	94	
28911	59279	A	29086	3	148	YAEHMLEVMSSIGDYT/NPRPA SRPVTKFDQRGHRLGHGVWNL MFERVK
28912	59280	Α	29087	27	227	
28913	59281	Α	29088	344	1067	
28914	59282	Α	29089	798	1049	
28915	59283	Α	29090	1	1473	
28916	59284	Α	29091	1	720	
28917	59285	Α	29092	45	208	
28918	59286	Α	29093	1	2499	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28919	59287	Α	29094	1	725	MHPRFQTAFAQLADNLQSALE
20717	3,20,	` `	2,0,1	1	1,23	PILADKYFPALLTGEQVSSLKSA
						TGLDEDALAFALLPLAAACART
						PLSNFNVGAIARGASRRSAKNIP
		ļ.				RAVRQVFWRILLFYVFAILIISLI
						IPYTDPSLLRNDVKDISVSPFTL
						VFQHAGLLSAAAVMNAVILTA
						VLSAGNSGMYASTRMLYTLAC
						DGKAPRIFAKLSRGGVPRNALY
		l				ATTVIAGLCFLTSMFGNQTVYL
		l				WLLNTSGMTGFIAWLGIAISHY
	:					RFRRGYVLQGHDINDLPYRSGF
						FPLGPIFAFILCLIITLGQNYEAF
		1				LKDTIDWGGVAGTYIASGGEPA
		1				VNSHAFGVLRNVVSIAVFFHQF
					1	GDAIKRLFPTDLLPFIRTWRTVF
	1					RKLQTAFGVDEIHQASAFRTKC
	1					TAVDRVIRIAFDMDRLDFFSWR
			:			SGYISRIPLIGLYFACALERHQN
						ERQPIILLSDQNAIATINQLAIER
	Ì					DVLNCRVIIARSLSELVAIREEIE
						PLLIINNSHYLLDDAVNNYITVK
	į	l				NIITAAGIEQIKHFLATAFIRQQP
	1					ERFFSAPGSFHYSNVRGESWQH
	1					ITRQICAQLVAQHHITADEAQRI
		}				IAREGEGENLIVNRLAIPHCWSE
		ł				QERRFR*TVAWWRAA*CAVCD
]				DGDCRSVLPDLHVWQPDGIPV
		Ì				AAEHLRDDGFYRLAGDCH
28920	59288	A	29095	3	453	THE TOTAL PROPERTY OF THE PROP
28921	59289	В	29096	1	3684	
28922	59290	A	29097	1	231	LLVFINQEEADFHTQRGGPVFQ
						QATFTL*QLALFAIEPGLMTDP
		-				DIQVRGTTLPYGRGAAHGVYT
						SNWKLTFRRILY
28923	59291	Α	29098	1	2862	
		1				

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
						1911
28924	59292	Α	29099	1	1567	MKLNKAGFNVPESYSLLKMPP
}						VGCLISALKKAEDRQEVILRLF
						NPAESATCDATVAFSREVISCSE
						TMMDEHITTEENQGSNLSGPFL
						RVRAGESIKFFNVLLADTPGLDI
						DTMDKDVAHDSRSIQLAMLRD
						DEILTHPVFNRYHSETEMMRY
						MHSLERKDLALNQAMIPLGSCT
						MKLNAAAEMIPITWPEFAELHP
						FCPPEQAEGYQQMIAQLADWL
} 				1		VKLTGYDAVCMQPNSGAQGE
1						YAGLLAIRHYHESRNEGHRDIC
						LIPASAHGTNPASAHMAGMQS
						RKTAGICCVHLWAGFGKVAIIG
	•					AGPAGLQASVTLTTQGYDVTIY
	ŀ					EKEAHPGGWLRNGIPQFRLPQS
						VLDAEIARIEKMGVP\IKCTTEV
						G\NTLTLEQVKAENRAVLVTVG
						LSSGSGLPLFEHSDVEIAVDFLQ
						RARQAQGDISIPQSALIIGGGDV
						AMDVASTLKVLGCQAVTCVAR
						EELDEFPASEKEFTSARELGVSII
						DGFTPVAVEGNKVTFKHGDLR
						TAPFLGVADKRNKSAGNHP
28925	59293	Α	29100	107	892	LAICTGTYSGRQVLPRFVDRGA
						SLIAEERNGAGRRRAGIRTTSA
						GGGLCAYAIVEF*CWRNCARFE
						LN/AGISVPI/SEFIGATMQQTVH
						AEQSAISHAWLSGEKALAAITV
						NYTPCGHCRQFMNELNSGLDL
						RIHLPGREAHALRDYLPDAFGP
1						KDLEIKTLLMDEQDHGYALTG
						DALSQAAIAAANRSHMPYSKSP
						SGVALECKDGRIFSSEYAENAA
						FNPTPDIQRAVLAEKADAPLIQ
2002		<u> </u>	22121		2100	WDATSATLKALGCHSIDRVLL
28926	59294	Α	29101	1070	3100	CTADNI TVOI CI CVCCC CODCNA
28927	59295	Α	29102	1878	2699	GTARNLTVSLSLSYSSSGTPSNA
}						PNARMEELGPHPGEASSLFHPE
						SPLLDELFLPEYKAGRTPNPDI\
						GHYVRRADV\DGKSRLLRGLDS
						NKDQSYFLYTLSHEQIAQSLFP
						VGELEKPQVRKIAEDLGLVTAK
[KKDSTGICFIGERKFREFLGRYL
						PAQPGKIITVDGDEIGEHQGLM
						YHTLGQRKGLGIGGTKEGTEEP
						WYVVDKDVENNILVVAQGHE
]		HPRLMSVGLIAQQLHWVDREP
						FTGTMRCTVKTRYRQTISLGPL
		<u></u>			11.60	RKPPHNRCLEI
28928	59296	A	29103	358	1160	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28929	59297	A	29104	234	930	KRAFLCSFCANRRNAANSALAL PGNCPVAHAQKRHSAPGTLSPD ARNEKQPLYG\GAAPETPNPRL PPLDSGILGGYIAPDNLTITLSV GHSLFDERFGLAPQMPKKLQK MTRFPNDSLDAALCHGDVLLQI CANTQDTVIHALRDIIKHTPDLL SVRWKREGFISDHAARSKGKET PINLLGFKDGTANPDSQNDKLM QKVVWVTADQQEPAWTIGGSY QAVRLNQFRSVMN
28930	59298	В	29105	1	837	
28931	59299	A	29106	1	1701	
28932	59300	Α	29107	733	1323	
28933	59301	A	29108	1	736	MKPSVILYKALPDDLLQRLQEH FTVHQVANLSPQTVEQNAAIFA EAEGLLGSNENVNAALLEKMP KLRATSTISVGYDNFDVDALTA RKILLMHTPTVLTETVADTLMA LVLSTARRVVEVAERVKAGEW TASIGPDWYGTDVHHKTLGIVG MGRIGMALAQRAHFGFNMPI/R L*RAPPP*RSRRTLQRPLLRFGY SVTRVRFRLPDPAVN**DASSV WRRTIRGPSLGLSPGWNTRVSL CAFFG
28934	59302	В	29109	1	1359	
28935	59303	Α	29110	874	1926	
28936	59304	Α	29111	1	777	
28937	59305	Α	29112	137	376	
28938	59306	A	29113	1197	1391	EIRATIVRSSTEGGRNSGLQSGN FC*RHGS*KITAGYIVPLPEESA TATGASWTHPWGRQDASW
28939	59307	A	29114	1846	2126	LMELIEKHVSFGGWQNMYRHY SQSLKCEMNVGVYLPPKAANE KLPVLYWLSGLTCNEQNFITKS GMQRYAAEHNIIVVAPDTSPRG SHVADADRYDLGQGAGFYLNA TQAPWNEHYKMYDYIRNELPD LVMHHFPATAKKSISGHSMGG LGALVLALRNPDEYVSVSAFSP IVSPSQVPWGQQAFAAYLAEN KDAWLDYDPVSLISQGQ/LRCG NHG*SGVE**FLRRQLRLQI*KD WPQ*EAAHVH

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28940	59308	A	29115	184	985	LGKRLVTYHTDANGQPVNQIL VEAATDIAKELYLGAVVDRSSR RVVFMASTEGGVEIEKVAEETP HLIHKVALDPLTGPMPYQGREL AFKLGLEGKLVQQFTKIFMGLA TIFLERDLALIEINPLVITKQGDL ICLDGKLGADGNELFRSLILRE MRDQSQE\DPREAQAAQWELN YVALDGNIGCMVNGAGLAMG TMDIVKLHGGEPANFLDVGGG ATKERVTEAFNPPGYIGPYQGV PPAGPGVTRMGKSVRRIVQVG CQVAAGSH
28941	59309	Α	29116	1825	3186	
28942	59310	Α	29117	366	1903	
28943	59311	Α	29118	1	2139	
28944	59312	A	29119	345	431	AASGSADDNLHHQYN*GDIAF CLHALLP
28945	59313	В	29120	1	2616	
28946	59314	A	29121	1	1521	
28947	59315	Α	29122	1	783	
28948	59316	Α	29123	96	215	
28949	59317	Α	29124	1	292	MWWGGLLYWLAALVTLLWA ASQIQALKKLTCAISQTLEEQPV LNSKSWLTSLQNDYSLPDSLTE RIWLTLISQRISRGELREF*TGRR KLVTEQCLV
28950	59318	Α	29125	3	529	
28951	59319	A	29126		884	MVDSLIARVGVMARGNAITLP VCGRDVKFTLEVLRGDSVEKTS RVWSGNERDQELLTEDALDDLI PSFLLTGQQTPAFGRRVSGVIEI GDGSRRRKAAALTESDYRVLV GELDDEQMAALSRLGNDYRPT SAYERESRSEGLDLLRMKVEEG DVILVKKLDRLGRDTADMIQLI KEFDAQGVSIRFIDDGISTDGEM VLDKLARGYADLSKAESQWDE MMRTAGSLKLGTIHASELIRSL LKSSRPSGLAQAIMEVGRVNKT LYLLNYIDDEDYRRILTQLNR GEGRHAVARAICYGQRGEIRKR YREGQEDQLGALGLVTNAVVL WNTLYMEEALSWMRRNGEEII DEDIARLSPLMHGHINMLGHYT
						FTLPEDILKGELR*RHLPPPSSSA SPALPIGIHVHKHLLGDNRYPI WIMQPSAHHPARQPEHDNHFR

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	F .	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
28952	59320	A	29127	143	523	NQTLMIKGAAHGIFNPLCIKAT AG\AGAYHGARKRLCANAALA N*RNAGISVSCATTAPLSLALFT GAGQIAASNTGELDVLQQLGFS PIPRLILPGRSSARNRSARPRIGS AGAAVMFSNNELMDA
28953	59321	В	29128	1	4107	
28954	59322	A	29129	1892	2720	PTAWSPPRPTSMTSISWVICCM ERSNLSQPMPATKGR\QARGAG \EVDVDWLIAERPGKVRTLKQH PRKNKTGINIEYMKASIRAQVE HPFRIIKRQFGFVKARFKGLLK NDNQMGDVFHAGQPVSGGPN DTIGKFADVACAGPLLAAELDA LGKALKEPARPMVAIVGGSKIV GALILLIAGFAILRLLFRALISTA SALAGLILLCLFGPALLAGYITE RITRLFHIRCAGSAYFIKNIQQN GITPEDISKRNGRVFLLVFILPFS LRRVGHAHH
28955	59323	A	29130	1332	1635	
28956	59324	C	29131	1	1677	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28957	59325	Α	29132	I	1114	MAEACNIGLEPLIKHNIPALTRH
						RLSWVKQNYLRAETLVSANAR
						LVDFQSTLELAGRWGGGEVAS
						ADGMRFVTPVKTINSGSNRKYF
						GSGRGITWYNFVSDQYSGFHGI
			Ì			VVPGTLRDSNFVLEGLLEQQTG
İ						LNPVEIMTDTCGCLEKQEEPPS
						LLRLNNRIKQLLPPVDLTELLLE
	·					IDAQTGFTHEFAHVSESGARAQ
						DLHISLCAVLMAEACNIGLEPLI
i		1				KHNIPALTRHRLSWVKQNYLR
						AETLVSANARLVDFQSTLELAG
						RWGGGEVASADGMRFVTPVK
						TINSGSNRKYFGSGRGITWYNF
						VSDQYSGFHGIVVPGTLRDSNF
		ļ				VLEGLLEQQTGLNP/D*NHDRH
		1				LRLSGETGRATIIASSK*SDQTA
						TPTGRFNGTVT\EIDAQTGFTHE
		1				FAHVSESGARAQDLHISL\LRY*
						WLKPVIS/ALEPLIKHNIPALTRH
İ						RLSWVKQNYLRAETLVSANAR
						LVDFQSTLELAGRWGGGEVAS
						ADGMRFVTPVKTINSGSNRKYF
					,	GSGRGITWYNFVSDQYSGFHGI
						VVPGTLRDSNFVLEGLLEQQTG
						LNPVEIMTDTCGCLEKQEEPPS
						LLRLNNRIKQLLPPVDLTELLLE
						IDAQTGFTHEFAHVSESGARAQ
			i			DLHISLCAVLMAEACNIGLEPLI
		l				KHNIPALTRHRLSWVKQNYLR
						AETLVSANARLVDFQSTLELAG
					:	RWGGGEVASADGMRFVTPVK
28958	59326	A	29133	1	2908	
28959	59327	A	29134	735	932	
28960 28961	59328 59329	B A	29135 29136	1	1413 1469	
28962	59330	A	29137	177	361	
28963	59331	A	29138	1	849	
28964	59332	A	29139	1	564	
28965	59333	A	29140	1	1593	
28966	59334	A	29141	1164	1635	EGPNRQNGRDYRSVMPTNL\LL
20,00		-			1.055	RRFHEATAQNAPDVVVWGSGT
						PMREFLHVDDMAAASIHVMEL
						AHEVWLENTQPMLSHINVGTG
						VDCTIRELAQTIAKVVGYKGRV
						VFDASKPDGTPRKLLDVTRLHQ
						LGWYHEISLEAGLASTYQWFLE
						NQDRFRG
28967	59335	A	29142	538	1116	
28968	59336	C	29143	1	2967	
28969	59337	С	29144	1	2214	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
28970	59338	A	29145	1	469	
28971	59339	Α	29146	780	1052	
28972	59340	Α	29147	617	2408	
28973	59341	Α	29148	2	488	
28974	59342	Α	29149	1	1083	
28975	59343	Α	29150	527	3213	SWRSVQLLPATSIPSWQTETNQ
						FMGRDRPTPTAESPYAVLLRQP
				•		LAKLNIIQ/RPVMNMVENMLDQ
						AFKKLNPHEHPVLHSDQGWQY
						RMRRYQNILKEHGCGVTPIMS
						MRRWLAKNRPQADVRVIYNVR
						TPQDVIFADEWRNYPVTLVAE
						NNVTEGFIAGRLTRELLAGVPD
						LASRTVMTCGPAPYMDWVEQE
						VKALGVTRFFKEKFFTPVAEAA
						TSGLKFTKLQPAREFYAPVGTT
						LLEALESNNVPVVAACRAGVC
						GCCKTKVVSGEYTVSSTMTLT
						DAEIAEGYAVVALIKPGAQIGR
ŀ						SPVNCDVASCHVISFNLRVELAI
						MRRLLCRIAVLMSYRIEQRLMF
.;						LERLRHVGLIAHPAKKAIKKTR
						KPGMKVTFEQLKAAFNRVLISR
						GVDSETADACAEMFARTTESG
						VYSHGVNRFPRFIQQLENGDIIP
						DAQPKRITSLGAIEQWDAQRSI
						GNLTAKKMMDRAIELAADHGI
						GLLRLAGGGKRLYWHLLDQLH
						RRNDNISLDLGNNAEAVILRED
						MLPRENFRPGDRVRGVLYSVRP
						EARGAQLFVTRSKPEMLIELFRI
						EVPEIGEEVIEIKAAARDPGSRA
						KIAVKTNDKRIDPPTQHEDEED
						EGLYDDPFPLNECSVGPGHRHR
						FAPPEAQFRRPETLKGAPTSRIP
						ETSVGVSAGSDFEPHLMRELTC
						RLTALTWCYPGSAYAVHQPDE
28976	59344	Α	29151	1	812	
28977	59345	Α	29152	1	1830	-

SEQ ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	1	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	:	
28978	59346	A	29153	1	1308	MMPLIDLEDPRLLVRREIGMLL
		ĺ				HVDYLDLVHEKVTCRGRNGGQ
						DREKTTMEKVRSSGTICPQAPE
						VVNHYFTTDDGYRIISARFGVP
						RTQVRTWVALYEKHGEKGLIP
						KPKGVSADPELRIKVVKAVIEQ
						HMSLNQAAAHFMLAGSGSVAR
						WLKVYEERGEAGLRALKIGTK
						RNIAISVDPEKAASALELSKDRR
			i			IEDLERQVRFLETRLMYLKELK
						ALAHPTKKVTLSLHREGKQINH
						KAVQRLMGTLSLKAAIKVKRY
						RSYRGEVGQTAPNVLQRDFKA
		ŀ				TRPNEKWVTDVTEFAVNGRKL
						YLSPVIDLFNNEVISYSLSERPV
						MNMVENMLDQAFKKLNPHEH
						PVLHSDQGWQYRMRRYQNILK
						EHGIKQSMSRKGNCLDNAVVE
						CFFGTLKSECFYLDEFSNISELK
						DAVTEYIEYYNSRRISLKLKG\L
28979	59347	Α	29154	1	836	
28980	59348	Α	29155	1	1566	
28981	59349	Α	29156	297	936	RTSSSLMRSSSSLLRICSGVSPRS
						IPRWFTSVSLPSSFIR\RITTFRYT
						PGHVAPASRRSCYKYRR*PMRL
						YTMIQSLS/VGSRPSGLRAFSSD
						CSPLPRTCSLSRRRVLMITTSRS
						*SLTYGVDPSVRPVLAAASEYF
						SRR\YAGFQNPHNLLVSG*YQG NYRHFGILRGYPG/TLKNSNFQL
						TRSARISLSSRSSICTSTGGNTTL
			:			PPSSPPDC
28982	59350	A	29157	5	861	SWRSVQLLPATSIPSWQTETNQ
20702	37330	1	27137		001	FMGRDRPTPTAESPYAVLLRQP
						LAKLNIIQ/RPVMNMVENMLDQ
						AFKKLNPHEHPVLHSDQGWQY
						RMRRYQNILKEHGCGVTPIMS
						MRRWLAKNRPQADVRVIYNVR
						TPQDVIFADEWRNYPVTLVAE
						NNVTEGFIAGRLTRELLAGVPD
						LASRTVMTCGPAPYMDWVEQE
						VKALGVTRFFKEKFFTPVAEAA
						TSGLKFTKLQPAREFYAPVGTT
		}				LLEALESNNVPVVAACRAGVC
						GCCKTKVVSGEYTVSSTMTLT
						DAEIAEGY
28983	59351	Α	29158	1818	1991	SPSHIRRTAPNGLRHYQR*IQQ*
		[APSDQKRDFLVPHGADSAMAK
						HGGSHRAVLPQGW
28984	59352	A	29159	3	601	
28985	59353	Α	29160	415	549	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
28986	59354	Α	29161	2	501	
28987	59355	Α	29162	1	1347	
28988	59356	Α	29163	3	2461	
28989	59357	Α	29164	1419	1640	IFCASLSLGLYAGIEARILTKGY
						TRK*IQQ*APSDQKRDFLVPHG
						ADSAMAKHGGSHRAVLPQGC
	ŀ					DPHMESLI
28990	59358	Α	29165	1135	2067	
28991	59359	Α	29166	1	1364	MAGNRRFMCTPKTHGLSISQH
						GTFPEHAGCKIRCAGRSGRVRP
		1				AELLAPYTGDIAAEGISKAMRG
						GAKFLHHGIKRQQRYVAEAITE
						EWRMAPGPLEVAWFAGVIYHL
						YYYRARFFCAAQPLVSGFHEAE
						LSLDDAKWVLHPGPDAGFHVF
						DVDGRFVLAWMLFQGSYLAG
						ALGDQPVHIHLGQLLALWRPL
						QITQLIEVMLVGRGGDQAVGQ
						ATLGIDTNGGLYAKGPLIAFLG
ŀ						LMHLRIALLLFVLGRTGCAYDG
						GRPQLAEKLYSELRAQGIEVLL
						DDRKERPGVMFADMELIGIPHT
	1	1				IVLGDRNLDNDDIEYKYRRNGE
						KQLIKTGDIVEYLNAALLIAVT
						VLTSMEASDLVDLGMTLSPAD
		1				YAERLAALTQKCGLDGVVCSA
						QEAVRFKQVFGQEFKLVTPGIR
						PQGSEAGDQRRIMTPEQALSAG
						VDYMVIGRPVTQSVDPAQTLK
						AINASLQRSA*CRDAGTLRLRA
						WLC*FLQRRYHRYKGPAVPQV
	ļ	<u> </u>		-		ELCQICQRNEFCTQRVPGMCHV
28992	59360	Α	29167	627	854	NAGDRRNRNPSCTAARQYG*S
						RFYNCRR*RHGRKNLSAERNGL
						PEYRNCNPDHRPSVFLAAGRCF
		<u> </u>				APTMCHDASE
28993	59361	A	29168	1	1593	
28994	59362	В	29169	940	3789 1326	
28995 28996	59363 59364	A A	29170 29171	1	1377	
28990	59365	A	29171	1	2547	
28998	59366	A	29173	561	845	AKIVQLRPRILRPSRSARRCPSA
20796	3,300	, , , , , , , , , , , , , , , , , , ,	127173		10.15	PRSRRQRRRSGPLPEPAPRVS*Q
					1	IFPSQYWRYRQSTENQKQRLDP
					1	RGQIVNVPARRIIRQKRKCCKV
		1			1	AGSA
28999	59367	A	29174	1	1284	AUSA
29000	59368	A	29175	624	866	
29001	59369	A	29176	1	1384	
->001	12,207	١٠٠	1	1	1	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29002	59370	A	29177	2268	2684	RCRRCKRRLLRRFRRSLLSLAG
27002	37370	``	27177	2200	2001	SPENHARFYCRNSLPDEWFFRH
						HPRST*PPRSREIRRCHCG*RQC
						SSDGRKITSVHRGRNADGRELT
						HQAVRLLAYLSDRFARHHRHL
						RNAHRRGPDRIPKERHFPATKL
						RHTPAV
29003	59371	A	29178	1	2142	
29004	59372	A	29179	1	2463	
29005	59373	Α	29180	3	126	
29006	59374	Α	29181	1	2013	
29007	59375	Α	29182	891	1000	FDSFHWHSHPMLCCDRGQHKE
ļ. !						NPQSRGPISCQ*IQQ
29008	59376	Α	29183	1	846	
29009	59377	Α	29184	90	411	
29010	59378	Α	29185	1	1580	MSKPKYPFEKRLEVVNHYFTT
						DDGYRIISARFGVPRTQVRTWV
	l					ALYEKHGEKGLIPKPKGVSADP
	1					ELRIKVVKAVIEQHMSLNQAA
						AHFMLAGSGSVARWLKVYEER
						GEAGLRALKIGTKRNIAISVDPE
ł						KAASALELSKDRRIEDLERQVR
						FLETRLMYLKKLKALAHPTKK
	•					AAEIPRSTFYYHLKALSKPDKY
						ADVKKRISEIYHENRGRYGYRR
	ŀ					VTLSLHREGKQINHKAVQRLM
	ŀ					GTLSLKAAIKVKRYRSYRGEVG
						QTAPNVLQRDFKATRPNEKWV
						TDVTEFAVNGRKLYLSPVIDLF
						NNEVISYSLSERPVMNMVENM
		İ				LDQAFKKLNPHEHPVLHSDQG
						WQYRMRRYQNILKEHGIKQSM
						SRKGNCLDN\AVVECLFGTLKS
						ECFYLDEFSNISELKDAVTEYIE
						YYNSRRISLKLKDLYASCLTVQ
						LFGVSTVMGLLIRILGSIFQKAL
ŀ						NISKIESFVAVTTIFLGQNEIPAI
		1				VKRFMIAESHEVLPHLYGMGH
		1				CGSRRWYAEWRPLHRVHEPSG
29011	59379	Α	29186	1375	3174	
29012	59380	Α	29187	604	1268	
29013	59381	Α	29188	1	288	
29014	59382	Α	29189	1	2412	
29015	59383	A	29190	82	405	
29016	59384	A	29191	1287	1472	
29017	59385	Α	29192	1	3156	
29018	59386	A	29193	1	1824	
29019	59387	A	29194	1260	1922	
29020	59388	Α	29195	1369	1743	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29021	59389	A	29196	21	432	GPGCNGVHRLCTE\QRDVRGTV RIVLKTFNNCRDTVFVAFEVNN TVSLLVATTDMTSGDTAIVVTT TGFVSAANEVQILAFFQGDVSF FPVATTTDTLSVTFNFPFNYQG VNDFDFDFKQFLHSSFDFCFGR VFSNFE
29022	59390	С	29197	1	1743	
29023	59391	Α	29198	2005	2571	
29024	59392	A	29199	170	486	LQTQKDGIPAVVERLEYDPNLP RTSRWFRNDFSVPVLQLLGSP*
29025	59393	Α	29200	1	1713	
29026	59394	A	29201	1	6729	
29027	59395	Α	29202	1	753	
29028	59396	A	29203	1	1470	
29029	59397	A	29204	665	1773	ASSQVKSGWLSAKIPVISSIYGP LLSVRLLSHAWPNSLCPQLHCF LPGAIWSASSLLKSGNRPLIRLA SIVLPVPGGPISKRLCPPAAV/HF QSSLSLFLTDNITEIML*RPDTW THVMYVLHHADKPNLYHGLPE NPEISETVKFWKGIWKPLAAVG FAATFAASIFHYVGVGPNRADE EENNLHEEKDEERKCSQDIQLV KERVIFLTGQVEDHMANLIVAQ MLFLEAENPEKDIYLYINSPGG VITAGMSIYDTMQFIKPDVSTIC MGQAASMGAFLLTAGAKGKR FCLPNSRVMIHQPLGGYQGQAT DIEIHAREILKVKGRMNELMAL HTGQSLEQIERDTERDRFLSAPE AVEYGLVDSILTHRN
29030	59398	Α	29205	948	1620	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29031	59399	A	29206	1782	3667	HRRRCRHGYPVPAYRCRIWKC
						GQFHPTGIAGCGRTGHRRLPW*
						RRLSAEQTWRTFYGALCAERQ
						RPGGP*RG\SRSIMIEIREGRGCD
						GPWGPHAKLKLDHLGKEVLES
						RLPGILELSRTFAHVDPSRFRLS
						HLSLHDGRYSDQSYRYNDTRD
	:					MVPINGSIHRIGREPHYHYQRG
			1			QQYIGLCRNCNVIDTHICIYLVD
						QPIMDDIRRLLLYSEISSAIIWLL
						PVVQGEHYMLVDPDTNEREER
						GRSETRGFPRVPLGRTVSTVWY
						PLSNAATLAATRCSRSPHAFAE
						PSSNNGFITATPLGRTHFLGMA
					1	FPPSACWRLLRAEPERVEAVLS
	1					ASGMNKAMRCGVSLICNFRLD
						YAPIEKQWDLHFADYFAEDLK
						LLAPLAKDGLVDVDEKGIQVT
						AKGRIRRLRRIRHLSMMPDAAL
						1
						VASYQAYDFLRIRHKQRASAK
•						QPNHCGTQHGSNGSLRTLWNSI
	-					DSGSVLTWCASLIFSSRKSLSPI
						QLVRSVDRGDVKKRYSMREFS
						LGETHSEAEFRELLEQNPSFVFF
	1					KPQSFAPVKGASAVPLVGRASV
						ASDRSIIPPGTTLLAEVPLLDNN
ŀ						GKFNGQYELRLMVALDVGGAI
						KGQHFDIYQGIGPEAGHRAGW
		ļ				YNHYGRVWVLKTAPGA
29032	59400	Α	29207	1351	1806	VIVGITSNSVTVAAVSSWCRTW
						VPVSVLCLNCYPASMALVRGVI
						RGV*TCLSLCPNCAAIFIFAFGA
						VIFCITSVGFLFPPMVYKSGLRF
						FVFT*MRDTGVPQRLRAPRRSL
						SAKLGPACPFAYIVPHIWCRWI
						GWGTCVCLAICVCVCVAD
29033	59401	Α	29208	1308	1647	RSWEVSIVEFYVVRPTGHV*HA
						SGNLSHHRKRHPLADQAARKG
						ETVPPRGRRS\WRTQAHP*HLR
						QHRGQHPASLPTRTGTPQPGRR
						AIYRIPVRTAGQFQRIEVGDFQR
						VGHQ
29034	59402	Α	29209	1	2184	
29035	59403	В	29210	81	1356	
29036	59404	Α	29211	1	2349	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	-	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
:				sequence		
29037	59405	Α	29212	514	1136	ILRIMQRGMKQFAGLLRLSGIK
						MLPSA**LGELLHAAGSFFQRG
		ŀ		-		CLLFSTGGKIGVARRNFTGTGI
						DGI*TFADMSDGVSQRALHM*
						NALRQVAHFTAPVNGQGIRQV
						TTGDFANVSNNFCQRSKQHTA
						NAVPRHQQNQYHHQRDNRQLP
						LGKSVIICVVSDDIAIQFFTAEG
						VLSKRFAHCLMPSLGGLSKIGP
						SMPLFRIISQFS
29038	59406	A	29213	1	2992	
29039	59407	A	29214	1	168	
29040	59408	A	29215	1	537	
29041 29042	59409 59410	A	29216 29217	1532	1881 2160	KHWSDSIPGTEADWSASTTSGC
29042	159410	A	29217	1552	2100	AGFAAFACSSS*VICLLSGAVA
			1			AYAPQLRHQAIRKVIIRRTSAFP
						LMD*TWSFLSSTNGLASCSASIS
						SAGSGAGSASGVTKVSVDTAS
						GWPIFVTDRLSSCSTRFTLPGAN
						RLITVEPSLKRPISWPFSSATEPS
						FSPAGQVQRLMIPSRGGVMVP
						AQTVSMLPTIVAPTGPYSSHLL
						GSFTLSPP
29043	59411	Α	29218	1	1713	
29044	59412	Α	29219	2159	2715	TIPAKPVPSMVASGTVRFGFLTI
ŀ		İ				PVLTAADSTPTKAHRQSRILLMI
ŀ						A*PSVVSAVFQLAA*VAASNQC
						QPTIAVITTGIRTSTRPIVA/CITG
						FVTGAVEIVLVANSVIDISVGSP
						FSIPQMFSARLGIATMAICPIMV
						SFSVAAINSASHNRQGFALQFFF
		ł				NDAACGSGEFRILMQEEHPDSV
00045	60412	 	20220		102	VFC
29045	59413	Α	29220	2	102	DFADFGTTIKQDFRLLGQTSVD
						RLLQLSQGQAVKGNQLLPVSL
					i	VKRKTTLAPNTQTASPRALADS
}						LMQLARQVSRLESGHHWRSGE SGVPAACINLVCSALYAAGNM
						SVDLCHRDFADFGTTIKQDFRL
		1				LGQTSVDRLLQLSQGQAVKGN
1						QLLPVSLVKRKTTLAPNTQTAS
						,
						PRALADSLMQLARQVSRLESG\I IGGAGSLAFPLPALIWCAVRYT
						PQVTCLLTFVTGILPISEPPSNRI FACWGKPAWTACCNSLRARR
20045	50414	 	20221	1	1464	FACWURFAW FACCISERARK
29046	59414	Α	29221		1404	<u> </u>

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29047	59415	A	29222	3	29	MQTEQQR/AVTRLCIQCGLFLL
						QHGAESALVDELSSRLGRALG
						MDSVESSISSNAIVLTTIKD/GQC
				:		LTSTRKNHDRGINMHVVTEVQ
						HIVI/LAEHHLPDPEP*EQQRR
29048	59416	Α	29223	5	307	
29049	59417	Α	29224	5	948	
29050	59418	В	29225	1	696	
29051	59419	Α	29226	1	1083	
29052	59420	Α	29227	817	978	LAGCYTMLPGNGPAGMHACIS KLDK*AAVKKRISEIIHENRGRY GYRRVPLSLH
29053	59421	A	29228	198	362	
29054	59422	Α	29229	1	2907	
29055	59423	Α	29230	1	2541	
29056	59424	Α	29231	1	1566	
29057	59425	Α	29232	3	601	
29058	59426	Α	29233	1	1347	
29059	59427	Α	29234	940	1326	
29060	59428	Α	29235	1	2547	
29061	59429	Α	29236	527	1383	SWRSVQLLPATSIPSWQTETNQ
						FMGRDRPTPTAESPYAVLLRQP
						LAKLNIIQ/RPVMNMVENMLDQ
	l					AFKKLNPHEHPVLHSDQGWQY
	i					RMRRYQNILKEHGCGVTPIMS
						MRRWLAKNRPQADVRVIYNVR
						TPQDVIFADEWRNYPVTLVAE
						NNVTEGFIAGRLTRELLAGVPD
						LASRTVMTCGPAPYMDWVEQE
			٠			VKALGVTRFFKEKFFTPVAEAA
ļ						TSGLKFTKLQPAREFYAPVGTT
		l				LLEALESNNVPVVAACRAGVC
						GCCKTKVVSGEYTVSSTMTLT
				:		DAEIAEGY
29062	59430	A	29237	1	2496	
29063	59431	A	29238	3	2056	
29064	59432	Α	29239	1135	2067	
29065	59433	Α	29240	1	1566	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29066	59434	A	29241		1605	MKVPRGDVMFQLNLRKDDGQ FEDQLLLLVLLPKHRGHLLLQV ADDVWFKNRRAKCRQQRQQQ KQQQPPGGQAKARPAKRKAG TSPRPSTDFRSRDGIPEKATRTS CPSDSSVFSLQRPPLSSTGRGSS LSWDSSQVLVILSTLTPSGTIVT AEPKYPFEKRLEVVNHYFTTDD GYRIISARFGVPRTQVRTWVAL YEKHGEKGLIPKPKGVSADPEL RIKVVKAVIEQHMSLNQAAAH FMLAGSGSVARWLKVYEERGE AGLRALKIGTKRNIAISVDPEKA ASALELSKDRIEDLERQVRFL ETRLMYLKKLKALAHPTKKVT LSLHREGKQINHKAVQRLMGT LSLKAAIKVKRYRSYRGEVGQT APNVLQRDFKATRPNEKWVTD VTEFAVNGRKLYLSPVIDLFNN EVISYSLSERPVMNMVENMLD QAFKKLNPHEHPVLHSDQGWQ YRMRRYQNILKEHGIKQSMSR KGNCLDNAVVECFFGTLKSECF YLDEFSNISELKDAVTEYIEYYN
29067	59435	A	29242	3	1119	SRRISLKLKG\LTPI
29068	59436	A	29243	1	846	
29069	59437	A	29244	1	3383	MSEKLQKVASARAGHGSRREIE SIIEAGRVSDDGEIAKLGDNVE AWYRARLAGAFTLQECVMAA STFFIPSVNVIGADSLTDAMNM MADYGFTRTLSVTDNMLTKLG MAGDVQKALEERNIFSVIYDGT QPNPTTENVAAGLKLLKENNC DSVISLGGGSPHDCAKGIALVA ANGGDIRDYEGVDRSAKPQLP MIAINTTAGTASEMTRFCIITDE ARHIKMAIVDKHVTPLLSVNDS SLMIGMPKSLTAATGMD
29070	59438	A	29245	104	1381	
29071	59439	Α	29246	1	375	
29072	59440	В	29247	1	5082	
29073	59441	Α	29248	119	343	RMPKRRRWGKLSTIRCSTTCKK RLT*IVLPVRTPGRLCSSLKSVP ASHCLASCKAYSNKPWKRQPS KRHYVTMR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29074	59442	A	29249	468	935	VPLAVPYGRLWRTIFSPLPSSFR STRVR*EVSGRSSPSISSLASLVR PIT/SLLIVNAHPVELLQVVFPTL DKHIAAARIHAVFDNRHFATRL FTRRVFRTVNKAAQVTLFNPTE AVDLFFHFNAVTKGFHLRQGD KEGYVQAHTNNGDLRVRTSNP
29075	59443	Α	29250	407	2145	
29076	59444	Α	29251	1	177	
29077	59445	Α	29252	1	1767	
29078	59446	Α	29253	1	2499	
29079	59447	A	29254	2	607	
29080	59448	Α	29255	2	314	
29081	59449	Α	29256	2977	3913	
29082	59450	Α	29257	1	2091	
29083	59451	A	29258	1	751	
29084	59452	Α	29259	1	927	
29085	59453	Α	29260	1	1113	
29086	59454	Α	29261	1	875	
29087	59455	Α	29262	1	450	
29088	59456	A	29263	1	522	
29089	59457	Α	29264	I	912	

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SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29090	59458	A	29265	1	2416	MLAQSLQALEQDGFLNRIAYPV
						VPPHVEYSLTPLGEQVSEKVAA
						LADWIELNLPEVLAVRDERTRY
<u> </u>						DIAVPRKRYGHAVSRNTFALRS
						QERYGHSVLETVGNSGSSKQFS
						MDILDPCARGPGQISLITVNHKL
						HVRCESIAYSVQTMVVKGGSA
		١.				FAAFFIAVVLWMIGYVPNVEQS
			İ			TQALLGMQFIMIALPTLFFMVT
						LILYFRFYRLNGDTLRRIQIHLL
						DKYRKVPPEPVHADIPVGARLS
						FAERVMEGLSDGGQSLQSPSAL
						FSKQTLKNMSIYKIPLPLNILEA
						ARERITWTLNTLPRVCVSFSGG
						KDSGLMLHLTAELARQMGKKI
						CVLFIDWEAQFSCTINYVQSLR
						ELYTDVIEEFYWDALPLTTQNS
						LSQYQPEWQCWEPDVEWVRQP
						PQDAITDPDFFCFYQPGMTFEQ
						FVREFAEWFSQKRPAAMMIGIR
						ADESYNRFVAIASLNKQRFADD
						KPWTTAAPGGHSWYIYPIYDW
						KVADIWTWYANHQSLCNPLYN
						LMYQAGVPLRHMRICEPFGPEQ
						RQGLWLYHVIEPDRWAAIGSP
						ADREEDAEEYLEAIMEARVTV
						AGMGLVMEVQDYFDGEA\DRL
						AKAWLP\EYTPQIKSLKDERKE
						AYRQIVEMSTEPQDVDLVRPA
						NKFEMTRVREGEKEADLPVWK
						HHLLCDESGNYPALLNHWETK
						VFEIETKREGFAFWYRNPQYTG
29091	59459	A	29266	786	1265	
29092	59460	В	29267	1	10161	
29093	59461	A	29268	1	882	
29094	59462	A	29269	1	2484	
29095	59463	A	29270	548	945	
29096	59464	Α	29271	17	352	DLQDTGCFMLMNTGEKAV/KS
						ENGLLTTIAC/GPTGE/VNYALE
						GAVFMAGASI/QWLRDEMKLIN
						DAYDSE/YFATKVQNTNGVYV
1						VPALPGWSLLWTRTCHRIFPRH
						RISGAAGYK
29097	59465	A	29272	799	984	QGDIALVIATNQFCIKLAPIIELN
						TDFLCLINHMVVGQHIAFTGVD
						DDTGA*TFEGLCRLIR
29098	59466	A	29273	1	975	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29099	59467	A	29274	65	562	DFRWHGDSRKVHRKNRLIKPL MILLTRLSNRTNWPLTAAVIWP GKV*SACRKSANAPKNIRRLCV SGWKSANWMSTQSSSSSSSTSS SIIIIINSSSSLQCQPCASKYLAH YFTVSSIAAYSTPVVSTQEPWA TRHHPHHQQTDRRRPATRKSPR QYHNETNRQ
29100	59468	Α	29275	1409	1641	PENGRPVYAGGRDAAWRDVY AEFPRLSLPDGFRAAAVHRADA ALHHADL*HHE*APSALGLCL* RLAGGDWCRDYSL
29101	59469	Α	29276	1	3252	".
29102	59470	С	29277	1	2760	
29103	59471	Α	29278	1	723	
29104	59472	Α	29279	14	338	
29105	59473	В	29280	1	1201	
29106	59474	В	29281	1	1866	
29107	59475	A	29282	1067	2753	
29108	59476	В	29283	1	1144	
29109	59477	Α	29284	3	724	LAQLYGDPPAWPTPTRGVSEIR LALRFKSNDSLLRHFKDTSTLY LEIVDYPGEWLLDLPMLAQDY LSWSRQMTGLLNGQRGEWSA KWRMMSEGLDPLAPADENRLA DIAAAWTDYLHHCKEQGLHFI QPGRFVLPGDMAGAPALQFFP WPDVDTWGESKLAQADKHTN AGMLR/ERFNYYCEKIVLVD/CL Q/PLNSGHSIYDMRWPDALIKFS YG/QRTVQRCFITPRAQSA*SGT TSGDLTRR
29110	59478	A	29285	1	1863	
29111	59479	В	29286	1	813 546	
29112 29113	59480 59481	A	29287 29288	1	2691	
29113	59481	B A	29288	1	1212	
29114	59482	A	29289	1	2328	
29113	59484	A	29290	1	531	
29116	59485	A	29291	188	358	
29118	59486	A	29293	2545	2713	LLVVQFFFQHL*VPSGTSP*L*H LSGILWHFLLQALLYPRVFLVL LCRSLGAVCLY
29119	59487	Α	29294	1	2046	
29120	59488	Α	29295	3	654	
29121	59489	Α	29296	2	182	
29122	59490	Α	29297	1	1215	
29123	59491	Α	29298	141	266	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29124	59492	A	29299	669	887	VYRSSVYRDSGCLSGGDLRSGN
						ASGHAKRQSDGDLRSRAATGG
	ł					DHSAGDWCGRRVQTSAG*LWR
						KARPWPNR
29125	59493	Α	29300	2353	2758	SQAYHQVLPVCEAAPIPDDNHT
				:		LAALR*HGVYEKHMDQDCWA
				:		SFLPEERLFWRPIPAPRSDRVEC
ĺ						VDSLPLTAVGKVDKKQLRQWL
						ASRASARAQRRSPLAEARKPQY
İ	1					VHQGMDNARTALQKPEQARA
						НТЕVНЖТ
29126	59494	Α	29301	5	793	FLQRFVADLPCGAQVVKFSTFR
						TQCRQTEATLKVLFLHGTFNVV
						TSIGATTQVTNDARTDLRKQLV
						IDILFGIRRQTLLHFLDRHNRHF
ĺ		1				CRCRSRNTFLFQLLRMIRDFND
l						FELV/NPLSLDSVLGMQPLREEI
						QQADRDDDKHHQGAGLLELET
ĺ						ANRFPQGDADPACADHADDGR
		1				RADVGFEAIEGVGDQQWHHL
	1			-		WQHAVEDLFELVGTGGANAGP
		1		•		GSIASTASESSLESTPVVWINSA
		1				STPARQRTGRGRRRPRTAWRRP
29127	59495	Α	29302	1	2457	
29128	59496	A	29303	1	292	
29129	59497	Α	29304	1	440	
29130	59498	Α	29305	593	864	RTSAEPINPAPPVIRIFLISARLC*
ĺ	į]				WTLSPLITLN*L*STSITSTSAVA
ĺ		1				SASSSCARVQSPVSFFGNWWM
		1				LGSTTRVSPLCHWAISSADF
29131	59499	Α	29306	2	696	VPAGRYTGRDLHLHI/ILPFRES
l		l				LPARHRVRRYRPLEAC*TPCTD
		l				GYHRIFYRLKGESAKDGSVMT
]	LRSFLDKDGHPIDVEDINDQAR
						HLVRLMPVLRLRDARFMRRIR
		1				NGTVPNVPNVEVTARQLDFLA
	İ	l				RELSSHPQNLSDGQIRQGLSAM
						VQLLEHYFSEQGAGQARYRLM
						RRRASNEQRSWRYLDIINRMID
		l				RPGGRSYRVILLGLFATLLQAK
						GTLRLDKDARPLLLIE
29132	59500	Α	29307	3	1405	
29133	59501	Α	29308	1204	1411	LRPALYQPARLSDAAVRKTG*F
						AVVSGSEHAESDAG*SGELLEQ
	1	l				LSEVLR*PDEIFLWRCRAEREQL
	1	ı	1			`
29134	59502	A	29309	236	645	GL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29135	59503	A	29310		776	MELAALRSENPQPDEKPLGETL KDLFSRPVLPEMTDVHLPLNLN IEEFMGEQLHVTGDTDIYREHH AAEMSNIDGNTKLDALDIDSSQ GIVDASGTAHLSDNWPVDITLN STLIVEPLKGDKVKLKMGGAL REQLEIGVNLSGPVDMDLRAHT RLAEAGLSLNVEVNSKQLYC/L AHCMSSMPKESGADEKNSDNR WCRVYWLGAGALYHQRNERR GGSGR*ADLRRKPDVAGTGRA
29136	59504	A	29311	955	1095	KRALCL*ES*YLRSGRTGTRIH HRRHPIPFLIHHRDQPFRHQLRK SFP*RPNAKCITRCQQTHS*FFIR
29137	59505	A	29312	1029	1490	RLPPAVDPTARLRRPASGRRYP CIPAFVGTPAVSLLCWPTGADD SYCRKSLFRRWRGIRAAGKAAF RGWSGL\DRQANPAQVEIIEIRQ L/VRKSPQTAHSPARIWRRLRSA SSRTYARRCCRFQCSKGPADGF PSVGSGKYQRSRRARRPASAG
29138	59506	A	29313	22	443	RRRHSCNSPTDEGASHTWTQTL SLSDKCRQGTVSGRLSLRKSDC TPISHASCSSSSLHGH*VSVAVR LRMTDFSRTVGKDVQRFDAGL GWTLERLLSAHAAFRVALKAG DMAILASRPPTVTPNSMRLLGR LYRSGVYGR

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29139	59507	A	29314		2104	STLAQQWQAGDSIWSRPAIRVF ATYAKWDEKWGYDYTGNADN NANFGKAVPADFNGGSFGRGD SDEWTFGAQMEIWCSYLLALR QCQADIHSAGCICHGVVLVND QCLPPVKCWGRCGAKSPFCAIT FRVRWTIRKSTKCCANRAYKR NITVGRIRRLRRIRQPLPDATLC VLSGLQTEHNRRWPNSVCHFSP DSTFYNDLSGRMKNVRLMFNG IHRDNGFSKRPTDLNYTRKPLV LAFQTAWFITVRVEIVGFRGINR LSLMLEQNNVLIGENAWGKSS LLDALTLLLSPESDLYHFERDD FWFPPGDINGREHHLHIILTFRE SLPGRHRVRRYRPLEACWTPCT DGYHRIFYRLEGESAEDGSVMT LRSFLDKDGHPIECRGI*PIKAR HLVRLMPVL\RLRECPVLMRR IR\NGTVPNVPNVEVTARQLDF LARGGQARYRLMRRRASNEQR SWRYLDIINRMIERPETRYTREI GFTSTNIDLIYGLPKQTPESFAF TLKRVAELNPDRLSVFNYAHLP TIFAAQRKIKDADLPSPQQKLDI LQETIAFLTQSGYQFIGMDHFA
						RPDDELAVAQREGVLHRNFQG YTTQGDTDLLGMGVSAISMIGD CYAQNQKELKQYYQQVDEQG NALWRGIALTRDDCIRRDVIKS LICNFRLDYAPIKKQGDLHFAD YFAEDLKLLAPLAKDGLGDVD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29140	59508	Α	29315	1	2237	MLTGYRAVSRHKSQRYTADDA
						EEMIGKLTGMPIPLNSLRQWIL
	1					GLPGDATDYKLDDQYRLSEITY
						SQNGKNWKVVYGGYDTKTQP
	1					AMPANMELTDGGQRIKLKMD
						NWIRADGYHTLQTLFQFLDYG
						DTISIELRDDGDIRLLTPVEGVE
						HEDNLIVRAARLLMKTAADSG/
	1					LSSDGKR/RSSSCARVQSPVSFF
						GNWWMLGQTTRVSPLCHWAIS
						SAISHRRAFAQVINIRFKRQTKA
				'		GDFQFTGAFIGSRQAISHRRFHL
						IDNPERFVIVHFARGTDKPRLLG
į						VLCHDKPRINSNAVTAHARAR
						LKNINARVTIRQANQFPDVNPLI
						GTNQRHFISKSDIHIAEAVFEPSI
						IAADRLNPLVNELIIMPDIEKRL
						DAFVRIAHEELLYLLGILMNPA
						NKDHVLPLILTGPKESADYFRV
						LDEFVVHTLGENARRHYRIIIDD
						AAEVARQMKKSMPLVKENRR
						DTGDAYSFNWSMRIAPDLQMP
ŀ						FEPSHENMANLKLYPDQPVEVL
						AADLRRAFSGIVAGNVKEVGIR
						AIEEFGPYKINGDKEIMRRMDD
						LLQGFVAQHPGSYNDLLLMEL
						,
						HLSCVANISKRQLICAVPLPKPP
						KAGLLGKNIMGTGFDFELFVHT
						GAGRYICGEETALINSLEGRRA
						NPRSKPPFPATSGAWGKPTCVN NVETLCNVPAILANGVEWYQNI
29141	59509	A	29316	1	2892	INVESTIGATION OF THE PROPERTY
29142	59510	A	29317	19	649	
29143	59511	Ā	29318	2471	3036	KVTWVTCSILPMTLSPSAAFSSL
						FRMKILSLK**KRILR/SSGKPAA
					1	ROGDMTQYGGSIVQGSAGVRI
						GAPTGVACSVCPGGVTSGHPV
		1				NPLLGAKVLPGETDIALPGPLPF
						ILSRTYSSYRTKTPAPVGSLGPG
		1				WKMPADIRLQLRDNTLILSDNG
						GRSLYFEHLFPGEDGYSPQRVT
						VACAPRRGKTG
29144	59512	Α	29319	1	1476	
29145	59513	Α	29320	688	1578	
29146	59514	Α	29321	1	1653	
29147	59515	A	29322] 1	218	MLIVFSLPSDTLVLSPL*PNFRT
						RPFRPSSVPR**PKKDLKIATSA
						MMEAAYSSVIANVVLVPVMDA
	1-25::	1_	00000	<u> </u>	0.00	KWLAR
29148	59516	A	29323	3	260	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29149	59517	A	29324	1	1545	
29150	59518	A	29325	443	1041	LSSLKIVKLLRSTANSQVIDFQR WLGHDKRATLLLWKLEAAGSP LRPLSVQVTTPQEVAETDNHAD NSYNAGLFIVNSLYTAEGVMD KHSLWQRYVPLVRHEALRLQV RLPASVELDDLLQAGGIGLLNA VERYDALQGTAFTTYAVQRIR GAMLDEL\AAVTGCRAACDAT RVKWHRQ*GNWSRNLAAKPR KLR*RNV
29151	59519	A	29326	1	2349	
29152	59520	В	29327	1	747	
29153	59521	A	29328	275	729	
29154	59522	В	29329	1	2469	
29155	59523	A	29330	1	969	
29156	59524	Α	29331	148	1180	
29157	59525	A	29332	56	170	VHA*GSLFFPELSMHQDLSQGH EVQLPPVNRSLKPNQK
29158	59526	A	29333	1	3246	
29159	59527	Α	29334	482	765	
29160	59528	В	29335	1	1713	
29161	59529	A	29336	123	287	GDCSGCVEKQERCCNRNTT**A SAPGN/ARWNSYVG*KHH\SCQ WGDYRRQCFRGE
29162	59530	Α	29337	1	3189	
29163	59531	Α	29338	1	1344	
29164	59532	В	29339	1	1233	
29165	59533	Α	29340	1	1572	
29166	59534	Α	29341	1	3591	
29167	59535	Α	29342		843	MNYSHDNWSAILAHIGKPEELD TSARNAGALTRREIRDAATLL RLGLAYGPGGMSLREVTAWAQ LHDVATLSDVALLKRLRNAAD WFGILAAQTLAVRAAVTGCTS GKRLRLVDGTAISAP/GGGSAE WRLHMGYDPHTF\TDFELTDSR DAERLDRFAQTADEIRIADRGF GSRPECIRSLAFGEADYIVRVH WRGLRWLTAEGMRFDMMGFL RGLDCEVPDPKRRTNSLWRITK MVIWSLQVAIRGTVSLTAYKTQ LKNARHRLNEAPRRRILQMVQ PLS
29168	59536	Α	29343	2	3203	
29169	59537	A	29344	227	634	IKTLPLSPDKLTRISKSIYRKQR AALFTHSFTTWVLAILEHRRFF AK*TRSISKAHVISCVAGHTLA AAPQPHYFTRETYSPERVSTLM TSPICTNSGTLTTAPVDRVAGLP PVPAVSPFRPGSVSTISSSTKFG

SEQ ID	SEQ ID NO:	Met	ISEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amiño acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29170	59538	A	29345		1425	
29171	59539	A	29346	918	1022	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29172	59540	Α	29347	1	1203	
29173	59541	A	29348	918	1021	IQTMQAACSPYQTGLSGHCW* W*GSRRPLEPPFH
29174	59542	A	29349	656	1629	GIINVRKNRHTGSPGHRGKPGT REDEHGV/ELRDRRLNFEWWK PEYGINLYQDYYKQDGFVEIPD QNNPSLGDMVIMQIGQNVPVW NHAGIYLGDNQILHHAFGSQT MNDVKLIKLSGSLGRRFGVFHR FAVDSYPEAIRALSSQVDGFKE YMQSEIGSRSKFAIFVDGVNVG HHEEEKFKCAKEIRIVPIPTGSK TGGLFQVVLGAAIMVAAFYTG GASLALMGTMSSSLFMMGGA MVLGGVMQMISPQPGWRNFEV QSSKNKPSYAFGGAVNTTGGGI PSPGPVWISRRRWRNFLSRFLC RGYELKLTRLARVFFRLYNEST
29175	59543	Α	29350	1	8043	
29176	59544	A	29351	1	876	
29177	59545	A	29352	2020	2224	CVESRCCHATRCGSK*YSGP\PE DTDLKTEAAGAGVACDAAEAP DEAPPAKLHVLPPIIPEIVLKITI
29178	59546	Α	29353	1	2346	
29179	59547	В	29354	50	340	
29180	59548	Α	29355	284	520	
29181	59549	Α	29356	2	304	
29182	59550	Α	29357	79	177	
29183	59551	Α	29358	236	373	
29184	59552	A	29359	1693	1961	RRLAIFHDQVGGKRRLCQLKAF MQSIAVALNHDRHHWH\GNRE NKVNCQLICVDIIINTAQPITSES /DQRQH/TLLRRQTRRDRRHWS HEP
29185	59553	Α	29360	2		YTVSFLLVITQLGFCSVYFMFM ADNLQQMVEKA/TRDLQHLPA QGDSDADPHPGHSFLHADNPA LPDPVGVYPEPQGAVRLLDIGQ HHHPWEHGSDL*VYHGGDSIS QQPTLDGKLEDLLAVLWYSHL
29186	59554	Α	29361	467	3014	
29187	59555	Α	29362	1	1174	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	l .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29188	59556	Α	29363	1	986	MKVTFEQLKAAFNRVLISRGV
	İ	1				DSETADACAEMFARTTESGVY
				1		SHGVNRFPRFIQQLENGDIIPDA
		[QPKRITSLGAIEQWDAQRSIGN
						LTAKKMMDRAIELAADHGIGL
						VALRNANHWMRGGSNGWQA
						AEKGYIGICWTNSIAVMPPWVP
						KECRIGTNPLIVAIRSTPITMVD
						MSMIKHTLPQRAAGTDRKLAM
						SREAQLLERHGYAFNELDLGK
						REPVTEEEKLFVAVCRGEREPV
						TEAERVWSKYMTRIKRPKRFH
						TLSGGKPQPGKKIVIRPLPGLPV
						IRDLVVDMGQFYAQYEKIKP/V
						PVE*WTKSASSRAFTDARAARK
29189	59557	Α	29364	99	375	THQPARRFPAYHYAHPAAAAA
						PGDPLGADLQLCARHYHRQRH
						CVPRHAGYPRSDGLHPQPRGR
						WRIRCSDCLRVP\SDRGDAGDY
20100	50550		20265	0.51	1206	FHL*LADR
29190	59558	Α	29365	871	1206	DDI DVCEMCETOVON TOLVO
29191	59559	Λ	29366	1784	1966	RPLDVSFMSSFTSNSPLTDLVG
						YLTFSAIFLSWRLSLLSDAA*TP
29192	59560	A	29367	1	1276	YPPWGSVHCRRFCSL FHIKLVLTGATWTALPYCHSHV
29192	39300	A	29307	1	1270	
						GLRASLKPTPPFWGRAPLGTRP SQQKTECRLINFPETPIFGNSFK
						YDIEVSNKSPDEEVKLRRHHLA
		1				RCMKNFKTDIYFVSTFEPSTKS
		l				VDLLTVETFAGTVCEYADMPK
		l				EWTTTRGLYDPTHLISASCHKV
						EGLFSFEDRTVATLIRLFIHPVK
						SMRGIGLTHALADVSGLAFDRI
						FMITEPDGADIAVKTFTGIRLKV
						PCPPDHPAFSITNHQTEVTALV
						VFECDIAVRGSDRLRLSPGPGG
						SNTDWVIFGLLIKENPGSLLAV
				ŀ		GVNLLGKILLSVVAAVSESGQN
						FLSVLPVRSEGPCFVVIDVDVEL
		1				PGLRDIADEVKTGVIAVTPAVIP
						ALWEAEVDVNIAAFRSQKAYIS
						GQVNKSGQQAITN/DATDYSRG
						HQKLPCLQSECFHGIYHRIDVA
L	ــــــــــــــــــــــــــــــــــــــ	Ь	L	L	L	I WYLL CLYSLCT HOLL HYDVA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29193	50561	<u> </u>	20260	11	1015	CTI PDPINAVIII A EVODINAVIONA
29193	59561	Α	29368	1	1815	STLEDPHYYHIAEVSPVVIIISIY
						GATGEKYGFITYRCSEHAALSL
						TKGAALRKRNEPSFQLSYGGLR
						HFCWPRYTDYGYFELQINRLAL
						FSTNVTAETPYMHLAPPVGTQL
						PLPHLSHDNSSKNSGGCLPGAS
						VSCNYREPAVRLALASTLPLLR
						AQSPFFMHKDKDPLFWFLTVPP
		ŀ				KWFRKGEVILSSRPRKKTEGSW
						FPKTFFGFGKSHVLVKEFYNRK
						HHIAKQQHAVERT\RELFCPKG
						LG\YSKPQTQGDYAIAQHF/L*T
1						NLPTGCWAKYAVISFMRTD/TV
						DDKH\WPEEHLAKN*LGLLADS
						G\IR\IKLPWGAPHEEERAKRLA
						EGFAYVEVLPKMSLEGVARVL
						AGAKFVVSVDTGLSHLTAALD
		l				RPNITVYGPTDPGLIGGAPENG
						DSDSALYRLRKEMEEFHLVVG
						SDIFGKHQHGTETDSTTCPSTLE
	ŀ					EFETQWFITGGINRILLATDGDF
		1				NVGIDDPKSIESMVKKQRESGV
						TLSTFGVGNSNYNEAMMVRIA
						DVGNGNYSYIDTLSEAQKVLNS
						EMRQMLITVAKDVKAQIEFNP
						AWVTEYRQIGYEKRQLRVEHF
		ł	}			•
						NNDNVDAGDIGAGKHITLLFEL
29194	59562	1	29369	12	1993	TLNGQKASIDKLRYAPG
29194	59563	A A	29370	3	1782	
29195	59564	A	29370	1	3858	
29197	59565	A	29372	1	705	
29198	59566	A	29373	104	471	LWWAGA/SYLCWMGYQMLRG
27170	37300		27373	104	7	ALKKEAVSAPAPQVELPKSGRS
						FLEAIIYFGSVFSLFVGDNVGTT
						ARWGIFALIIVETLAWFTVVAS
						LFALPQMRRGYQRLAKWIDGF
			<u> </u>			-
29199	59567	A	29374	50	620	AGALFAGFGIHLIISR
29199	59568	A	29374	194	767	LWW/AGGLYLCWMGYQMLRG
29200	139308	A .	29313	134	707	-
						ALKKEAVSAPAPQVELAKSGRS FLKGLLTNLANPKAHYFGSVFS
						- [
						LFVGDNVGTTARWGIFALIIVE
						TLAWFTVVASLFALPQMRRGY
						QRLAKWIDGFAGALFAGFGIHL
						IISRLALIVPGLLQKNGGWRRM
						AIISAVIALVCHAIALEARILPDG
						DSGQNLSLLNVGSLVS
29201	59569	Α	29376	1	1038	
29202	59570	A	29377	1	513	
29203	59571	Α	29378	485	1166	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29204	59572	В	29379	54	275	
29205	59573	Α	29380	2		IFLLLLPPHHLLLLLLLLLLLLL LLLLLLQ/MIPLEFCRLYRKQG CICFWGSLGEILLMAEGEAGAS PSH
29206	59574	Α	29381	100	393	FLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL
29207	59575	Α	29382	264	911	ILGFLRDGNFWRKSQSFFPVHH LLICLLRKSSETMQLTDEHLIHD HPKRPPITELVVPGLHEHLRSN VGDYRCEPPHLTKRNIFCILSEA TDITY*LTSISFPGFCFRLT*LLPL TEITGEAVVQIPIKFCPMCFFQS CAKIWTRGMQWHLEAWRCQK PQSPKGGVTALAQEAPKSGLLE GQFMPMPPQYLAVQKKVVWF DVSVDESKLVNRVYG
29208	59576	Α	29383	1	261	
29209	59577	Α	29384	3	195	
29210	59578	Α	29385		399	LERLSAPCISLLLSRSLSSLSSS LLFFFFFFLLLLLLLLLLLLLLL LL/SPPPLLLLLLLLLLLLLLLLL
29211	59579	Α	29386	15	159	SPLHESLV*VKQLELLELLEL LLLLLLLLLLLLLLLLLLLL LLLLLLSSSSFLPS
29212	59580	Α	29387	17		SFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
29213	59581	A	29388	3	282	RELLRGGNVYIGP*SILSFFLLLL LLLLLLLLLLLLLLLLLLLLL LLLLVN*GVCCTLLSGPEISCRS DFAQGPTPLQGAPQTALGNLAS
29214	59582	Α	29389	3	264	
29215	59583	Α	29390	296	421	
29216	59584	Α	29391	3	210	
29217	59585	Α	29392	1	252	
29218	59586	Α	29393	1	1731	
29219	59587	A	29394	1102	1362	NLGTAATLFFLFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
29220	59588	Α	29395	3	2368	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29221	59589	Α	29396	1	318	MEKKSPAYFCCRDMQVIHSDA
						ALQRLLTRFNDPEGWSNLAKN
						QYLSTSMKQKIWQRALSHRKN
						NPKADSDAYETSADMILSELIS
						HGEVDDQMLLNATALIRSDDW
						DFLESALISWDNLPAVVLKELQ
						QNTPRNDIWAKFFLRQENSSRA
						QVDEALRVYYALDPDALAQLD
						VLAKRPYKTAAFRGEKTHRVP
						RRSVRQNIIDQADRLHGAQRLV
						INTNRTRVVDQLIEFLHHQHVN
						AHLAEIVRHHQPNRAGTSDRHL
į		l				NAMVNSRLDVRNNEQTEYKTV
						RGLTRGLMLLNMLNKLDSTSP
						CRMLVCCVPRAPPNPGGLNPR
						AHSLNRSP*NPLKLLSPTGPFEG
						MRPLGTHFWGGIGHGQGPEWG
		İ				PQFGLGMNLLVKSLGHWATW
						VLARAKILRFELGASMMVAST
29222	59590	A	29397	2	4002	WQE*VHYIWGVMHGDLGISMK
27222	37370	' '	2,3,7		1002	SRIPVWEEFVPRFQATLELGVC
						AMIFATAVGIPVGVLAAVKRGS
				5	_	IFDHTAVGLALTGYSMPIFWW
						GMMLIMLVSVHWNLTPVSGRV
l		ŀ				SDMVFLDDSNPVTGFMLIDTAI
						WGE/DHGTFMGAAPIRILPAYG
]						LGTIPVAGFGRMTRSSMLEVLG
ļ						EDYIRTARAKGLTRMRVIIVHA
						LRNAMLPVVTVIGLQVGTLLA
						GAILTETIFSWPGLGRWLIDALO
		ł				RRDYPVVQGGVLLVAT
29223	59591	Α	29398	187	1710	RRDITVVQGGVELVAI
29224	59592	A	29399	1	791	
29225	59593	A	29400	353	646	FYWNWVPFTNWQNPRLMGQK
2,223	3,3,3	' '	25 100		0.10	*HARWLHLRSLLPAM*ATLL*R
						ENNR*LLLLTLTSIFKTFRIRRLS
i						VSKP*VKAKKKTRLIIWSTSKFL
						SCMMLKFT
29226	59594	A	29401	406	1023	GCMIVILIA: 1
29227	59595	A	29402	1	1129	
29228	59596	A	29403	1759	2100	FAGIGRSPGEALVLLLIEKMRES
						GDIHSHHGWLHLPDHKAGFSE
						EQQAIWQKAEPLFGDEPWWVR
						DSPGYFALMVRAKFNNCVIVFR
						R*AQQRHRYTDVVVEIACRIKR
						VAALA
29229	59597	Α	29404	86	426	
29230	59598	A	29405	657	3595	
29231	59599	Α	29406	1973	2582	.,, .
			·		1	1

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29232	59600	A	29407		1483	MFVLADFGHTRRTNRSLGHNIL PARIAPDAINKWLSGFFSREVQ LRWVGPQMTRRVKRHNTVPLS FADGYPYLLANEASLRDLQQR CPASVKMEQFRPNLVVSGASA WEEDRWKVIRIGDVVFDVVKP CSRCIFTTVSPEKGQKHPAGEPL KTLQSFRTAQDNGGGEGEARA ANTGATHRGRHRSPSAVRYRD RLNMYVLRRMDLLYRVKTLW AALRGNHYTWPAIDITLPGNRH FHLIGSIHMGSHDMAPLPTRLL KKLKNADALIVEADVSTSDTPF ANLPACEALEERISEEQLQNLQ HISQEMGISPSLFSTQPLWQIAM VLQATQAQKLGLRAEYGIDYQ LLQAAKQQHKPVIELEGAENQI AMLLQLPDKGLALLDDTLTHW HTNARLLQQMIRAGGWSVKEG REKEYFQSPRGWGRSLMPSLGI IIRPP*RKPKNTENRRCISASVTS EKEAPETINQYKAAVRRPFLFL ATALAQSEVRVCIAWTN
29233	59601	Α	29408	2	1406	
29234	59602	Α	29409	1	1818	
29235	59603	A	29410	441	583	GVYRFPWRFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPGLSS VSSR
29236	59604	A	29411	835	1143	RQLPVSLYVRAVAFENGCFGSC SVGG*GPPAARLGEEQVRGGSS SPCIIRAPRRLHSFLLLLLLLL LLLLLLLLLLFHLSSSSFSST SSSSSCSRSFM
29237	59605	Α	29412	3	1487	
29238	59606	A	29413	149	534	
29239	59607	A	29414	1002	1145	GVYRFPWRFSSAGYGRSGLLV QVEPRLDA*HPGLHEARPGLSS VSSR
29240	59608	Α	29415	2	289	
29241	59609	Α	29416	1	919	
29242	59610	Α	29417	329	405	
29243	59611	Α	29418	48	268	
29244	59612	Α	29419	2	4625	
29245	59613	Α	29420	1	867	
29246	59614	Α	29421	1	684	
29247	59615	Α	29422	409	543	-
29248	59616	Α	29423	1	1128	
29249	59617	A	29424	2	664	
29250	59618	A	29425	3	202	
29251	59619	A	29426	222	296	RSPRD*LPFKFSDPSLQSLKRGH S

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29252	59620	A	29427	1	1774	
29253	59621	A	29428	3	184	MSENMRCLVFCPCDTLLRMMV SSFIHVPPKDMMSIFSICLSAASI SSL*ASVCSYPSLNF
29254	59622	Α	29429	667	834	
29255	59623	Α	29430	1	738	
29256	59624	A	29431	39	230	QMAQHLPHLVFGSHSGSLWEL LSH*VYLLILSLPPPHTPQQAPV WDVPLPVSKCSHCSIPTYK
29257	59625	A	29432	985	1205	IPGSRGKNWVVTGTGQGCHRG PAESDGPAG\GARHWEQPPA*Y LVLFLCSQRRWPGRQQRGQSG RSWPSVRAAP
29258	59626	A	29433	339	592	PLQAWGPSLCS*AIGTPSRKPSP STAHVKHRRLCIPTRRGFSSDN WDPVSSPTCNDARQLHAQVDL EIPVRTCSVWFFVLVIVC
29259	59627	A	29434	633	894	FAENDGFQLHPCPFFQGS*LLCI GLAHAPLAQRSLLLSTF*CLLLS IHQTHSPSSFCPLLARSCDPLEE KRHSGFRNFQPFCSGFSS
29260	59628	Α	29435	517	603	
29261	59629	C	29436	1	1188	
29262	59630	Α	29437	1	1722	
29263	59631	A	29438	1064	1330	MCGIISEGSVLFHWSISLFWYQ YHAVLVTVVL*YSLKSGSVMPP ALFFWLRIDSAMRALFWFHMN FKVVFSNSVKKVIGSLMGMAL
29264	59632	Α	29439	1	1308	
29265	59633	A	29440	162	377	YSHCSIYTRKIQFLCCPSIKTHL GTNLTS*TFFT*VNIISIYLEASLF FSFLDLGRADKGSSLTGVRSIIT
29266	59634	Α	29441	1	480	
29267	59635	Α	29442	731	850	
29268	59636	Α	29443	531	845	
29269	59637	Α	29444	11	649	
29270	59638	Α	29445	1	2433	
29271	59639	Α	29446	1247	2420	
29272	59640	Α	29447	29	94	
29273	59641	Α	29448	1637	1830	
29274	59642	A	29449	3769	4263	RGGRRSSTSGKGTAGCPQSPCF CRCSTLRRTAASPGISPPCPKICS CSPLESIWMSNGLCRSCPPSEDS TCGC*GCCCCCCCCCCCCR RRCPSLGSDAGTELETQRPGAG TGPGPTVAPATFLQSRRLMVGA GTPTLGVRTPGFGLQLGFFYWL EDVERDTS
29275	59643	Α	29450	492	585	
29276	59644	A	29451	2909	3174	
29277	59645	A	29452	1	1617	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29278	59646	Α	29453	1	599	
29279	59647	A	29454		504	MWNCLTNKLLFQESLQKTATR LSAFSWEEAKVQLSWVVLNLA TSAMLPKFYPNEIKVTYLRCTG DEVGATSVLAPKISPLGLSS/VK ALKEPPRARKKQKTIKHSG\NIT FDEIVNVAQHMWHRSLARELS GIIKEILGTPQSVGCNVDGCHPH DIIDDINGGAVECPAN
29280	59648	A	29455	1	1269	
29281	59649	A	29456	434	655	PFSSPASSSGR*KTTSFPAKLFN ACRISLLASAEVNPNISAYLAT WISQIPSCSCRVPSDFLIWSTNR YSIRF
29282	59650	Α	29457	1	801	
29283	59651	Α	29458	2	722	GRVGGGGQGANYLRVVPESGV YSTPSRLPPLPPKVRPPTRFKSV YLEVAPKGE\VGA\TSALGPQRI GP\LGPVSKKKLG\DDISKA\TG\ DWKGP*GITVKLT\IQNRQAQD *GGCLSASALIIKALK\EPPRDR KKQKNIKHSGNITFDEIVNI\AR QM\RHRSL\ARETLWNHLKRSL GTAQSVGCNVDGRHPHDIIDDI NSGAVECPAVSDIFIVTVGVKG GPPSVFTEISWEVLEMVTGGVG
29284	59652	A	29459	1	330	
29285	59653	A	29460	140	214	
29286 29287	59654 59655	C A	29461 29462	181	381 957	
29288	59656	A	29463	3	241	WLRAERAPEGSPETKGS\PPPPP RSVLHLSA\SSPGLRPPEGL*TC RGSPSADSPRRGKHGGKTTHLV SWLSQQKIPMAR
29289	59657	Α	29464	122	473	
29290	59658	Α	29465	1	771	
29291	59659	В	29466	1	1017	
29292	59660	В	29467	1	2568	
29293	59661	A	29468	1680	1899	NASRMSAGGRTAQNAD*LSE*I SQ*PQQRYECRDNQQPLDQL/V/ EQFIQTLEKAITQHRQQLNQWT QKVDIARRR
29294	59662	Α	29469	1343	1714	
29295	59663	Α	29470	321	2645	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29296	59664	A	29471	611	1215	RWCVWSLFLQML/EMCPEFLPS
						GGFVVSLTSGVKLQTFTVNVTA
						HKGSVDPKRVKLKTLAVSVTA
		1				LKAACLELFLLPGGFVVFAGFR
						SEAADLCAEGASSGLGQPREGL
						PRCSGGLKGSSSAARMGAEAK
						GAPRASQGCEGRHHAVTSHRS
						DMGEEEGESQRYLSCPQPSCPI
						NLLQEDASKVIVFAESGINPDSV
						LDLIMLH
29297	59665	Α	29472	335	453	KYIWNVNLQHSVSMLL*FITS*L
ŀ					1	SGMDSLFPAAHCV
29298	59666	Α	29473]	1041	
29299	59667	Α	29474	3	874	TEGQKNLIVEVTSNDAVRFYP
	1					WTIDNKYYSADINLCVVPNKFL
		1				VTAEIAESVQAFVVYFDSTQKS
				1		GLDSVSSWLPLAKAWLPEVMI
,						LVCDRVSEDGINRQKAQEWCI
						KHGFELVELSPEELPEEDDDFPE
						STGVKRIVQALNANVWSNVVM
						KNDRNQGFSLLNSLTGTNHSIG
						SADPCHPEQPHLPAADSTESLS
			1			DHRGGASNTTDAQVDSIVDPM
						LDLDIQELASLTTGGGDVENFE
	-					RLF\SKLKEMRDKAATLPHEQR
						KVHAEKVAKAFWMAIGGDRD
		ļ				EIEGLSSDEEH
29300	59668	Α	29475	1	1773	
29301	59669	Α	29476	1	1023	
29302	59670	Α	29477	2	616	
29303	59671	Α	29478	1	972	
29304	59672	Α	29479	1	339	
29305	59673	Α	29480	3	441	PLTCTSRAAAAMHKYEKLEKIG
						EGTYGTVFKAKNRETHEIVALK
						RVRLDDDDEGVPSSALREICLL
						KELKHKNIVRCAGGGCSLPVW
						PLGGGGG*HWTSVRRTCLAEPF
						FCPRLHDVLHSDKKLTLVFEFC
						DQVKGGVWRTVALGR
29306	59674	Α	29481	1	843	
29307	59675	A	29482	1	873	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29308	59676	A	29483	13	945	NRGPAGVPAAAAMQKYEKLE KIGEGTYGTVFKAKNRETHEIV ALKRVRLDDDDEGVP\SSALREI CLLKELKHKNIVRLHDVLHSDK KLTLVFEFCDQDLKKYFDSCNG DLDPEI\VKSFLFQLLKGLG\FCH SRNVLHRDLEAPATWLINREW GSWKLG\DFGPGVRAFWGFPV\ RCYSAEV/VSHLW\YRSPDV\LF GAKLYSTSIDMWSAGCIFAELA NAGRPLFPGNDVDDQLKRIFRL LGTPTEEQRPSMTKLPDYKPYP MYPATTSLVNVVPKLNATGRD LLQNLLKCNPVQRISAEEALQH PYFSDFCPP
29309	59677	A	29484	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIADCGQLE
29310	59678	Α	29485	3	1225	
29311	59679	Α	29486	1	864	
29312	59680	A	29487		1413	MVNPVFFDITVDGEPLGRISFEL FADKVPKTTENFRALSTGQKGF GCKSSCFHRIIPGFMY/QGGDFT RHNGTGGKSI\HGEKFDDENFIL KHTGPGTLSMAIAGPNTKGSQL FIYTAKSEWLDGKHVVFGKLSR GDSLKEPTSIAESSRHPSYRSEP SLEPESFRSPTFGKSFHFDPLSSG SRSSSLKSAQGTGFELGQLQSIR SEGTTSTSYKSLANQTRNGSLS YDSLLTPSDSPDFESVQAGPEPD PPLGYTSPFLSARLAQQREAER HPRLVPTGPTHREPSPVRYDNL SRHIVASLQEREKLLRQSPPLPG REEEPGLGDSGIQSTPGSGHAPR TSSSSDDSKRSPLGKTPLGRPAV PRFGKPDGLRGRGVGSPEPGPT APYLGRSMSYSSQKAQPGVSET EEVALQPLLTPKDEVQLKTTYS KSNGQPKSLGSASPGPGQPPLSS PTRGGVKKVSGVGGTTYEISV
29313	59681	Α	29488	1	3126	
29314	59682	В	29489	46	114	

SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29315	59683	A	29490	1	704	AALLALGPRNPWTLWTPLTPN
						YPDRQPWTDKHPDLLTCGRCL
ŀ						QTFPLEAITAFMDHKKLGCQLF
						RGPSRGQGSEREELKALSCLRC
						GKQFTVAWKLLRHAQWDHGL
						SIYQTE\QRPRRPRSWAWPRWL
						QPCRQWWGQQLRPRAPV/HSG
						SGLTRRSPTCPVCKKTLSSFSNL
						KVHMRSHTGERPYACDQCPYA
						CAQSSKLNRHKKTHRQVPPQSP
						LMADTSQEQASAAPPEPAVHA
29316	59684	Α	29491	3	1605	
29317	59685	A	29492	1	453	
29318	59686	Α	29493	2	128	_
29319	59687	Α	29494	1	543	
29320	59688	Α	29495	39	1092	
29321	59689	Α	29496	165	439	PPRQAKMQNLAAPGSHSQSPW/
						TLRPKAL*LTPSQIFSA*RLKTD
						TARSPRKPPSFQGPVSLASITVV
						GIDGQASKPLKTPQLWCQLRQ
						YSFK
29322	59690	Α	29497	1	281	VSDHAGTPALVLHP*RQVPLF*
						GRGKYPSTPSPSPLAELATSAR
					#	NLTTRPRNACSPGFLPSRVPSVR
						DPTGNRTVQLTWQPLPEPLEL
						WPKAL
29323	59691	Α	29498	1	542	MRAPPKSGQLQHCRPSRGALRS
		l				GDLPWEINPLSSCSLLHEKDPP
						MTSGPQTNQPKEHLTNFKSGV
						RP/LQGRLPWSFTLSGKSRFSGE
						GASTPTPYIS/GAPIPYFRTPTSY
						LCAPIPYVRTPTSYLCALTPFPL
						FWRHIRTSKRLN/LQQPGIPPEPP
						PPG/CLLQVPEI*PPGQGMPAAQ
29324	59692	Ā	29499	1	1044	
29325	59693	A	29500	596	833	LLLDLPAED*CCLIASEAP*TITD
						AEL*VTLTVEGKSVPFLINTEAT
						HSTLPSFQGPVSLASITVVGIDG
						QASKPLKNE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29326	59694	A	29501	1006	1118	RSKYPNLVSLCPSPLFPRPDLLS
		`	2,301			LWPNPLFLHPNLLYLCAPIPYFH
						APTSYLCTPTPYFHDPTPFPLFW
		ŀ				KELATCAGNLATGTRNAGSPG
						FLLSRVPSVWDPTENRTVQLT
						WQPLPEPLELWPKA/HLTDSFP
						DLLGLAA\ED*HCTIASEAP*TI\
						TDAELWVTL\TVEGKPFPFLINT
						ſ
						EATHSTLPFFQ\GPVSLASIT\VV GIDG\QA\SKPLKTPQ\LWCQH*
						TIRRFKHSFLVIP\TCQVPLLG\E
				1		1
ĺ						DTLTKLSASLTIPGLQLYLIAAL LPNPKPPLRPPLVSPDLNPQV*D
						IGVEWGKGD
29327	59695	A	29502	6958	7935	IGVEWGRGD
29327	59696	A	29503	1	486	
29329	59697	A	29504	1	492	*
29330	59698	A	29505	2	502	RRAHACARRRRKKEMLGVNVL
27550	37070	``	27303	-	502	TSHSSQERMKLTFKKKAVNFA
						DAAAAQGPLLPAMVNPTMFFH
				j		IAVDGEPLGCVSFEVRGLESKK
						*LLI*SIKLC*QIG\LFADKVPKT
						AENFHALSTGEKGFGYKGSCFH
						RIIPGFMCQGGDFTRHNGTGGK
						TSKKITIADCGQLE
29331	59699	A	29506	2	727	NRVLLAMVNPTVFFDIAVDGEP
2,331	3,03,	` `	29300		, 2,	LGRVSFEVRGLDTKK*LLI*SIK
						LC*QIG\LFADKV\PKPAENFR/A
						L*SIEEKGFGL*GVPCFHR\IIPGF
						YVSRGGDFTPP*MAPGGQVHL
						MGKKFER*RTSSLKHTG\PGHL
						VPWANAWTQTQMGSQFFICTA
]					\KT\EWLDGK\HVVVLAKVKER
						HEILWEAM\ERFWVPGNGKT\S
						KKIISIADCGQLLISFDLCFYLNH
		ĺ				QDHSLLCSPLRESTPLPHLLAGS
29332	59700	A	29507	1	380	LCCSPCRRRLLGREEAGEEPTSP
						VTQYLQPRSPEECKMFACAKL
						ACTPSLIRAGSRVAYRPISASVL
	:	İ				SRPEASRTG/EGAATVGVAGSG
						AGIGTVFGSLIIGYARNPSLKQQ
						LFSYAILGFALSEAMG
29333	59701	A	29508	76	385	EEPTSPVTQYLQPRSPEECKML
						ACAKLACTPSLIRAGSRVAYTP
İ						TSASVLSRPEASRTGEGSTAFN
						GAQNGALHL\IQRELHTSAIRRD
						IDTWCKFIGCSAATE
29334	59702	Α	29509	2	230	
29335	59703	A	29510	242	427	SAPDLTCNSKTWKNGRIICFHP
						ASLVSLY*QPQLASWTMKKQD
						ENTQEGKSWDSFSRDVIHI
	<u> </u>					ENTQEGKSWDSFSKDVIHI

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29336	59704	Α	29511]	1497	
29337	59705	A	29512	199	766	EEPTSSCHPNISSRAVPEECKMF ACAKLAMRPPSLIRAGSRV\AY RPIS\ASVVISTQRLSRTG\EGST GI*MGPQNGVS\QLIPKGSFQTS CNQAGGHLITGCQIYLGAGCLQ Q*GVGWFLVAGIGNSLLGKPYP LGYGQKTLSPESQQLVPP*CYP GDFALALKLKAMGL\FC\LMVA FLILFADVTEITA
29338	59706	Α	29513	427	840	
29339	59707	Α	29514	1	477	
29340	59708	A	29515	45	344	PKGTVIDLEKRRQ*DGTLLC\RR CGS*GLPTFKKSTCGKCGYPAK RKRKYNWSAKAKRR\NTFGTG RMRHLKIVYRRFRHGFREGTTP KPKRAAVAASSSS
29341	59709	Α	29516	1	668	
29342	59710	Α	29517	649	992	
29343	59711	Α	29518	1	2994	
29344	59712	Α	29519	3	486	
29345	59713	A	29520	2	898	NSRVDDFVCPRSRRSKRDLIEFS CRIILFPLPSLPPRISFHPSPTLAR VRIGGAVRRPHQSHSISSSSFGA EPSAPGGGG\SPGSLPRPWGPKS CSSSLCGARS*FFWRDVKN\TGL VFG\TTLIMLLSLGSFSVSSVVV S\YLILGFSSSVHHQLSGI*QSSVI PSCNRKFRKKGHPFQKPNWNV DITLSSKSFSINNMNAAMVHIN RALKLIIRLFLVEDLVDSLKLAV FMWLMTYVGAVFNGITLLILAE LLIFSVPIVYEKYKTQIDHYVGI ARDQTKSIVEKIQAKLPGIAKK KAE
29346	59714	Α	29521	24	93	
29347	59715	A	29522	2146	2313	VSSIFFMSMKLGFFFTQVANIIS VAWNLVFCIRFLENTVGIVTI*R RCPIPFSWAF
29348	59716	Α	29523		4368	MLFSYLEKYFYVADELSHCVEP EPSQVPGGSSRDRQQGKPPPLP ALKAKTSSRSGPYATEIKKSTD DSIFKVLDWFNRSSYSDDNK/LI PPTSPRNRVQRKNR\PKSQVAV DLVTDDTTLRENGSKTLSPSKIE LKPVRSDSPFQAEGDMLVSESC QDNNVNIKSKFMNLSQKGTPK EGPGILQPFESYGTPSQGSKNM DYSQDSKSPGKGNGASPSNSNY SYSVLKESDAENQVPCNTNNIG NLGEEEPKFHAH

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence		in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29349	59717	A	29524	33	3339	TDQAKVDNQPEKLVRSAEDVS TVPTQPDNPFSHPDKLKRMSKS VPAFLQDESDDRETDTASESSY QLSRHKKSPSSLTNLSSSSGMTS LSSVSGSVMSVYSGDFGNLEVK GNIQFAIEYVESLKELHVFGAP VEGLNSSGWKKTGVIPY*KG\Y LLPNKGQMGKKKTLVVKKTLN PVYNEILRYKIEKQIL*TQKLNL SIWHRDTFKRNSFLGEVELDLE TWDWDNKQNKQLRWYPLKRK AKALQRFQLKAMGNS
29350	59718	A	29525	946	1183	
29351	59719	A	29526	2048	3359	
29352	59720	В	29527	1	300	
29353	59721	A	29528	1	1495	
29354	59722	Ā	29529	1	2769	
29355	59723	Α	29530	450	3061	
29356	59724	Α	29531	421	1464	
29357	59725	A	29532	238	930	RLSLVSSHCGTILSSEVVCAPPT AYIDFARQKLDPKIAVAAQNCY KVTNVAFTGEISPGMIKDCG/AT WVVLGHSERRHVFGESDELIGQ KVAHALAEGLRE*FACIG\EKL DER\EAGIH*GRLFFEQTKVIAD NVKD\WSKVVL\AYEPLLAIGT CKTSTPQQAQEVHEKL\RGWLK SNVSDAVAQSTRIIYGG\SVTGA TCKELASQP\DVDGF\LVGGASL KPEFV\DI\INAKQ
29358	59726	A	29533	1	929	
29359	59727	_	29534	3	623	
29360 29361	59728 59729	A A	29535 29536	1	202 1046	
29362	59730	A	29537	1	1320	
29363	59731	A	29538	1	1052	
29364	59732	A	29539	922	1245	NRCLGNSFKCFLCILQVGRAHA FLLCSDFMPCEAVCSSIIYSFIPV TKTQGAAPHTR\AHSLTPDPKPS CCCCCCPRPGEDPGHMCVVWP WQPSVIYAKYWTYEHAQW
29365	59733	A	29540	3	130	RPEPEGRGC*GILGGGGGAGPS GHYALQEAQETSQSGRESQA
29366	59734	Α	29541	1364	1916	
29367	59735	Α	29543	1	451	ALPAPRRKVGLNLAPVTEPRDQ PWAMIIDVFS\RYSGS\EGSTSDP *PKGE\LKVLMDKELPRLSLQS GKDKDAVDKL\LKDPGRPMGD AQGGTFSEVHPCSVAAIT\SA\C HKYF\EKAGLKLMPWEMFTDF LGQSIGSQGFPKMFCLGIYFP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	;	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	
29368	59736	Α	29544	175	355	FSQQLLGQAD**SFLL\GCSRLL TAVSRPKRPGEAGITPRVRCLLS NMKDILVASKFWQL
29369	59737	Α	29545	482	1196	
29370	59738	Α	29546	196	818	
29371	59739	Α	29547	170	370	
29372	59740	В	29548	147	257	
29373	59741	Ā	29549	1	1278	
29374	59742	Α	29550	2	152	
29375	59743	A	29551	2	187	
29376	59744	Α	29553	1	915	
29377	59745	A	29554	62	430	RQQDELALIAETLKCVDH*LSL DVLPRGCA*HRELCIHDLLKGN PLRRNILAG*TQERMQLQVESQ SIPEEILGLQPQLGPMGGLWNV RFLLIPTVLWGFHCSQERAFPR KLQVKSFPVAQG
20279	50746	_	29555	149	381	RLQVK3FFVAQO
29378	59746	A			656	
29379	59747	A	29556	1	<u></u>	
29380 29381	59748 59749	B A	29557 29558	146 629	1320 1417	WCASHWGSGHAARHA*ASHPL
29382	59750	Α	29559	318	608	HGLLCSPSLPEEHHPLLHGAQS HRPPKG*GM*AHGTGLAGSSTC SPAQGL*IHQSAPCV*LKVCECT NRHSVSSCSDEDVCICSLCLGQ* GP/ECI*CRIFLGPFNRLIEGAPH L/CRSAMLNPLQEGAREQASAR SGWLLRLLTQEQLLCRACIQTR RDREGKTRHRKGTPEIGKGRAF WKKSLKIILILFNCLRYWNAYM EIWVPALTGIPPNVTVNYATSSS KDSRTDGRVDLLMAVTDGM ISQARRAAPWGPVQPEPSR*APP
						PASGHPVPSTTQRLRSAGARRG TGGQLHLQPRCGDPLGETSWA PESRRSAASLLKPARPRAHWEE QTTPDALL
29383	59751	A	29560	88	564	SCLPVLRRALAFLSPWVVDGTG RRGAAGGGRWGGSGRTGAHG VGGRLRHGGLQVPSPALQEGS* GSVRNRAQ\PGGLALLGDPVHP LQPLARVLSPSLPG/DQQGWPA APSVGPTKPTPTRNSSWPPSAA HSPGSCSCLSLHTSLESCRCPSIN TSLHKHA
29384	59752	A	29561	3	339	RYKDSPRPHQTQEPSWLHLVDP APRLQVELPASPALCARIPQPLG G\HGTGRRGQGAALVGEARAG LPSLPSFFFSFLLSFLSFFLPSFPL FFSLFFPFCPVNCGEQCPIGKM

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	D.	*=Stop codon, /=possible nucleotide
	sequence	·	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29385	59753	A	29562	327	890	VMRIQVLLYYLRFADQGTGFH
		'	2,002			LVLCLRHTAGVQ*SWDS*SGLT
						PELV/HLDGSHV/LAASPRGSPG/
						SPK*MGADQRSSESSPGPQPGG
						PRAEGPHHIQEAPRSA*AQGAG
		l				AEAARLGAGQASGCQSTRRPA
		1				GSRREPGVSLDGGHRAVVGIQF
		ł				QAPSRRAAWGHPLHDAPGRRL
		ļ				MSRQLLTPRRRRHRGD
29386	59754	A	29563	609	972	HPGQWLRKVYWVPQQCRPTG
						AVLDFSPGCSCLPAGQGSGPAA
						RHA*ASHPLHGLLCGPSLPDEH
						HPLLHGAQSQRPPKG*GMRAH
						SAGLAGSSTCSPGAGSTR*SQL
						GS*VW*GRGESLCL
29387	59755	Α	29564	1	2715	
29388	59756	Α	29565	3	644	KMPASPLPSAMNGSLLRPPQKQ
		İ				KLLHFLYSLQKGISPNAIPPHSP
						HPTTAPVYSSQCERRRRQVISAF
						PT/GD*SLHSN*E*QGGVEGEAP
						AGTWAVRGA*GPAGVPGGRGL
ŀ						GGLRTRSSWPALLAPGRQGSGP
						AARH/GLSLPQPPWAPVQPEPP*
						GAPPPAPRRPVPSATQGLRSAS
						ARRRTGRQLHLQPPCGIHLVKP
		İ				AGLLSLVGTWRVFMS
29389	59757	A	29566	1	470	MGQPLLLVRDSGGLQLWQKV
j						KGEPVQQHERRIIPPAREEKVK
						RSPAGPPPSGGLDSSRHKIPSHE
						QA/SGVQPACRTNHQPRGIWCS
	ĺ					PSLPDEKCPLLHSAQSHRSPKG*
						GVRAHGVGLAGSSTCSPSAGSN
]						G*SQLGS*V*NKGR*IYPRTGRC
29390	59758	Α	29567	777	1063	QLPPPSVFPTTPKTELVLGTPGH
						GQPHRGGHESSDSAGGHLP/LR
1						ALRSGWDPSPPSSVCATPTSSGL
						SSTPQLPLHQRTSSSTASWSPG
						WGMGSC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	l .	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29391	59759	I A	29568	195	1899	GSASGVVRSSRWARGLAGFRS
29391	33133	^_	29300	193	1000	EAADLHSECYSS*KQCGPKD*A
						EARFIAKSEGTKLPQCGRGPH*I
		1				QRFSTSPPDSGAQLASPSGSRTR
		i				AAGGAACQSWCRAP/STPQPLG
	Y	1				` `
		1				GRWDWAPWSRGWRSSGTSGR
						TGAHGAGGR/PQAWRAAGPQP
		į.				CPAGRQLRPETLKQNIILSLIQCI
						GASLVPTGTAELEPSPSLQLRGT
						TDAAQAIKNEFARVQKRNLCR
						RGPICFEGDALSWFFEKINKIDR
						RLARRIKKKREKNQIEAIKNDK
						GDITTDPTEIQTTIREYYKHLYA
						NKLENLEEMDKFLDPYTLPRIS
		ĺ				QEEVESLNRPITGSEIEAIINSLP
						TKKSPAPDGFTAEFYQRYKEKL
	ļ					IVLEVLARAIRQEKEIKGIQLGK
						EELKLSLFADDMIVYLENPIVSA
					<u> </u>	QNLLKLISNFSKVSGYKINVQK
					1	SQAFLYSNNRQTESQIMSELPFT
1						IASKRIKYLGIQLTRDVKDLFKE
						NYKPLLNEVKEDTNKWKNIPC
						SWIGRINIVKMAILPKIEKQTWN
				ŀ	ļ	NSQTLQCQPFCESDVCTSTLQIQ
						ERFEVAPLHKKALSSEEITIDKT
					ļ.	DPSPAIEELTV
29392	59760	Α	29569	77	640	
29393	59761	Α	29570	384	746	APWSRGWCSSGRLGLHRSPWS
						GWEAQAWRAAGPEPRPAGRQL
					İ	GAMSCKVETGT*DSEQRHRFG
						ESWGHPWAGAQPTGPVLSGIL
						NVLSSFSVLALPRPTGWPRPCS
				1		AASPSRCPAQSHQH
29394	59762	Α	29571	189	545	GLSCLPAGQGSGPAARHV*ASH
						PLHGLPCGPSLPNEHHPLLHGA
						QSHRPPKG*GMQAHDAGLAGS
	}					STCSPGAGSTR*SQLGS*VCCTG
1					1	RLVGTQQLRPESG*VSQPSPRL
						WAAAEGSC
29395	59763	A	29572	87	374	AYSSQLGESRRYSLDQCLAK*I
	1					CEGRTCIFEEPCNCSSLYVRSNG
		1				GNHSHSTTTFKYNGSNWIPRW
						QGPSGSTQPSKARRPVAFSQGN
						CAMEKGN
29396	59764	A	29573	1	2453	
29397	59765	В	29574	182	1356	
29398	59766	A	29575	28	340	IWISIGGFLFGCNFLFGAVLCFS
	1				1	LGLSCLPVEQGSGPAARHA*AS
	}					HPLHGLLCGRSLPDEHRPLLHG
						AQSHRPPKG*GMRAHGAGLAG
		1				SSTCSPGAGSTRNREN
Ь	L	1		<u> </u>	<u> </u>	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29399	59767	Α	29576	142	442	PKGVGRALAAFPQDRAPGPAA
						RHA*ASHPLHELLCGQSLPDKR
		ł				HPLLQGAQSHRPPKG*GVQAQ
						GTGTGRQLHLQPWCGIHWVKP
		1				AGLLSSLGPRCFYKL
29400	59768	В	29577	1	2464	
29401	59769	Α	29578	985	1292	WIPHRGCRWSCLPVLCRALTFL
		ļ				SPWVVDGTGCRGAGGGAHRG
						GSGRTGAHGVGGR/PQAWQAA
						GPEPCPMGRQVRPGEKSSAVPV
						GQPGWGTQYTLRSHWLGC
29402	59770	В	29579	1	2598	
29403	59771	Α	29580	1	2028	
29404	59772	Α	29581	5917	6355	QEAQPEESANDAQGDGPPGGK
					PQPQPEERSSCAQGVGPPGGQQ	
						ESQDEERSSDAPEDGPPGGQQK
•						PQPEERSSDAPEHDPPGGQQQP
						QPEERSSDAPEHDPPGGQQQPQ
						SEERSNDAPGDGPPGGQQQP*P
						EERSSGAPGHSSPDV
29405	59773	Α	29586	875	2090	
29406	59774	A	29587	228	505	MLGRKPNHTSASRNTRLRHCSR
İ		İ				ARAQVKRMRQQRREEREAK\R
						QPGTASGTSGIAERDSGKCSRK
						RGVQKVPG**NTRQSKLRPREQ
						CTTADP
29407	59775	Α	29588	188	592	AAPPRSPSYRMIRKTR*MLGR/E
						AEPHVCQQEHQVEALQHGQGP
		1		1		GETDATAAERR/RGRQRRQPGT
						ASGTSGIAERDSGKCSRKRGVQ
	1					KVPG**NTRQSKLRPREQCTTA
						DP*TLSTFPEGRGTELEPGFDSG
						ASVLMRGCRAALSASSSP\QGP
						GPQEM*ATRNSWGRRQ*GRHC
						KLPVLITGLQGDVVEGVHVGC
						ASQEPLIQNDQEDEVDAWQKA
						EPHVCQQEHQVEALQHGQGPG
						ETDATAAERRAGGKDASLVQH
						LVPAVLLSVTQGSVPEKEEFKK
						SLVNEILGKVNYDQGNNVPQQ
						TLEHCPPFPKGEARSWSLASTP

ŠEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29408	59776	A	29589	524	1318	NGCDSSGEKSGRQRRQPGTASG TSGIAERDSGKWSRKKREFKKS LVNEILGKVNYDQGNNVPQQT PSHHPNLEHCPPFPKGEAGAGA WLRLRGLGSYEGLPGCALCFFF PSRVLGLRRCEQQEIAGQQQGR DTQHGQQ/RSAEGRGRPG*GPG RTGPPAAQLPQSLRTTRRSRPW GRRQ*GRGR*PPQGLMRC*RRP HHTGWSPQNEKRQPGRSFQQH KSH*RE/RR/RARPVGQQVKAK RSQQFDDECGEDVRQEHSSRRD RVAVKS
29409	59777	Α	29590	2	394	
29410	59778	Α	29591	353	693	GSLFLVKRREPER/QVQHEELTE GEADHSGYAGELGFRAFSGSG NRLDGKKESPSPIKPGDIKRGIP NHEFKLGKTPFIRNACPLVKKF EEDEAGGRFVAFSGEGQSLSKK
29411	59779	A	29592	1	561	
29412	59780	A	29593	725	922	VFKRVYIPFRSKLSSFFKCFP*W TALWEMLYAEEANPFSTIRILF QLEQPALGTSQYKILCLSST
29413	59781	Α	29594	2	704	WRGGSGSGGWESGRRGFFVAL PERSGVCQVVSIMFSFNMFDHP IPRVFQNRFSTQYRCFSVSMLA GPND\RIMPPSALDQLSRLNITY PMLFKLTNKNSDRMTHCGVLE FVADEGICYLPHWMMQNLLLE EGGLVQVESVNLQVATYSKFQ PQSPDFLDITNPKAVYLFQISGV LLDKGECAGECVCRLENALRN FACLTTGDVIAINYNEKIYELRV METKPDKAVSIIECDMN
29414	59782	A	29595	1	1680	
29415	59783	Α	29596	1	2220	

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SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29416	59784	A	29597	2	1114	SGRRGFFVALPERSGVCQVVSI MFSFNMFDHPIPRVFQNRFSTQ YRCFSVSMLAWPNDRSDVEKG
,						GKIIMPPSALDQLSRLNITYPML FKLTNKNSDRMTHCGVLEFVA
						DEGICYLPHWMMQNLLL\EEG
						GLVQVESVNLQVATYFQELSSC
						YLPHW\LMQNLLL\EEGGL\VQ
						VESVQPFKWATY\SNFQPQSPD
		ŀ				FLDITNPKAVLENALRNFACLT
		ļ				TGDVIAINYNEKIYELR\VMETK
						PAKPVSIH\ECDMNVDFDA\PLG
						YKEPERQVQ\HEESTEGEADHS
						GYAGELGFRAFSGSGNRLDGK
						KKGVEPSPSPIKPGDIKRGIPNY
						EFKLGKITFIRNSRPLVKKVEED
						EAGGRFVAFSGEGQSLRKKGR
29417	59785	A	29598	15	569	
29418	59786	A	29599	30	525	YCLHHFFFQVSLLVFAWCSEM
						HGNRQLWE\RTGEMGRRTPGL
						SWTAKSPIGR/RSLRSARVPRTV
						AHSQRAKGSHSLWVLRPQKRR
		ŀ				CAGKSPPPSRLARSPRCPEPLVA
						LARQPLCVRRAGPEERARAQR
į.						RPPRVPPLLSQPGRALLLLLRS
						SFLRSPASGSEQQP
29419	59787	A	29600	1121	1420	
29420	59788	Α	29601	758	1076	LPMNRPPRWTGTILAPIIELLLE
						LQQKENMALGSRTHHGSSPNS
						GSAFCQMACCSSLKPAL*SGRC
						SQP*WLWMSPLSRIFSISNSTSA
			20/22			SSSIGNAIRRRRSRPGP
29421	59789	-	29602	632	835	
29422	59790	Α	29603	428		FIAITVLPHWRSPQWYYPYWRG
						PVTA/LVRKVPAVAGERSSLWS
						VVGLIWKPGLGLALQGVGFAVI
						GTFVSLYFASKGWAMAGFTLT
						AFGGAFVVMRVMFGWMPDRF
						GGVKVAIVSLLVETVGLLLLW
						QAPGAWVALAGAALTGAGCSL
						IFPALGVEVVKRVPSQVRGTAL
						GGYAAFQDIALGVSGPLAGML
						ATTFGYSSVFLAGAISAVLGIIV
						TILSFRRGQETAHQPDQQRAAY
						DLQRSNRRVLPASPASACRCSD
20422	50701	_	20604	1		AHSR
29423	59791	Α	29604	1	825	

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29424 59792	A	29605	242	945	NGCIVRGKTSGSTFICVAMSVA ASTVRR*CWLPGRKAAAWRTC WAPMT*AVMC/WSRLMYGAR LSLLVGCLVVVLSLIMGVILGLI AGYFGGLVDNIIMRVVDIMLAL	
						PSLLLALVLVAIFGPSIGNAALA LTFAGLPHYVRLTRAAVLNCL APLIVQASLGFSNAILDMAALG FLGMGAQPPTPEWGTMLSDVL QFAQSAWWVVTFPGLAILLTV LAFNLMGDGLRDALDPKLKQ
29425	59793	A	29606	1	2433	
29426	59794	Α	29607	1	1383	
29427	59795	Α	29608	1	218	
29428	59796	Α	29609	1055	1873	
29429	59797	Α	29610	3	823	
29430	59798	Α	29611	183	1163	
29431	59799	Α	29612	4375	5125	
29432	59800	Α	29613	1800	2031	
29433	59801	A	29614	2	848	
29434	59802	Α	29615	886	949	
29435	59803	Α	29616	123	315	
29436	59804	A	29617	34	343	HLCSYGRVYAADPYHHALAPA PTYGVGAMNAFAPLTDAKTRS HADDVGLVLSSLQASIYRGGY NRFAPY*MTKP*KPSNVGRKEA FRGLSIAIHAVVHHFSNS
29437	59805	A	29618	1	305	AAAYRGAHLRGRGRTVYNTFR AAAPPPPIPAYGGVVYQDGFYG ADIYG\VMLHTATPSLPLPLPLP TVTVTDEFMTFSPLSPLTCSSPH LRRWCHECFCTFD
29438	59806	A	29619	1	2115	
29439	59807	A	29620	1		FFSRVVPP\DSYQAQA/MVDIVT ALGWNYVLTLASEGNYGESGV EAFTQISREIGYPSLFGIQGCLHE CFAILCQVVYQFLLLMQLSDAQ TVY
29440	59808	A	29621	1	405	
29441	59809	A	29622	1	582	

SEQ ID NO:	SEQ ID NO: of peptide	Met hod	SEQ ID NO: in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29442	59810	Α	29623	1	3429	MAAGGGSGGAGRRPIAAAGGS
			ŀ			ICYSHGRDLAPARPAQPPQPRD
						QPQVRPLCSPHAAAAAAAAAL
	İ					TWSCGPPAGFLTAPSAGSRVRL
	1					AARQQKAAPRKASAEPRDKKP
						LAPKLPQNALLVGKGESPRFIPL
						SVFFSKTFQRTARILKRSASDRL
						PWVTSRTCPGGIRTCPAEMTRY
						LRFANLTGGISEVSGFRDESGIN
						FGSWIAIPPVEKMVCEGKRSAS
		İ				CPCFFLLTAKFYWILTMMQRTH
						SQEYAHSIRVDGD
29443	59811	Α	29624	1	2740	
29444	59812	Α	29625	1	1614	
29445	59813	Α	29626	88	540	
29446	59814	A	29627	2	577	
29447	59815	A	29628	1	2169	
29448	59816	A	29629	1	1619	L DODGUDODIGI GOVGURUDIGA
29449	59817	Α	29630	674	867	LDGDGIESINSLGQYGHFHDIDS
		ŀ				SYP*AWNENVLPFVCILFYFVE
29450	50010	 	20621	746	1985	QWFVALLEDVLHVPCKLDS
29450	59818 59819	A	29631 29632	1	2211	
29451	59820	A	29633	139	247	KTSAAHEKPKWRKE\RNARG*
29432	39020	A	29033	139	247	KRKRRKMLQRSQVNR
29453	59821	A	29634	335	556	THE CONTROL OF THE CO
29454	59822	A	29635	1	586	
29455	59823	A	29636	908	1260	
29456	59824	A	29637	222	1686	ICRTCEVACAVSHHENQDCAA
						LSPDEFISPVCWLARLVRWRCF
						FAQKAR*SPAKYGILGELTTGS
						KLVKANGLMEASTIAAILLGSV
		1				AGGVLAYWHVLVAWPHAHWP
						TVSRQQQQLMASTLPFTSPLAQ
		1				IFPWRAITQRTMRMPFVIDARD
·						ALLQGVFAAVNPSAHLNDSRH
İ						RRINKNVIEPGISCQRPQHLDRI
1			-			AHPFGIHIHQLNAFTGRQFHRQ
						QLLYLRQTFVVDIDHHHPRRLY
	}					AAVNGVIDSANAHRTCTRQQC
		1				NIAARFDAHAMLINILRGVIIGM
}						ISTNNAAHRLCQRRRSKIRSRDT
[GNTQPKLMQI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29457	59825	A	29638	59	600	KWSRSEAGIDELCS/RNRVIIDH
29437	39823	A	29038	139	000	
						CWTTAVACHQCEDAPCANVCP
						VDAISREHGHIFVEQTRCIGCKS
						CMLACPFGAMEVVSSRKKARA
						IKCDLCWHRETGPACVEACPTK
						ALQCMDVEKVQRHRPRLNFLR
						LWYVVHAHTLMRMRPRFIQPW
	<u> </u>					EEVVPRHHQHAACFQALIELLG
						RNGQILKP
29458	59826	Α	29639	391	812	HSALCSCRMRRERLIRPTKTCK
						FNRLQRLCRPDKRSASGNFAVV
						IRLERVSLLAPFFYGVLLLKCL
						MPKRQCNEADHHQTHTCAGQ
						KKMATHPLPGENKFIIGEDREY
						RWALMFPNENAPVCWVGHVR
į l						*KSPLHQHIDRA
29459	59827	A	29640	589	1075	
29460	59828	Α	29641	l	435	
29461	59829	A	29642	9	661	
29462	59830	A	29644	403	567	
29463	59831	A	29645	404	706	
29464	59832	Α	29646	114	851	CDHRNIVIRSAENISANFSHTGS
						V*GWMFTVP*SPSGRVVF*FCH
						L*ATCGN*LN*THSLSQGQRAF
						CILGFLPWHSRRIRSHVGLENEC
						KVLLSGRSSQQMGEP*GR*FSP*
			:			VGPLGGRALLQLPQPNSV/YVL
						PVSGLLVPAGE/CPLNV*PLVCS
			į			SANVLLSTSSCFCLCLARVSGF
						YRHRMGA/SGGFL/M*V*RKGS
						SFNFLHMA\ASSWDSYSGHHFF
						*AGADYFFASSVSSLPLVLLHSL
						HSFF
29465	50022	-	29647	1	1422	<u></u>
ムプサロン	59833	Α	 	1 1	1 1 1 2 2	
29465	59834	A	29648	1	768	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29468	59836	Α	29650	1	1253	MVSVTALKAAFLELFIPPSGLV
						VSLASGVKLQTFAVSVTAHKG
	İ					SVDPKSDQHGLVVSLASGVKL
		1				QTFARRAEFPASQQQREVPRHD
		1				GGNHADRFTHDHRQLMATGG
1	ŀ					RHFAIHFVDRFGVPANGARRAG
	1					NIITQTVTNRFAGVESFQQCQLF
						GIYAVCERQGAEIPGPYARLFL
		1				ATFFIYTSSFKPPLPWLRSLPRN
						TTPAVVRTAKGQVTAKYVIVA
		1				GNAYLGDKVEPELAKRSMPCG
						TQVITTERLSEDLARSLIPKNYC
						VEDCNYLLDYYRLTADNRLLY
						GGGVVYGARDPDDVERLVVPK
ļ						LLKTFPQLKGVKIDYRWTGNL
						QLTLSRMPQFGRQDTNIYYMQ
						GYSGHGVTGGSSRVGLMAGSQ
		l				ISRVSV/CINP*YHRFNLHWRYV
						ADAISADGAFRTVSGGGGRRSG
29469	59837	A	29651	3	354	IFSRTDISLYQHTAEQKHPYCW
						YPYPADSADI\SVNKHRRNATQ
į						LHVSCSFFLLSDQRFHHEAVPR
						RVVLFTFNTCVDKYIADIRSRT
						NGLGFLYAFKQRNSHFVFNAQ
						RHRHSACLR
29470	59838	Α	29652	1164	1273	
29471	59839	Α	29653	1	1161	MKNKLPPFIEIYRALIATPSISAT
		•				EEALDQSNADLITLLADWFKDL
						GFNVEVQPVPGTRNKFNMLAT
						RRHEGRYITCMQPLPIIAEQEQE
						PEMTVRYYISSADLTAEKFATA
						IRNHWHVENKLHWRLDVVMN
						EDDCKIRRGNAAELFSGIRHIAI
						NILTNDKVFKAGLRQGWEDIED
						FGETHLDFLKQYGDFENGIPVH
						DTIARVVSCISPAKFHECFINW
						MRDCHSSDDKDVIAIDGKTLRH
						SYDKST/RRRGAIH\VNNAFSTM
						HSLVIGQIKTDEKSNEITAIPELL
						NMLDIKGKIITTDAMGCQKDIA
						EKIQKQGGDYLFAVKGTQGRL
						NKAFEEKFPLKELNNPEHDSYA
						ISEKSHGREEIRLHIVCDVPDELI
						DFTFEWKGLM
29472	59840	Α	29654	2	1587	
29473	59841	Α	29655	236	666	
29474	59842	Α	29656	1	1953	
29475	59843	Α	29657	2202	2333	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29476	59844	Α	29658	1	1126	MHEVTLEDPSSAQILITVITGHG
						EIITLKRSSRRQNDIRMYCRRRP
						EAFRDHHQLRFLPGTDQAIGIL
						MMSKVGTARPPDKTNIREMSV
						HTVVLICATRVFQCFNNAGNR
						DFIHRIAATRQAALHGREHRRT
				i		PRGVTTIGKMVRKTKTAAGWE
						HESGFYLDGVVKLNRFKSNVA
•					<u> </u>	GKMSSGGAANGSYHSNGLGGH
						IETGMRFTDGNWNLTPYASLTG
						FTADNPEYHLSNGMKSKSVDT
						RSIYRELGATLSYNMRLGNGM
						EVEPWLKAAVRKEFVDDNRVK
		ļ				VNSDGNFVNYLSGRRGIYQAG
						KDLDRFKNLVLVHAARYAADL
						SYLPLMQELEKRYEGKLRIQTV
						VSRETAAGSLTG\GYRH*LKVG
						NWKARLACR
29477	59845	Α	29659	1	1989	
29478	59846	Α	29660	3	159	YKELNLADSSLSEEALIQAMVD
:						IPKLMKRPKVVANGKARIGRPP
						EQVL\EIVG
29479	59847	Α	29661	360	744	
29480	59848	Α	29662	1	996	
29481	59849	Α	29663	441	446	ICRQYPSPDDRTASGAGGGDHQ
						QYGAGLRQTFCLCQRLSARTC*
						RLSASVCAT
29482	59850	В	29664	1	1608	
29483	59851	A	29665	1	2568	
29484	59852	A	29666	116	283	
29485	59853	Α	29667	207	1270	
29486	59854	Α	29668	114	503	
29487	59855	A	29669	1124	1216	LSGKMVM*SIKATCQRVPLKYF FTFECYML

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29488	59856	Α	29670	1	1167	MPWLSTGAAALITALAVVELN
]				DDDDHHHRNNSPLPPTPPDDES
						DDTPVPPTPGGDEIIPDDPDDTP
		l				TPPKPVSFNNDVILDKTEKTLTI
		l				RDSVFTYTENADGTISLQDSNG
						RKATINLWQIDEANNTVALEG
						GNTSACRQALKIPKGSSDYTVT
						WKGGHFTFYRRWRCKVHKVV
		ŀ				FEGSPPVTICRYVLNRKNSWHV
						AHIFRRHAKPEEQ/CSHLFPYPF
		1				H\HDLDEVLNDPDVKLVVVCT
						HADSHFEYAKRALEAGKNVLV
						EKPFTPTLAQAKELFALAKSKG
						LTVTPYQNRRFDSCFLTAKKAI
					ESGKLGEIVEVESHFDYYRPVA	
				ļ		ETKPGLPQDGAFYGLGALFTNQ
						QGFFKSSLLSIFADSSSSVAGRS
						PHNLVKKRGGIVAISAFAG
29489	59857	A	29671	285	431	
29490	59858	Α	29672	112	314	
29491	59859	A	29673	1	1191	
29492	59860	Α	29674	282	660	GPSSSEPSWAVAPGKAGDPHHS
						AEWARNSTPSKDQA*RRPHT\IC
						VTAYQGKVLLVGQSPNAELSA
						RAKQIAMGVDGANEVYNEIRQ
						GQPIGLGEASNDTWITTKVRSQ
29493	59861	_	29675	720	4525	LLTSDLVKSSNVKVTTEN
29493	59862	A A	29676	218	990	
29494	59863	A	29677	54	723	
29493	59864	A	29678	 	2229	
29490	59865	A	29679	2	235	
29497	59866	A	29680	279	1275	-
29499	59867	A	29681	692	1052	
29500	59868	A	29682	1	515	
29501	59869	A	29683	21	267	TLRFGANSVLKPEIKRGFEYSD
		`				CWVDDARLVLANAQMVVRKG
						GEVLTRTRATSARRENG\GKKY
						SWQARGLESLSQPVERLSP
29502	59870	A	29684	1	1941	<u> </u>
29503	59871	В	29685	1	4107	
29504	59872	Α	29686	840	1006	CHESHRQTDGGAVFRVYPGGG
						PRRECWFGSSLDEATPGWLLQ/
						LYERDRH*PASTG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29505	59873	A	29687	1475	2280	NAPGIKTSWRTLRKRLLLLSRK TRMP/GFTNPRYGAGAATNPDP EVFSWAATQVVTAMEATHKLG GENYVLWGGREGYETLLNTDL RQEREQLGRFMQMVVEHKHKI GFQGTLLIEPKPQEPTKHQYDY DAATVYGFLKQFGLEKEIKLNI EANHATLAGHSFHHEIATAIAL GLFGSVDANRGDAQLGWDTD QFPNSVEENALVMYEILKAGGF TTGGLNFDAKVRRQSTDKYDL FYGHIGAMDTMALALNIAARM IEDWQLDKRIVQR
29506	59874	С	29688	1	2130	
29507	59875	Α	29689	238	1879	
29508	59876	A	29690	22	219	RIFPTMCSMPTPIKQPRRW*VR KSVRTQV\LSAADVRAKLFTLK VQDPKIDRANPTMVNMRWMM SA
29509	59877	Α	29691	596	723	MCASAP*WCELPAGVVRPPAST TADYFPLFTLVHGGCAHGRF
29510	59878	В	29692	1	441	
29511	59879	Α	29693	1	1422	
29512	59880	A	29694	1	2856	
29513	59881	A	29695	2	367	QKAGAVQVLLSLWSSLSAAAA GTSLLKEPQWSQRIEALGDTGK ITEQGLSNTAIFSIRHTMAFLHS GSLDRPSALHSGTILSGKITSDIC CPHF*SPGRPCSKQHWAEMLV HHVCLPCRCT
29514	59882	A	29696	735	956	SRLLGEITSPAHFSPTLHSPAAH HQYRKALHGRFPARSRDPPALA PGWRSARRER*SSPARAAARW CRKFAG
29515	59883	A	29697	217	378	ADGTGRRALGG*ATGPAGRWE SYSFTDSV
29516	59884	A	29698	279	732	PPGATLPTVARGTPQMGKEGSS PAKSLAPPLCEQMGQEDGHWG AGWGLAQVLLIALDGLLDAQQ HGGEPLGPAGRWSRIPSPTRCS CPHSAPRGPLAIFSSTCIPGNQR KLGTAPHTFGQPAWR*ACRCRS GRGPP*RSSLWRCTEEGAVH
29517	59885	Α	29699	353	2776	
29518	59886	Α	29700	158	605	PERSGLQEAGGGSRGWGKRSL PPAETAGLSGYMCFRAWLSLSR WDSEDGHWGAGWGLAQVLLI ALGWSS*CASNGWLSHWFQPG R*SRIPFTDSV*LVHILLPVGPL AIFFINLAFPGIRESWEQLLILLE KPVGLEACPCKSGKGRP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29519	59887	I _A	29701	1	753	MLALDQREAMRMIFPA\AGAP
2,31,	37007	ľ.	27701		,,,,	APALSPYAS/ARILVDQQFCYRQ
		l				VVEQNAIAKSCAMIVAADEFIP
						GNGIPVDSVVIDRKINPLQIKQD
						GGKALKLLVLWRSDEDAQQRL
						DMVKEFNELCHSHGLVSIIEPV
						VRPPRRGDKFDREQAIIDAAKE
						LGDSGADLYKVEMPLYGKGPQ
						QELLCASQRLNDHINMPWVILS
						SGVDEKLFPRAVRVAMTAGAS
				ļ		GFLAGRAVWASVVGLPDNELM
						LRDVCAPKSGEPIL
29520	59888	A	29702	294	479	KIHFGFFCHCAESGSLDGRHFA
23220	3,000	ľ.	-,,,,		>	PGV*RSEQHESGSGAVSGTGY
	:	İ				WCSRDYRSREIDGLYRNW
29521	59889	A	29703	1446	2103	IHTDHRPGEIAATTLANRAALS
						GAALRRRRRQNQTIAVGWRLA
			:			GTAHACNIISIRGYGSDEDA/Q/
						QRLDMVKEFNELCHSHGLVSII
						EPVVRPPRRGDKFDREQAIIDA
						AKELGDSGADLYKVEMPLYGK
		l				GPQQELLCASQRLNDHINMPW
						VILSSGVDEKLFPRAVRVAMTA
		1				GASGFLAGRAVWASVVGLPDN
						ELMLRDVCAPKLQQLGDIVDE
		1				MMAKRR
29522	59890	Α	29704	370	1080	
29523	59891	Α	29705	547	928	RLTKVEMPFYGKGPQQ\ELLCA
						SQGLNDHINMPWVILSSGVDEK
1		1				LFPRAVRVAMTAGASGFLAGR
1						AVWASVVGLPDNELMLRDVC
						APKLQQLGDIVDEMMAKRRFIP
						LLRRWVDLALTRWLITVSKP

SEQ ID	SEQ ID NO:					Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	l .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29524	59892	Ā	29706	1	550	MESGVATRPIADFDVYIDKLTE
						FVYKTNLFMKPIFSQARKAPKR
						VVLPEGEEARVLHATQELVTLG
]			LAKPILIGRPNVIEMRIQKLGLQI
						KAGVDFEIVNNESDPRFKEYWT
						EYFQIMKRRGVTQEQAQRALIS
						NPTVIGAIMVQRGEADAMICGT
						VGDYHEHFSVVKNVFGYRDGV
						HTAGAMNALLLPSGNTFIADTY
						VNDEPDAEELAEITLMAAETVR
						RFGIEPRVALLSHSNFGSSDCPS
						SSKMRQALELVRERAPELMIDG
						EMHGDAALVEAIRNDRMPDSS
						LKGSANILVMPNMEAARISYNL
						LRVSSSEGVTVGPVLMGVAKP
						VHVLTPIASVRRIVNMVALAVL
		İ				FVNADETTVVNFHACFACVEV
		l				
		l				FTVRHTTNRYQHGVVTLRFSG
		l				CFFAFHRHINAVFFRFNIQAVFV
		l				ALRPEVIAIMHKLREQGHRVVV
		l				LSNTNRLHTTFWPEEYPEIRDA
						ADHIYLSQDLGMRKPEARIYQH
						VLQAEGFSPSDTVFFDDNADNI
						EGANQLGITSILVKDKTTIPDYF
						AKDKARHRTRPLWAWLKLLW
						QRIDEDNMTTLAGNLAYVSLLS
						LVPLVAVVFALFAAFPMFSDVS
						IQLRHFIFANFLPATGDVIQRYIE
		l				QFVANSNKMTAVGAGQSGDQF
						LFALFNCQCFDADELKRIKNEL
						EPKMGMELNLVQLIAYTDWNE
						TQQKQPDGSWVNYNYDWMFK
29525	59893	Α	29707	898	1163	
29526	59894	Α	29708	81	454	NRLLAGRISSGTGDHFSGAAGI
						DSSLRPVW*T*TLRDQMSGGQS
						AKQPGRFAQWFYP*RLPETG*V
		l				PE*CL**CELIRAN/DHFLVSILPL
		l				RSPCVPLHLSTTPLRLAMDLTG
		L				LSGFPIPLSQSA
29527	59895	A	29709	1321	2973	
29528	59896	A	29710	1	2218	
29529	59897	Α	29711	68	432	
29530	59898	A	29712	740	859	
29531	59899	С	29713	1	3126	
29532	59900	A	29714	642	825	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29533	59901	Α	29715	107	1315	KCADLPVRGLRHCWRRREDPS
	,	` `				GADRSFSALIHSGRAAFWPCR*
						QGALMSEDIFDAIIVGAGLAGS
						VAALVLAREGAQVLVIERGNS
		ļ				AGAKNVTGGRLYAHSLEHIIPG
						FADSAPVERLITHEKLAFMTEK
		ŀ				SAMTMDYCNGDETSPSORSYS
						VLRSKFDAWLMEQAEEAGAQL
						ITGIRVDNLVQRDGKVVGVEA
						DGDVIEAKTVILADGVNSILAE
						KLGMAKRVKPTDVAVGVKELI
1						ELPKSVIEDRFQLQGNQGAACL
						FAGSPTDGLMGGGFLYTNENT
						LSLGLVCGLHHLHDAKKSVPQ
						MLEDFKQHPAVAPLIAGGKLV
						EYSAHVVPEAGINMLPELVQIP
						CIERNAINAVKAVNAARMAMR
		1				RTSAPRVSLDKVIETMYETGKD
	i	1	:			MNDKYRETSRGGLAIKV
29534	59902	A	29716	3	264	
29535	59903	В	29717	85	737	
29536	59904	Α	29718	171	820	LGVCAMTNSQCG/CDEYRSKN
						GYEGARKALTGLSPDEIVNQVK
						DAGLKGRGGAGFSTGLKWSLM
						PKDESMNIRYLLCNADEMEPGT
						YKDRLLMEQLPHLLVEGMLISA
						FALKAYRGYIFLRGEYIEAAVN
						LRRAIAEATEAGLLGKNIMGTG
	1					FDFELFVHTGAGRYICGEETALI
						NSLEGRRANPRSKPPFPATSGA
						WGKPTCVNNVETLCNVPAIL
29537	59905	В	29719	1	486	
29538	59906	Α	29720	1	605	
29539	59907	Α	29721	285	449	TPAARDAQLSGGRGWY*CSAG
						NGLMQHRSQSGDWRAGRPFTE
						GW*PTPDWQIEA
29540	59908	A	29722	411	557	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29541	59909	A	29723	1244	3261	KTINRTSLWYWTLHDHWSVTG
		ļ				RCAFTDVTKVEDHHEPQTQTR
		ľ				GLVMTTS*ATT*KLTVSLTTAC
		ŀ				VMNWV*MQVIPSPTAKIRL*LR
		ŀ				TSNWLTSTTTLTT/NNDVNGDSI
						DNGTEGSAVRVGLGTQFSFTK
						NFSAYTDANYLGGGDVDQDW
						SANDLTGITAKDAQMLSVVKP
						LQEFELFVLAALESRGTLADILK
						AAGATTANITQAIEQMRGGESV
						NDQGAEDQRQALKKYTIDLTE
						RAEQGKLDPVIGRDEEIRRTIQV
						LQRRTKNNPVLIGEPGVGKTAI
						VEGLAQRIINGEVPEGLKGRRV
						LALDMGALVAGAKYRGEFEER
						LKGVLNDLAKQEGNVILFIDEL
						HTMVGAGKADGAIDAGNMLK
						PALARGEWHCVGATTLDDIAS
						TVKRCWTSHQHQTKNRTRRTT
						TRNIRFPNQMIEQINIALEQKGS
						GNFSAWVIEACRRRLTTGGPHV
						MYVLHHADKPNLYHGLPENPE
						ISETVKFWKGIWKPLAAVGFAA
						TFAASIFHYERVIFLTGQVEDH
						MANLIVAQMLFLEAENPEKDIY
						LYINSPGGVITAGMSIYDTMQFI
						KPDVSTICMGQAASMGAFLLT
						AGAKGKRFCLPNSRVMIHQPL
						GGYQGQATDIEIHAREILKVKG
						RMNELMALHTGQSLEQIERDTE
						RDRFLSAPEAVEYGLVDSILTH
29542	59910	Α	29724	1487	1821	QYRPESVLEDPRRSDHHRRTDS
						FRETSFIVQSIVCRVSLSRAILQS
						KRL*EPGEFPPPDPSSPEQRWPV
						CYPPK*SDR*PEYPHSPPGRQES
20542	50011	<u> </u>	20725	1062	(544	QSRYLPAFRHRYSYQTTAY
29543	59911	A	29725	4063	6544	
29544	59912	Α	29726	174	556	
29545	59913	A	29727	1	1926	
29546	59914	Α	29728	1	1443	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29547	59915	A	29729		817	MAFNEPLMLEPAYARVFFCAL AGQLGITRLTDTVSGITLDAGQI AEPLALFGEDDDMDPRPSRSYQ VANGIAVLPVSGTLVSKTRALQ PYSGMTGYNGIIARLQQAISDP GVDGILLDMDTPGGMVSGAFD CADIIARMRDIKPIWALANDMN CSAGQLIASSASRRLVTQTART GSIGVMMAHSNYGAALKTNGV EVTLIYSGDRKV\DGNPYEKLP\ KDVRADFQTRIDATR\SAYTGM SVQDV/LDTEAAVFSGQESWDN GLAE*LVHTDWL
29548	59916	Α	29730	68	98	
29549	59917	Α	29731	215	871	
29550	59918	Α	29732	1	2360	
29551	59919	A	29733	5	194	RGADAGERLNMLTVAEGVETP EQRDGAGRFCSLAKETVTPQW *GVLTSLIIHSEACRIAANDE
29552	59920	A	29734	3	290	WRIIGIPLLLGYSLVCSRVLLAC FWPGSDFWPRSRRKTSHLTVEA FPV/VVIFVSWRNPQVAPTSAH QNRPSRNPVSRPPNTQRVARRK HYALADGY
29553	59921	Α	29735	403	588	
29554	59922	Α	29736	1	743	
29555	59923	Α	29737	5	97	
29556	59924	Α	29738	756	935	
29557	59925	Α	29739	1	1056	
29558	59926	A	29740	1193	1405	
29559	59927	Α	29741	1	2718	
29560	59928	Α	29742	3	357	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29561	59929	A	29743	3	1307	KYGFVHYTLHTLGGTARALVA TDYRPLTKLSLDNGFQTVDHLQ ISQCPYIPPYNFPTDTSPGTPGLL QPPEGHAYDAYWRCVRAVRG QRVSALHGPPVHLRSVYPSASA */WFAPRNPLGVWRSGYRIAPG YGSGVRSWVQPGGFARYKYDQ TGNASTVKCDYYRMAAFGHH AYRMQALTCSMTACPCTTRQE TSSAWGSVSSMGDSRPPQEILG QPLLGRRIKYNCTGIGPWDGKG DESGASRPRKQQASGWLWACP RIFLVIPHSSHPAARRTNGSVGG SNRNRFVIITGPGPQLAPKGLW QWPIGQDPVTEIATLIGTHDLIM FDCIGSVSAPTIQPLEKLLSIVRY PAQVGLFFATRRCQAGATGKQ SQQRNPVLFIFYQRGISVFTSAF APVAVTAPPRQSRRQFPRLSPL DAHQRMGDVSIQAVKEARTC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29562	59930 59931 59932	A	29744	1 755	3075	MLPDSSVRLNKYISESGICSRRE ADRYIEQGNVFLNGKRATIGDQ VKPGDVVKVNGQLIEPREAEDL VLIALNKPVGIVSTTEDGERDNI VDFVNHSKRVFPIGRLDKDSQG LIFLTNHGDLVNKILRAGNDHE KEYLVTVDKPITEEFIRGMSAG VPILGTVTKKCKVKKEAPFVFR ITLVQGLNRQIRRMCEHFGYEV KKLERTRIMNVSLSGIPLGEWR DLTDDELIDLFKLIENSSSEVKP KRRPNRKQRASNVQSLRWKKR RKKAVARRPTQSSDDAIRGQQP DGVDCRDCRAGERQRQQTDSA MMELMVVHPHIFWLSLGGLLL AAEMLGGNGYLLWSGVAAVIT GLVVWLVPLGWEWQGVMFAI LTLLAAWLWWKWLSRRVREQ KHSDSHLNQRGQQLIGRRFVLE SPLVNGRGHMRVGDSSWPVSA SEDLGAGIRQCQQLVAHGLQLL NVSFDLRHLFQRGRLEFGCALR LLTDSQSRLSRKPRGWRGLYG YSPPCGDIVRYHHHDLSVATLH VHINHDDCLEIAVLKGDMGDV QHFADDVIAQRGFFFAFSYEDT VIKIIEKDFTMSGKPAARQGDM TQYGGSIVQGSAGVRIGAPTGV ACSVCPGGVTSGHPVNPLLGA KVLPGETDIALPGPLPFILSRTYS SYRTKTPAPVGSLGPGWKMPA DIRLQLRDNTLILSDNGGRSLYF
29564	59932	A	29746	755	1321	
29565	59933	A	29747	397	576	
29566 29567	59934 59935	A	29748 29749	1014	1266 724	TPGLTKTPCPWEKVTLFSLQWS AYRQANTSGLRHSASSLLPLAC RY*R*WRWQKLAAVLTASARQ SVKSLAYCWQRFVTWRWGRFS LRRVQLPFPLKWGLRR
29568	59936	A	29750	230	1829	
29569 29570 29571	59937 59938	A	29751 29752 29753	137	586 557	KTKTNIKL*AAPITRMVMVRHA \PHSGSVKK*SDITMSFATISVIG LGYIGLPTAAAFASRQKQVIGV DINQHAVDTINRGEIHIVEPDLA SVVKTAVEGGFLRASTTPVEAD AWLIAVPTPFKGDHEPDMTYV ESAARSIAPVLKKGAL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29572	59940	A	29754	63	202	RGRSNSGSTSSVTSPVYT**PTA QGLSARQGCTKGHQVRRYGFR HD
29573	59941	Α	29755	66	372	
29574	59942	Α	29756	1	992	
29575	59943	Α	29757	1	393	
29576	59944	Α	29758	1	3753	
29577	59945	Α	29759	1	1098	
29578	59946	Α	29760	320	703	
29579	59947	Α	29761	2	673	AAFLRECKDPQTMVPKAINSVI WRIGLFYVGSVVLLVMLLP\WS AYQAGQSPFVTFFSKLGVPYIG SIMNIVVLTAALSSLNSGLYCT GRILRSMAMGGSAPSFMAKMS RQHVPYAGILATLVVYVVGVF LNYLVPSRVFEIVLNFASLGIIAS WAFIIVCQMRLRKAIKEGKAAD AHFTPYHATPLRNVMLHIYVLN GVSRFSVIDTNQIAQRCNRFAL LCGA
29580	59948	В	29762	51	623	
29581	59949	A	29763	1184	2406	
29582	59950	A	29764	103	473	
29583	59951	A	29765	444	699	CWPGKMSWGGFPLFLLIGIVSE GIVPAPPCTSGRIQL*IRLVLDFF WLVGY*LLPQFQSLLLVYSGIQ LLPGLVLGGCMCRGIYA
29584	59952	A	29766	3073	3621	GVDNWRIIPIISARLQR*AGSFFS FLGETGSLSCGLSLSFKSCCEAK NCSGSRGSSP/G*IPGVQEWNQI FSRF/HGVGLASLRKQRAPGDQ SPTGLLGE*AHGEIPVGNGRSG KTRA/RGGPRGLEVSWSGSLTH SRG*ASLTSSHNSCHIRRGHGPQ KRSGDMTHASAGH*AEVILAAP RRSCPL
29585	59953	Α	29767	362	1850	
29586	59954	Α	29768	1	1401	·
29587	59955	A	29770	1366	1515	YDQAELDQLIHGSSSN/EQDPR/ RLPKGLTPQTLR/TLCQWIDAH QDYEFSTDG
29588	59956	Α	29771	1	1827	
29589	59957	Α	29772	419	1295	
29590	59958	Α	29773	167	451	
29591	59959	A	29774	94	304	SPAASLYVTGSDLCTARMGGL VTRTGGLSRRAAYPLCHPPSGS RPSATSRASVDSG*TCGELGDA GTRAN
29592	59960	Α	29775	345	652	
29593	59961	Α	29776	596	2297	
29594	59962	Α	29777	184	283	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29595	59963	В	29778	16	1058	
29596	59964	A	29779	715	1234	FTWIGFYANRHFHCPVTTNDFP
				:		HFMKWRAAAHGGENIAFKLAN
				;		LPFFGDIRESHYQVVINRADRG
			ĺ			FNPDFFTGARQQQKFVLIAGGF
						P*QLL*TNAVIGREFRNVQECIG
						LHTAGFANAVTKHF/W*M/PRL
	•					HCTIWRSGSRTITGRSRWSTAII
		ı				NCRVCSFCAISTLASRTSAR
29597	59965	Α	29780	938	1250	PGRVSGKADGSV/LAGNGLLPG
		İ				FFCPLRLRGKYQPEV/IASTIRRR
			ŀ			YQLLFLAVASHQATAAGCGVN
						ALSDLRLCSVCRPDKTHSVASG
						NGCRMRALPSSPFSVIL
29598	59966	A	29781	1	1389	
29599	59967	A	29782	3059	3537	SEGKTANLFNKAITCSGAGECT
2,2,5			25702	3003		RPWASDIKAQCAGGISRFATGN
						GFKRLCDTLRYLQAIENGLKN
						WRLIHIATVRRCPFPT/LSPATID
						AINVIGQWLAQDDFSGEVPYQ
						ADCVILAGNAVMPTIDAACKIA
		1				RDQQILAEGDFGLRCEIRDWCA
		}				NFVSDIR
29600	59968	A	29783	97	610	RCQTRQNAEYRVNAVLVHHFH
29000	39900	A	29/03	97	010	AITHIRQQSQITRYIKLLRHRRH
						TQRRFTACRLRVDAPFPGNHQC
						1 '
						CALHCLRKIDRIQHNFNARFNIR IEKYRRRNTHTARSAA/DPPSGR
		ļ				l i
		1				H*FQFAVVKHGRNFAAPVQVL
					:	RPSPALPLFAGQTPPPRRVPLPA
20601	59969	 	20704	260	750	GYQRHMLLQYDQATVN
29601	39969	A	29784	269	753	YRTPTLQLDQGRADARRGVW/
						HVPFSHESV/WENIVMTRQAQG
						ANFT*TLFCFGIGFAVIA*NCAI
						DPDISIRFFSKEETAT/GDRPDQI
						AAHLWRFPTPGGRFVHHRGAY
						AAIIFRP*YLNGRSMAEQSMILV
						TGELLVELNLEPSQVGNEFAEK
20.502		ļ	2070-		1106	YYGPASQVV
29602	59970	Α	29785	762	1182	
29603	59971	A	29786	3703	5889	
29604	59972	A	29787	925	1130	
29605	59973	A	29788	658	1212	1.5
29606	59974	A	29789	904	1473	
29607	59975	Α	29790	1205	2222	
29608	59976	Α	29791	1	194	
29609	59977	В	29792	83	970	
29610	59978	A	29793	379	1095	
29611	59979	A	29794	172	367	
29612	59980	A	29795	557	1475	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	ŀ			sequence		
29613	59981	Α	29796	1	738	MQPWALPTVGELWVCGRPGA
						ALRAGTEPSSRALGVSETALPA
						EIKLRVIRVGHSSPLAQLASFQK
						PVLFVLRLNSRRFLFLSLARSED
						GILFAKSKHSSPLSLTPLRCIVL
1						MRMYEQLMSGDLCQRVMMPS
1						RNNPGYWNPQ**SEIFKGSPAQ
ļ						TMATLTCSFKKPPPKIPYKAIAL
1						ATVLFLIGAFLIIIRLPSCCQGYI
						KQRGGRPGPFQLLIIGHSWCSY
						PGFYPPAHRFTMHPKGLPWVN
						PNE
29614	59982	Α	29797	1	186	DCRLRAGDPRRSHCAVSPTGGS
27014	J7762	Α	29191] 1	100	RALSGYRY*SVDQPRNDGVDQ
						*ATLRASAHLQTAVVEFSA
29615	59983	A	29798	724	1015	RSHPQCGYLQNHTSSASFSAPA
29013	139963	A	29/90	124	1013	RKG*NRHYAFARNDRLVPAPCS
	ŀ					
						HHHQ*PAFPAPVHLH*PVDLST
						AIDAPAVNGDGKARPSKRRYQ
20616	50004		20700	1	4102	RLSVPEVVQY
29616 29617	59984	В	29799	1	4182 1191	
29617	59985	В	29800 29801	167	504	
29618	59986 59987	A	29801	167	1852	FALFANRVSLAANVSGRGSPC
29019	39987	Α	29802	1341	1832	WWRRIAVVCCSTNR/RSALDIA
		1				HQVDVLSLVHRLSQERGLTVIA
						VLHDINMAARYCDYL\APCAA
		l				VK*LLRERLRKLCAAKPSK
29620	59988	A	29803	407	3584	VK LLRERLRRLCAARFSK
29621	59989	A	29804	3	150	
29622	59990	A	29805	1	921	
29623	59991	A	29806	300	560	IRDKNRVFLRESWRRLFTTAND
_,						QPHRPARRIISIAGIKWRYSDFLI
						NYCAGRAVF*RETGSVVERWH
						HHAGWKTPFRKRAGRTAGH
29624	59992	Α	29807	100	315	PIKITSALASASRYVRATLSCSR
2,02.	0,5,5,2	`	2,00,			NSTLRWKK*RKMALTKPSTTN
						GSRSNS**MNFFL*QAPPG*PSA
						LPFVH
29625	59993	Α	29808	3	116	
29626	59994	Α	29809	1	1469	***
29627	59995	Α	29810	1	2760	
29628	59996	A	29811	284	460	RNRQCYRARHLRWCLQYQRA
						CSGR*VPNLRLPEVQSTDRLLS
						QRRRVSPDRQWWLACH
29629			20012	l	1040	
127027	59997	Α	29812	438	1942	
29630	59997 59998	A A	29812 29813	1	1464	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29632	60000	A	29815	1252	1906	NTFKECKFSQAPFRFGNDPFLA
		ŀ				SVVSRDGFVIAGGGGMVVVEE
						LEHALARGAHIYAEIVGYGATS
						DGADMVAPSGEGAVRCMKMA
			ĺ			MHGVDTPIDYLNSHGTSTPVGD
		-				VKELAAIREVFGDKSPAISATK
		ŀ				AMTGHSLGAAGVQEAIYSLLM
	İ					LEHGFIAPSINIEELDEQAAGLNI
	1					VTETTDRE\LTTVMSNSFGFGG
a.						TNATLVMRKLMIISASTTSILR
29633	60001	Α	29816	1	2472	
29634	60002	Α	29817	1	469	LFNREVCCLGQGQS*QMAL*LL
						GIESYIT*L*SGGDN\ASIGVIPDP
						AAIAR*RPWRSACG**PKCPLA
						DVFAGHSGRKRPPSMAFTATLI
						SPGTGRRAINSVLAQFKAGESNI
						WLSALPTPLTPTIRITNGALPSTF
						SGSSTFARISPISSFSRP
29635	60003	Α	29818	884	1084	
29636	60004	Α	29819	1	1040	
29637	60005	A	29820	2711	3854	
29638	60006	Α	29821	1	957	MKIGTQNQAFFPENILEKFRYIK
						EMGFDGFEIDGKLLVNNIEEVK
						AAIKETGLPVTTACGGYDGWIG
						DFIEERRLNGLKQIERILEALAE
						VGGKGIVVPAAWGMFTFRLPP
						MTSPRSLDGDRKMVSDSLRVL
						EQVAARTGTVVYLEPLNRYQD
						HMINTLADARRYIVENDLKHV
						QIIGDFYHMNIEEDNLAQALHD
						NRDLLGHVHIADNHRYQPGSG
						TLDFHALFEQLRADNYQGYVV
						YEGRIRAEDPAQAYRDSLAWL
						RAGQVADKVHASYYCTRNDLE
						LVAVCDSRLSQAQALAEKYGN
						ASVWDDPQAMLLAVKP*FVGL
						V\GAGQVADKVHASYYCTRND
						LELVAVCDSRLSQAQALAEKY
			L			GNASVWDDPQAMLLAVKPDV
29639	60007	В	29822	96	821	
29640	60008	Α	29823	3	775	
29641	60009	Α	29824	961	2073	
29642	60010	Α	29825	1	849	
29643	60011	Α	29826	319	541	
29644	60012	A	29827	1142	1756	
29645	60013	Α	29828	44	283	
29646	60014	В	29829	1	1812	
29647	60015	Α	29830	685	1146	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29648	60016	Α	29831	202	918	AVDTGLADHRDRTEHGGAFAA
						IVHRIVKHFITAWAICQQRNHA
						ALVVIRRLEANHRRHRTGRG\S
						VDRVSAARSLSSGTMPGNGVW
						RIGVFTQLSVA/WHQ*VDLLIVF
						QFVRDTTDDHDVGIFALAAND
			•			RAAFDNILDPTGSVDVLLPLPG
						RHNIANALAAAALSMSVGATL
						DAIKAGLANLKAVPGRLFPIQL
i						AENQLLLDDSFLVNAAQQNILS
				ĺ		VHILNQQTGKPAADVTVTLQE
29649	60017	A	29832	1184	2409	TLKACCLVRSMCRAVP*RC/GR
						QLVSSDNISNDPMNVIDWINMY
						ALAVSEENAAGGRVVTAPTNG
						ACGIIPAVLAYYDKFRRPVNER
						SIARYFLAAGAIGALYKMNASI
						SGAEVGCQGEIGVACSMAAAG
						LTELLGGSPAQNMEGKIDRPEE
						YADIATKCVTNFREKNRDRCL
						VILSRNDEALNSQRTSEELHHY
						YEIVWDEEQTHKFKNISPHLQRI
						KAFKTLGGPHGNITVDMVISAQ
						ELLQEDMATFDGHIVEALMKM
						PEVNAMYPELKLHAIGWVKHK
						CIPGAKWPEIQAEMRIWKKRRE
						GERKETGKYTSVVDLARARAN
						QQYTENSTGKISPVIAAIHREYK
						QTWKTLDDELAYGRCFADRQN
						LMVCLRSMPNVFTGSCARMRC
						CLSENLLYRHRNGHIQAEWP
29650	60018	A	29833	1	3195	
29651	60019	A	29834	1	621	LLAGTALVGGVQPADAITVDA
						MIPNFNWAFLGVTTWIFMAAG
						GAESVA\CTLTTSKAVRNRSFK*
						SSSPGILSGYVSRSSGSPISSLISP
						ASLCAGHMRFFCSSSKPTCSNP
						RTFAAALSSAWSSPSPNEGFSSN
						PAFLGTSLMMFHLELRRCIAPIV
						TTDLLPLTSGDVGLVLLCVGLD
						GSLWSDCRMTESVSTTNTPPIIT
						SRNS
29652	60020	В	29835	46	893	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29653	60021	A	29836	3	2037	CTSSPDPPSGLPPGFAKLTSLIVT LVEVGVSPEPDEGWLYLAVVID LWSRAVIGWSMSPRMTAQLAC DALQMALWRRKKPRNVIVHTD RGGQFGDRWKGWLTRSIFRWI SFQPALAPTRKAALCYLAREVN PDMADYIKKLKLPGIHVREESR RYYPSGEVTAHLIGFTNVDSQG IEGVEKSFDKWLTGQPGERIVR KDRYGRVIEDISSTDSQAAHNL ALSIDERLQALVYRELNNAVAF NKAESGSAVLVDVNTGEVLAM ANSPSYNPNNLSGTPKEAMRN RTITDVFEPGSTVKPMVVMTAL QRGVVRENSVLNTIPYRINGHEI KDVARITTEEDFNHASAARFVC AAAERRCKTTINLVPENEVLNV LEGEDAETNALRAKRRCPKCG TAMDSYLIDPKRKLHVCGNNP TCDGYEIEEGEFRIKGYDGPIVE CEKCGSEMHLKMGRFGKYMA CTNEECKNTRKILRNGEVAPPK EDPVPLPELPCEKSDAYFVLRD GAAVAARFNDDRHRRGLAVLY ADQADLYGVADSVSAGDSLSA LYKHERRLVVPLLVSSSLLFLY RHGIRLPCGPSGGIWAPWQIRR GRQAVNCLAPM/HHPGKNRAW KTYCSQ*AIVPQLPVCGI*PRSD
						SYHDYQRDPRCQPLRALWRRS DSPIGGYSSAIGI*TERHCRSGNP
29654	60022	Α	29837	993	1832	
29655	60023	A	29838	124	276	QEGRCQVTITRKMPLSSDLGSL HGLAGNHSPPICARTPHVATVL RQLLELEDKHWNGSG*FARLG WKPQSPHLCQNPPCGHCPQTAP GA
29656	60024	C	29839	64	267	
29657	60025	Α	29840	3	86	
29658	60026	Α	29841	1	1481	
29659	60027	Α	29842	217	2040	
29660	60028	A	29843	1	132	LNTKSAK*VGGSSRVNVPQVFI SLVSQMFSENDLPLVRKRKTEP
29661	60029	Α	29844	115	903	
29662	60030	Α	29845	1194	2311	
29663	60031	Α	29846	368	502	
29664	60032	A	29847	1156	1359	SEPVYPLCYLRQLAVQANPRR MRCIARHFNINGNRHLTTTINFI *SMVSLIANRLLIIDLIHTVDFY
29665	60033	Α	29848	1	228	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29666	60034	Α	29849	102	296	YRNSHNLLQGWQIHRGDLLYH SSPHSR*KHRNRHNARARIPAAI HDNLACVQPTLSAFHQDMCS
29667	60035	Α	29850	1	4185	
29668	60036	Α	29851	1	906	
29669	60037	A	29852	19	195	GEFDVNIAAVVLPDVA*TPYPA YRRDLIAIGQCVVIDQCVFLIRV TNPAGSFFELRIHH
29670	60038	Α	29853	2	834	_
29671	60039	A	29854	2	193	DYAFILQSKRTVALDIKQTGVI QGLPLLFSGNNLVKAIRSGT/H* RCTNATAGGRSYRKR*IRTG
29672	60040	Α	29855	1591	3150	
29673	60041	Α	29856	2	222	
29674	60042	A	29857	16	359	TTHKTRWQAPVPLRGSPVVAL RIPSDQSEAV/HSLSGVLIALFRT HRFLSGRMFPDHRVWFRMIGSE LVPGYRLSWLSFFNRHYICFTRI RRFRWHRSSLFHGMNVKYRRS KINN
29675	60043	Α	29858	207	470	ATIL*GDFYP/GSRNWLGVSSSA IQMAGCVSLPGAGKRCSP*ICW SNWKQTSRTS\GHVLAGSCCW NGKTLRKSDSRWQQLLRRSLIR R
29676	60044	Α	29859	3932	4195	
29677	60045	A	29860	4424	4594	LISTPRKKVRT*SFAGLLRISSG VPTCTTSPFCIMAIRSPIRMASSR SWEIKTMVR
29678	60046	Α	29861	593	1881	
29679	60047	A	29862	3	198	
29680	60048	Α	29863	1	1590	
29681	60049	C	29864	1	5421	
29682	60050	A	29865	63	185	LCQSHAPRKFPARPFRFFR*RQD CQTSVFLLRPVANRAPA
29683	60051	Α	29866	1	715	
29684	60052	Α	29867	1	1212	
29685	60053	A	29868	886	1185	
29686	60054	A	29869	190	433	AFAKLFIMAAALTSGVAHLSSS GTPFRPFCLPSC*LSSSRAAAIST CSLYAAWFPLTLIRCRGIRKSPII CGISRCRCWRQ
29687	60055	Α	29870	1	439	
29688	60056	Α	29871	14	106	
29689	60057	Α	29872	2518	3024	
29690	60058	Α	29873	448	537	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29691	60059	Α	29874	463	889	FFGLVTSSPSADSPAMLDTRNV
		1			-	SHTGLGPIIPLTFEAGIHTRPTPN
		i			:	SPPRSCLAPAIKA*FFSPAARITT
		ŀ				CCASLYRSPLKTLRSVRFWRSS
						ASVLMRRSSSAAPMPEATLRVL
		İ	<u> </u>			SGLRGSRSDKAFTPHPTI*CLEA
						FPGSRAFVASAP*CLTLRANQR
						KGCW
29692	60060	A	29875	524	1006	SLLAWLSGINIFASSRIAIASPLA
						ASVPLSMDNISLCTPSGVPEKV
						TSTVLTSVPQSCKLMMKDFSGP
						*FP*EKRVSETSPNCTLICLLSCA
						STHVLRRNDPLMLTVPSWANS
						SQPHVNPNKNRIQIIPFNITPSLV
		ļ				NQIKIETRRAFTPLLPLCGLITK
29693	60061	Α	29876	2005	2517	
29694	60062	Α	29877	1	470	MQRRDGDIALIYRSKIGPRTSIT
						FTARRANPVQRIAARILLRDHLI
ŀ						CRMSCTAARHANTFDLIQGSG
						ADNFAAIYGGANDRITRADA/V
[SRGCWKLAPVRDIKRQTVAAF
						YHQDIQPGSCHDQNAL*STGFW
			:			REQSGGQ*P*AG*TNSRTRCCIT GR
29695	60063	Α	29878	734	1306	
29696	60064	Α	29879	743	901	
29697	60065	Α	29880	771	1013	RLGTVGTDSLWCYQYQLCYQ*
	ļ					ALPFSTLPAKLAGNGCQRRRCA
						GTHSLWHADLGSVWPDADSLF
						QRDGRAGGGATRLLRR
29698	60066	Α	29881	1094	1345	
29699	60067	Α	29882	2	751	
29700	60068	Α	29883	239	483	PTPQHLTYHALTGSTIMSQRGV
						DIPCHWHDITCGHAHSLPHRRG
						RKA*SMGNR*YSCTWCYCEGG
						TEKAIWPGDGCPGLSV
29701	60069	В	29884	228	803	
29702	60070	Α	29885	488	636	
29703	60071	Α	29886	1	2117	
29704	60072	Α	29887	665	795	

3823

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
29705	60073	A	29888	1743	2013	LQCTQYAVGENPAVNFAGRPK
		1				GSPCFGPGGGLIN*AAADIPVAS
		1				DNPAHYADAIRYNARTPLQAG
						VYFVRDGPGPLASVRNKERYF
						ANNYIYDMGRNKDGRQSTWY
						MGLGTDIDTGLPMSLSMNVYA
						KYQWQNYGAANENEWDGYRF
						KIKYFVPITDLWGGQLSYIGFTN
		:				FDWGSDLGDDSGNAINGIKTRT
						NNSIASSHILALNYDHWHYSVV
						ARYWHDGGQWNDDAELNFGN
						GNFNVRSTARGWLPGTICRPDK
						MRQHRIRHCAPIAGCGTGCRPD
						KTRQASHQAQMSNAYDYSEIQ
	1	:				PPSEGEILLDAQPLESWSSKAFA
					,	RKVAYLPQQLPPAEGMTVREL
						VAIGRYPWHGALALLGAADRE
						KVEEAISLVGLKPLAHRLVDSL
	}					SGGEPGVDRMLVAQDSRCLLL
						DEPTSALDIAHQVDVLSLVHRL
						SQERGLTVIAVLHDINMAARYC
			:			DYLVALRGGEMIAQGTPAEIM
		ł	:			RGETLEMIYGIPMGILPHPAGA
						APMNTAHAAAIDPNRIVALEW
						LPVELLLALGIVPYGVADTINY
						RLWVSEPPLPDSVIDVGLRTEP
						NLELLTEMKPSFMVWSAGYGP
						SPEMLARIAPGRGFNFSVRNTP
						LARTLQLILREGPRGHPALVQV
						VDLLIEPPQLPLLVPSVQTRIPRI
						QPQSHPAHGVNEAVRNPTVWV
20555	1.00.	<u> </u>	2000		1504	APFIDEIISSIHKYSI
29706	60074	A	29889	1	1584	
29707	60075	A	29890	1	1188	
29708	60076	A	29891	728	970	
29709	60077	A	29892	2447	2665	
29710	60078	Α	29893	255	1360	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29711	60079	A	29894	1	1890	MYSRFDIVVAEPICTLTTFGKET VVSDSQTRTTTTDDPLQVLQQV LDRADIRPTHNEDLPFQGGALG
						LFGYDLGRRFESLPDIAEQDIVL
						PDMAVGIYDWALIVDHQRHTV
						SLLSHNDVNARRAWLESQQFSP
						QEDFTLTSDWQSNMTREQYGE
						KFRQVQEYLHSGDCYQVNLAQ
						RFHATYSGDECQAFLQLNHGN
		l				RAPFSAFLRLEQGAILKLSPERFI
						LCDNSEIQTRPIKGTLPRLPDPQ
						EDSKQAVKLANSAKDRAENLM
						IVDLMRNDIGRVAVAGSVKVP
						ELFVVEPFPAVHHL\TITAQLPE
						QLHASDLLRAAFPGGSITGAPK
						VRAMEIIDELEPQRRNAWCG/SI
						GYLSFCGNMDTSITIRTLTAING
						QIFCSAGGGIVADSQEEAEYQE
						TFDKVNRILKQLENYRRALRDL
						KEEVAIRLSPFELSAFCSPSIASM
						ATRYPNGRHIPPDLRLPKERGIII
						VFTGNGKGKTTAAFGTATRAV
						GHGKKVGVVQFIKGTWPNGER
						NLLEPHGVEFQVMATGFTWDT
,						QNRESDTAACREVWQHAKRM
						LADSSLDMVLLDELTYMVAYD
						YLPLEEVVQALNERPHQQTVIIT
						GRGCHRDILELADTVSELRPVK
						HAFDAGVKAQIGIDY
29712	60080	Α	29895	159	475	VKVNLPWAMLLHSGYADHPYS
						RFDIVVAEPICTLTTD/GRCSHIS
						LYAAGIINSDSKGAVIMPPIIGA
						AIRLITSEPAPVPHRIGSRPAIITA
20712	(0001	n	20006	150	010	TVIAFGRTRRTAP
29713 29714	60081	В	29896 29897	158	810 2070	
29714	60082	A A	29897	1081	1218	
29715	60084	A	29899	289	1014	
29717	60085	A	29900	145	297	
29718	60086	A	29901	452	568	
29719	60087	A	29902	21	185	VHDQPSQEIQQRTEAPGAPRSS
2,717	00007	1	27702	21	103	RRVAQCHPQPGES*SRAQIPPAS TPKPGGGDL
29720	60088	A	29903	1	711	
29721	60089	A	29904	2	825	
29722	60090	A	29905	812	961	
29723	60091	С	29906	1	1587	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29724	60092	A	29907	3	403	LVFDDGDVQMGFWCGCPFCLL VFLLTVRSLSCRSVGVCWRSTR DLVCLGISSGGCRTVNIAEQQM LLPDCSSGIFVSEGYLAV*GVSL PLLGGASQLGLGSMAIFMILILP IHEHGMFFNLFVSSFILLSSCL
29725	60093	В	29908	168	863	
29726	60094	Α	29909	340	612	
29727	60095	Α	29910	1	834	
29728	60096	Α	29911	92	548	
29729	60097	A	29912	1251	1682	VPVALAAARRSELSRTAAADT G*SAAAELVNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGGQSSWAPFEWEGAPR GEEWTLVSVGALK
29730	60098	Α	29913	1	1278	
29731	60099	В	29914	1	2007	
29732	60100	Α	29915	406	615	
29733	60101	Α	29916	52	391	SNRLLKLMHSSRSSCVMFFSSIR SFKDFSLVFDDGDVQMGFWCG CPFCLLSFPF*QSGPSAARSVGV CWRSTPDPVCLGVSSRGCQTV NIAEQQMLLPDRSSGSFVSEGY PAV
29734	60102	A	29917	759	1190	VPVALAAARRSELSRTAAADT G*SAAAELVNPPDYVPDERKRH QSGCPASNSARDPSSYNHAPDD ARCRHRGSGFASIPGGRASRLP APDADQNRLSLAPVLLQSPPER TELHAGRRSALGQLSEWQSGQ SPAGAAIAAFDNR
29735	60103	Α	29918	84	3661	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	, , , , , , , , , , , , , , , , , , ,
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29736	60104	A	29919	1	1230	MDAGWSDVGSWSSLWEISAHT
						AEGNVCHGDVINHKTENSYVY
						AESGLVTTVGVKDLVVVQTKD
						AVLIADRNAVQDVKKVVEQIK
						ADGRHEHRVHREVYRPWGKY
						DSIDAGDRYQVKRITVKPGEGL
		1				SVQMHHHRAEHWVVVAGTAK
		1				VTIDGDIKLLGENESIYIPLGAT
						HCLENPGKIPLDLIEVRSGSYLE
						EDDVVRFADRYGRGNDMKKL
						TCFKAYDIRGKLGEELNEDIAW
		-				RIGRAYGEFLKPKTIVLGGDVR
						LTSETLKLALAKGLQDAGVDV
						LDIGMSGTEEIYFATFHLGVDG
ŀ						GIEVTASHNPMDYNGMKLVRE
1						
						GARPISGDTGLRDVQRLAEAND
		l				FPPVDETKRGRYQQINLRDAYV
						DHLFGYINVKNLTPLKLVINSG
		↓	20020		1000	NGAAGPV/VDAIEARFKALGAP
29737	60105	A	29920	1	1398	
29738	60106	Α	29921	426	1861	
29739	60107	Α	29922	863	1388	EPERTSIKSSGIFPGFSRQCVAPS
ŀ						GI*MDVVFTKQFDITINGDFCRS
						RDNHPVFRAVMVHLYRQALAR
				:		FHGDAFHLVAVARVDRVIFAPR
}						TIHFAMHPMLMATIGFDLLDHF
						FHILYRVTVGNQHRIFGLHHYQ
						IFHPDGGDQARFSIHIAVFSFVIN
		<u> </u>				HIAVANVALGGVGADLP
29740	60108	Α	29923	1	2055	
29741	60109	Α	29924		2047	
29742	60110	A	29925	1	1294	
29743	60111	Α	29926	1	1020	
29744	60112	Α_	29927	1	1422	
29745	60113	A	29928	1	1698	
29746	60114	Α	29929	210	340	YGDVEHESWLSCVRHAH\PRIP
		<u> </u>				FA*PTLISLQKRLGKWSGVTGA
29747	60115	Α	29930	1230	1404	TFSDCQLRQQPGRNHHHFLWK
						GYGHHHYRNLP/VPNGPPLSLL
						P*YCKAKFKPSTSQVP
29748	60116	Α	29931	63	281	
29749	60117	Α	29932	345	467	LPTRCTYTNLTRRRSPPAWYY*
				1		*YWHRDICRSTPARRQTE
29750	60118	Α	29933	29	281	MFGKELGRRDVSQLGAAEITYI
						LKD*T*ES*EILCGGRFLLPLRG
						RTLGQGEWPSLYFHSDCSSHAE
						QCLLYGFADWAPLAFFR
29751	60119	Α	29934	520	714	

SEQ ID NO:	SEQ ID NO: of peptide sequence	1	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29752	60120	A	29935	222	527	LPSKLASGRCSFCDHWY*SQKS SHSGTLKSKKGQTLTAELGHLI SFHLALLSQHLV*WQDRLQQR ELHSDHWYFSRSSRGSLSPDIEG DLIQGQRHRDHIGP
29753	60121	Α	29936	586	837	
29754	60122	A	29937	203	864	NSTKASQA/GRRVLLIDNGKKP GRKILRDPVESSDALFGVPAPA QVASGNRYGYSYLNDALNGGD AESAGLTPPELWPRHHGHGPA GVKLVEQLCQRLRVPNEIRDLA RLVAEFHDLIHTFPMLNPKTIV KLFDSIDAWRKPQRVEQLALTS EADVRGRTGFESADYPQGRWL REAWEVAQSVPTKAVVEAGFK GVEIREELTRRIAAVASWKEQ RCPKPE
29755	60123	A	29938	322	919	VRAVFSLREQIRSHEIRRSAAVS NHQHFRRACGHIDRRTVQTLA HLTFRFGDKGVTRPEDFVHFW HRFRTKGDPLLTFWPSAPVTAT ILRIPLANGFFRHDHKSSCMTR VPQVPEDPVKSHAPQQFWIHH GKWFAWYDVAIGIPGPFAGRS\ CVILLGDAVREVTRVSNAVPAK RYIGGSPRRGFINSCNMPGIISPG
29756	60124	A	29939	1	114	
29757	60125	В	29940	1	4191	
29758	60126	A	29941	512	661	
29759	60127	A	29942	1	1254	
29760	60128	A	29943	247	855	RKKPLP*QRDISSSSLLSLRAFW ASAPVTATNPPDTLGNGFFRHD HKSSCMTRVPQVRSPTELNRSQ GASRPRGVIQQLGHRDPNGDDS HRVRIGLIKHMP
29761	60129	Α	29944	1	2313	
29762	60130	A	29945	2	2687	
29763	60131	A	29946	1	936	
29764	60132	Α	29947	1	966	
29765	60133	Α	29948	1	675	
29766	60134	Α	29949	1	792	
29767	60135	Α	29950	2	929	
29768	60136	A	29951	1	969	
29769	60137	A	29952	1	420	
29770	60138	A	29953	1	549	
29771	60139	A	29954	1	450	
29772	60140	Α	29955	1	606	

sequence 09/540,217 codon for peptide of peptide sequence d	r=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
sequence	leletion, \=possible nucleotide insertion)
29773 60141 A 29956 L	·
167773 100171 173 1627730 1 1740 176773	MARGNAITLPVCGRDVKFTLE
1 1 1 1 1	VLRGDSVEKTSRVWSGNERDQ
1 1 1 1 1	ELLTEDALDDLIPSFLLTGQQTP
1 1 1 1 1	AFGRRVSGVIECDNLKTCHTSH
1 1 1 1 1 1	GSVMAETAVINHKKRKNSPRIV
	QSNDLTEAAYSLSRDQKRMLY
	LFVDQIRKSDGTLQEHDGICEIH
1 1 1 1 1	VAKYAEIFGLTSAEASKDIRQA
	LKSFAGKEVVFYRPEEDAGDE
	KGYESFP\WFIKRAHSPSRGLYS
	VHINPYLIPFFIGLQNRFTQFRL
29774 60142 A 29957 I 771	
29775 60143 A 29958 1 1491	
29776 60144 A 29959 145 1929 \	VSGVIEIADGSRRRKAAALTES
	DYRVLVGELDDEQMAALSRLG
	NDYRPTSAYERGQRYASRLQN
	EFAGNISALADAECDNLKTCHT
	SHGSVMAETAVINHKKRKNSP
	RIVQSNDLTEAAYSLSRDQKRM
	LYLFVDQIRKSDGTLQEHDGIC
	EIHVAKYAEIFGLTSAEASKDIR
	QALKSFAGKEVVFYRPEEDAG
	DEKGYESFPWFIK/RPSRGLYSV
	HINPYLIPFFIG\LQNRFTQFRLS
	ETKEITNPYAMRLYESLCQYRK
	PDGSGIVSLKIDWIIERYQLPQS
	YQRMPDFRRRFLQGFCRFRNH
	HQTGFSPAGANQRGPLAATLSG
	PGGEGQSAVARLTGEKKNHPG
	AQYANRLSPRVGRFINAAGTTG
	FPTWKAGSERNAINDDVTYAIK
	PTCWPGLDIIPSCLALHRIETEL
	MGKFDEGKLPTDPHLMLRLAIE
	TVAHDYDVIVIDSAPNLGIGTIN
	VVCAADVLIVPTPAELFDYTSA
	LQFFDMLRDLLKNVDLKGNSN
	GSQSPWMEEQIRDAWGSMVLK
1 1 1 1 1	NVVRETDEVGKGQIRMRTVFE
1 1 1 1	QAIDQRSSTGAWRNALSIWEPE
1 1 1 1 1	CNEISIGVSLDQDGGSNSVLRK
29777 60145 A 29960 1 1731	
29778 60146 B 29961 1 3345	
29779 60147 A 29962 1 1959	

NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29780	60148	Α	29963		1302	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPV NVSKSDDTLKINGVEDHKTIFD GDGKTYQNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSAKK RDAELANGALGIIELNNDYTLK KVMKPLITSNTCDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHDGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPE/EDAGDE KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL
29781	60149	A	29964	1	1557	SETK/EITHPYAMPLYESLCQYS
	60149	A	29965	1	2259	
29782	60151	A	29966	1	1959	
	60151	A	29967	1	2277	
29785	60153	A	29968	1	2418	
29786	60154	A	29969	1	2028	
29787	60155	A	29970	1	1650	
29788	60156	A	29971	1	1170	
29789	60157	A	29971	1	1446	
29789	60158	A	29973	1	1191	
29790	60159	A	29973	22	1893	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ļ		sequence		
29792	60160	A	29975	1	1375	MNMNIKKIVKQATVLTFTTALL
27172	00100	l'`	2,7,73	[AGGATQAFAKENNQKAYKETY
						GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
		1				DSWPLQNADGTVAEYNGYHV
		1				VFALAGSPKDADDTSIYMFYQ
		ļ				KIRRKNGPVSATFTSDGKIRLFY
						TDYSGKHYGKQSLTTAQCDNL
						KTCHTSHGSVMAETAVINHKK
1		ĺ				RKNSPRIVQSNDLTEAAYSLSR
						DQKRMLYLFVDQIRKSDGTLQ
		ŀ				EHDGICEIHVAKYAEIFGLTSAE
		ŀ				ASKDIRQALKSFAGKEVVFYRP
						EEDAGDEKGYESFPWFIKRAHS
l		ŀ				PSRGLYSVHINPYLIPFFIGLQNR
						FTQFRLSETKEITNPYAMRLYES
						LCQYRKPDGSGIVSL/KIDW/IIE/
						RYQLPKVPSPEARKITRRWRI\V
	ļ					KQRI*LGFLLRLSEMPRKQGDY
]						RTRIWKFEDGLSNVLVIQLNKLI
			:			ICVMCLVRDCDVLKTYFHR
29793	60161	A	29976	1458	2675	CDNLKTCHTSHGSVMAETAVI
					·	NHKKRKNSPRIVQSNDLTEAAY
						SLSRDQKRMLYLFVDQIRKSDG
						TLQEHDGICEIHVAKYAEIFGLT
						SAEASKDIRQALKSFAGKEVVF
		į				YRPEEDAGDEKGYESFPWFIKR
						AHSPSRGLYSVHINPYLIPFFIGL
						QNRFTQFRLSETKEITNPYAM/R
		İ				IPLH*LFR*TLRQTKPDNSAGKC
					•	VKI**HTQNQRSGRSQNDF*RR
						GI
29794	60162	В	29977	1	1317	
29795	60163	В	29978	78	215	
29796	60164	С	29979	225	422	
29797	60165	Α	29980	1	368	MAETAVINHKKRKNSPRIVQSN
						DLTEAAYSLSRDQKRMLYLFV
						DQIRKSDGTLQEHDGICEIHVA
						KYAEIFGLTSAEASKDIRQALKS
						FAGKEVVFYRPEEDAGD/EKGY
20555	10165	ļ	20001		100	ESFPWFIKRIYSR
29798	60166	Α	29981	1	409	MAETAVINHKKRKNSPRIVQSN
						DLTEAAYSLSRDQKRMLYLFV
						DQIRKSDGTLQEHDGICEIHVA
						KYAEIFGLTSAEASKDIRQALKS
						FAGKEVVFYRPEKDAGDEKGY
						ESFP\WFIKHSTNITSLSLWFFSS
20700	60167	 	20002	1	014	СТН
29799	60167	A	29982	1	814	<u> </u>

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
29800	60168	Α	29983	3	678	GSVMAETAVIN\HKKRKNSPRI
		` `				VQSNDLTEAAYSLSRDQKRML
]		YLFVDQIRKSDGTLQEHDGICEI
						HVAKYAEIFGLTSAEASKDIRQ
						ALKSFAGKEVVFYRPEEDAGD
						EKGYESFPWFIKRAHSPSRGLY
1						SVHINPYLIPFFIGLQNRFTQFRL
						SETKEITNPYAMRLYESLCQYR
						YSFPPDYFHGLALNVCGFSRYT
		ŀ				VQDVGGSIILGSGGQWLSSHSS
						SRQCP
29801	60169	Α	29984	2	660	BRQCI
29802	60170	A	29985	179	283	MGQGRNPQTRRTYGCQFRMV
27002	00170	` `	27703	1,77	203	K*HGIEMKCEELIL
29803	60171	Α	29986	i	643	THE TENNING SECTION OF THE TENING SECTION OF THE TENING SECTION OF THE TENNING SECTION OF THE TENNING SECTION OF T
29804	60172	A	29987	2	1073	
29805	60173	A	29988	1	1167	MNMNIKKIVKQATVLTFTTALL
						AGGATQAFAKENNQKAYKETY
						GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
		ŀ				DSWPLQNADGTVAEYNGYNV
						VFALAGSPEDADDTSIYMFYQK
						CDNLKTCHTSHGSVMAETAVI
						NHKKRKNSPRIVQSNDLTEAAY
						SLSRDQKRMLYLFVDQIRKSDG
						TLQEHDGICEIHVAKYAEIFGLT
	1					SAEASKDIRQALKSFAGKEVVF
						YRPEEDAGDEKGYESFPWFIKR
						AHSPSRGFYSVHINPYLIPFFIGL
		ŀ	ļ			QNRFTQFRLSETKEITNPYAMR
				,		LYESLCQYRK\PDGSGIVSLK/ID
						WIIKRSQLPQSAFYQPFMGLRR
						ESFYFRWERRTLGPLKSFSVKR
						GTEAGKFRLAALLVRL
29806	60174	A	29989	1	1692	
29807	60175	A	29990	1	1788	
29808	60176	A	29991	1	960	
29809	60177	A	29992	1	1385	
27007	1001//	1 .		<u> ^ </u>	1200	L

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29810	60178	A	29993		936	MWLVTTELESTDTEHFYHHSK CYWPRAHLGECILSIEAACQAA GGEAGNGGSAVTKATLGSRQG AQHWKALARTIRQEKEIKGIQI GKQEVKLLPFADDMIIYLENST DSSKKLSELCDNLKTCHTSHGS VMAETAVINHKKRKNSPRIVQS NDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHV AKYAEIFGLTSAEASKDIRQAL KSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAH\SPFQRALYS CTICNP*ILIPFSF\IGLQNRFTQF R\LSETKEITNP\YAL\RLYQSLC
29811	60179	Α	29994	1	1641	
29812	60180	Α	29995	1	1551	
29813	60181	В	29996	90	1515	
29814	60182	Α	29997	452	1523	
29815	60183	В	29998	9	2021	
29816	60184	Α	29999	1	960	
29817	60185	Α	30000	1	864	
29818	60186	A	30001	2	917	FLFSPLEMQIQRFTSPSPDIPYRA SSSNCAPRGISPQELTVDLQTKC DNLKTCHTSHGSVMAETAVIN HKKRKNSPRIVQSNDLTEAAYS LSRDQKRMLYLFVDQIRKSDGT LQEHDGICEIHVAKYAEIFGLTS AEASKDIRQALKSFAGKEVVFY RPEEDAGDEKGYESF\PWFIKR AHSP\SRGL\YSVHINPYLNSLFY GVQNRFTQFRLNFVQKSRLVD LALKGLRVLLVEGNDPQGTAS MYHGWVPDLHIHAEDTLLPFY LGEKDDVTYAIKPTCWPGLDIIP SCLALHRIETELMGKFDE

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29819	60187	A	30002		1756	MPASGNENDLNMPSGTIEIFVR CYVEVERIMDFADFGTTIKQDF RLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLES GHQAPCMKSNNALIVILGTVTL DAVGIGLVMPVLPGLLRDIVHS DSIASHYGVLLALYALMQFLCA PVLGALSDRFGRRPVLLASLLG ATIDYAIMATTPVLWIYPLCDN LKTCHTSHGSVMAETAVINHK KRKNSPRIVQSNDLTEAAYSLS RDQKRMLYLFVDQIRKSDGTL QEHDGICEIHVAKYAEIFGLTSA EASKDIRQALKSFAGKEVVFYR PEEDAGDEKGYESFPWFIKRAH SPSRGLYSVHINPYLIPFFIGLQN RFTQFRLSETKEITNPYAM/RIPL H*LFR*TLRQTKPDNSAGKCVK I**HTQNQRSGRSQNDF*RRPVL LASLLGATIDYAIMATTPVLWI YPLCDNLKTCHTSHGSVMAET AVINHKKRKNSPRIVQSNDLTE AAYSLSRDQKRMLYLFVDQIR KSDGTLQEHDGICEIHVAKYAE IFGLTSAEASKDIRQALKSFAGK EVVFYRPEEDAGDEKGYESFP WFIKRAHSPSRGLYSVHINPYLI PFFIGLQNRFTQFRLSETKEITNP YAMQSPYTDYSGKHYGKQSLT
						TAQVNVSKSDDTLKINGVEDH KTIFDGDGKTYQNVQQFIDEGN
29820	60188	A	30003	1	1653	
29821	60189	A	30004		1128	PWISAPVPVDVVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE IASTHIALAARHSDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDRNRERHTVS SSGGNRLPNPGPDRSCDNLKTC HTSHGSVMAETAVINHKKRKN SPRIVQSNDLTEAAYSLSRDQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGKEVVFYRPEED AGDEKGYESFPWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLYK\SL CQYRAFVNGGGEEKARGKPIL CRYGVGM

SEQ ID SEQ	ID NO: N	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
	• 1	od	in USSN	location of first	I .	*=Stop codon, /=possible nucleotide
sequ	ience		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29822 601	90 /	4	30005	2974	3878	PSKASELGRKQRRPVLSDSSYA
						QRKKKYPPWEKLQGSVRGETP
						VINHKERK\NSPRIVQSNDFPEA
						AYSLSRDQKRMLYLFVAQIRKS
						DGTLQEHDGICEIHVAKYAEIF
						GLTSAEASKDIRQALKSFAGKE
						VVFYRPEEDAGDEKGYESFPW
						FIKRAHSPSRGLYSVHINPYLIPF
						FIGLQNRFTQFRLSETKEITNPY
						AMRLYESLCQYRKPDGSGIVSL
1						KIDWIIERYQLPQSYQRMPDFR
	İ					RRFLQVCVNEINSRTPMRLSYIE
						KKKGRQTTHIVFSFRDITSMGFF
						LESPTQGLASPE
29823 601		$\overline{}$	30006	233	1538	
29824 601 29825 601			30007	1	2331	MADI DECCCODIDANAM I LIIZAA
29825 601	93	4	30008	1	1857	MPLRFSSSSRIPYYVNLLHKAA
						TGFERIDYNFETHSSLEIATDAL
					!	TISDHHPCESAAINAETRPSTVL
	}					EELARAIRQEKEIKGIQIGKEEV KLSLFADDMIMYLENPKDSSRK
1						LLEWIKESNKVSGYKTHVHKS
						VALLYTNSDQVENQIRTQPFYN
						SCENKIKYLAIYLTKESKDLYK
						RNYKTLLKEITDDTNKWKHIPC
						SWIVKVAGVESWIHHTQVEVW
						TPPEETAGSTAHGSQDQPDQPR
	1					YTCEPLEDLHLLFQKETSHTIKA
						STTDPEEKPLPPYKRYCDNLKT
						CHTSHGSVMAETAVINHKKRK
						NSPRIVQSNDLTEAAYSLSRDL
						KRMLYLFVDHIRKSDGTLQ\EH
						DGICEIHVAKYAEIFGLTSAEAS
						KDIRQALKSFAGKEVVFYRPEE
						DAGDEKGYESFPWFIKRAHSPS
						RGLYSVHINPYLI\PFFIGLQ\NRF
						TQFRLSETKIPVIIQEAGLSQSEK
						QAADGIQGVAHPAFQVCDGCG
						SSLQHFFLLMLVDFQLPPLLNL
						RVLIMATLFTIACYVELRGYML
						HAFQLVSLAMSHLHLAHNQDT
						HPAISDVLWVCALSHSLEFHRA
						SDVRADLSNAYSEEVRKFGFLL
						WGLDCASLHRSDFITSSETKYH
29826 601	94 /	4	30009	1	944	
29827 601			30010	1912	1915	
29828 601	~ -	4	30011	1503	1961	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29829	60197	A	30012	1	6552	MAETAVINHKKRKNSPRIVQSN
29629	00197		30012	1	0332	DLTEAAYSLSRDQKRMLYLFV
						DQIRKSDGTLQEHDGICEIHVA
						KYAEIFGLTSAEASKDIRQALKS
						FAGKEVVFYRPEEDAGDEKGY
						ESFPWFIKRAHSPSRGLYSVHIN
						PYLIPFFIGLQNRFTQFRLSETKE
						ITNPYAMRLYESLCQYRKPDGS
						GIVSLKIDWIIERYQLPQIRLGDP
						GSSRLSMEHGLRSIPAWTLDKFI
						EDYLLPDTTFGADVKSAVNVV
					,	CDFLKERCF
29830	60198	Α	30013	1	2679	MAETAVINHKKRKNSPRIVQSN
						DLTEAAYSLSRDQKRMLYLFV
						DQIRKSDGTLQEHDGICEIHVA
						KYAEIFG\LTSAEASKDIRQALK
		l				SFAGKEVVFYRPEEDAGDEKG
						YESFPWFIKRAHSPSRGLYSVHI
						NPYLIPFFIGLQNRFTQFRLSET
						KEITNPYAMRLYESLCQYRKPD
						GSGIVSLKIDWIIERYQLPKVPS
						PEARKITRRWRI\VKQRI*LGFLL
						RLSEMPRKQGDYRTRIWKFED
						GLSNVLVIQLNKLIICVMCLVR
			:			DCDVLKTYFHR
29831	60199	Α	30014	2641	5798	CDNLKTCHTSHGSVMAETAVI
			:			NHKKRKNSPRIVQSNDLTEAAY
						SLSRDQKRMLYLFVDQIRKSDG
						TLQEHDGICEIHVAKYAEIFGLT
						SAEASKDIRQALKSFAGKEVVF
						YRPEEDAGDEKGYESFPWFIKR
						AHSPSRGL\YSGHINPY\LIPFFIG
						LQNRFTHF\RFMEQKKSPSNRFT
						QVRLSETKEITNPYAMRLYESL
						CQYRKPDGSSIVSLKIDWIIERY
						QLPQSYQRMPDFRRRFLQVCV
						NEINSRTPMRLSYIEKKKGRQT
						THIVFSFRDITSMTTG
			l	L		THIVESTRUITSWITTU

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
:		İ		sequence		
29832	60200	A	30015	1734	6267	QQHRNPQKGKQWSYKSTFKFK
		-				SESDIHLAEHHKQVLYDGKLAS
						SIAFTYNAKATDAQLCLESSPK
						ENASIFVHSPHALMLQILTEQV
						CTQVVHKPHPEPDSTVKIQNPS
						EQMAVLYCIVLVGGEFDLEMN
		1				FIIQDAESITCMTELLEHCDVTC
						QAEIWSMFTAILRKSVRNLQTS
						TEVGLIEQCDNLKTCHTSHGSV
		1				MAETAVINHKKRKNSPRIVQSN
		İ				DLTEAAYSLSRDQKRMLYLFV
						DQIRKSDGTLQEHDGICEIHVA
,						KYAEIFGLTSAEASKDIRQALKS
						FAGKEVVFYRPEEDAGDEKGY
•						ESFPWFIKRAHSPSRGLYSVHIN
		i				PYLIPFFIGLQNRFTQFRLSETKE
						ITNPYAMRLYESLCQYRKPDGL
						SIVSL\KIDWIIERYQLPQSYQR
						MP\DFRRRFLQDVQNETHGNT
29833	60201	Α	30016	1514	6335	
29834	60202	Α	30017	2033	4226	
29835	60203	В	30018	1	5670	
29836	60204	Α	30019	1968	3130	
29837	60205	Α	30020	34	431	
29838	60206	Α	30021	320	528	
29839	60207	A	30022	1373	1868	
29840	60208	Α	30023	3	1771	
29841	60209	В	30024	1	2299	
29842	60210	Α	30025	2	488	
29843	60211	Α	30026	1	127	
29844	60212	Α	30027	1	812	
29845	60213	A	30028	1	1830	
29846	60214	A	30029	1	836	P. WOOD OF THE COURT OF THE COU
29847	60215	Α	30030	297	936	RTSSSLMRSSSSLLRICSGVSPRS
						IPRWFTSVSLPSSFIR\RITTFRYT
		İ				PGHVAPASRRSCYKYRR*PMRL
						YTMIQSLS/VGSRPSGLRAFSSD
						CSPLPRTCSLSRRRVLMITTSRS *SLTYGVDPSVRPVLAAASEYF
					:	
						SRR\YAGFQNPHNLLVSG*YQG
						NYRHFGILRGYPG/TLKNSNFQL TRSARISLSSRSSICTSTGGNTTL
						PPSSPPDC
29848	60216	1	30031	1818	1991	SPSHIRRTAPNGLRHYQR*IQQ*
27048	00210	A	1 5005	1010	1771	APSDQKRDFLVPHGADSAMAK
						HGGSHRAVLPQGW
29849	60217	A	30032	2	501	HOUSHIKA VLFQUW
29850	60217	A	30032	1419	1640	IFCASLSLGLYAGIEARILTKGY
2,000	100210	1				TRK*IQQ*APSDQKRDFLVPHG
						ADSAMAKHGGSHRAVLPQGC
						DPHMESLI
	<u> </u>					

SEQ ID			SEQ ID NO:	L		Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	<u> </u>					
29851	60219	Α	30034	1	1593	
29852	60220	Α	30035	107	195	
29853	60221	Α	30036	1480	1605	TILRITFQFCRSNRRRQRQ*NRF
		<u> </u>				STSQRRCYFLLNGEDVTLP
29854	60222	Α	30037	1	373	MPSYFTSRIAAVHVSALREEQA
	ŀ				HHESKHHESFIAQRMFRMFYQ	
		ļ				ARNLLHAGQENLFSGLTALTAE
						FTVGEEATRGKTTGKRGPSPDG
		ŀ				RILRTTKTRNPRGYMQGRYLES
						QRDVEATDKPFEFFMNRFRLLE
		l	}			AAPRVEFIAYTGLCEDVIRPQL
						DEAIAQGYLTECADYWQITEH
		ŀ				GKLFLNSLLELFLADGYHMWR
						MIGAGAHLAVGIDPTQLFLCQF
						EAVRKLLGNDQRAHLLPLGIEQ
						LPALKAFDTVFSMGVLYHRRSP
						LEHLWQLKDQLVNEGELVLET
						LVIDGDENTVLVPGDRYAQMR
		1				NVYFIPSALALKNWLKKCGFV
						DIRIADVSVTTTEEQRRTEWMV
						TESLADFLDPHDPGKTVEGYPA
						PKRAVSDCAQAVKMTNMISYQ
		1				GLVRTFLSTSPNNWLVFMQNG
						QEVVIDSGKSVS*RSVCFGCFIK
						HGICSMRDKKISFLV*RRLLLNS
						LSAKKLHGAKQRAKGDLPRMG
		1				AFCVPPKRVIRVVICKEGIWKA
20055	(0000	<u> </u>	20020		0.15	SVMSKPQISRLSSL
29855	60223	A	30038	561	845	AKIVQLRPRILRPSRSARRCPSA
		1				PRSRRQRRRSGPLPEPAPRVS*Q
		1				IFPSQYWRYRQSTENQKQRLDP
		1				RGQIVNVPARRIIRQKRKCCKV
2225		 -				AGSA
29856	60224	Α	30039	1	1090	
29857	60225	A	30040	1	1384	
29858	60226	A	30041	2268	1377	DCDDCVDDI I DDCDDCV I CI AC
29859	60227	A	30042	2268	2684	RCRRCKRRLLRRFRRSLLSLAG
						SPENHARFYCRNSLPDEWFFRH
						HPRST*PPRSREIRRCHCG*RQC
]						SSDGRKITSVHRGRNADGRELT
						HQAVRLLAYLSDRFARHHRHL RNAHRRGPDRIPKERHFPATKL
20060	(0220	<u> </u>	20042	1120	1210	RHTPAV
29860	60228	A	30043	1130	1310	RLDKQNRRQGKRQRNNGVFHQ
						QPQRR*RTDVIQMPHSHHRHA
20061	(0220	 	20044	205	690	QRRDHQQLGQHHAGRNFE
29861	60229	A	30044	395	689	VAASVSSSMSCAPVLMTVVTR
		1				CTLLILSQFMRRKAIKK/LSGSL
						LPASEVKVLKRDGDYSE/VQQ*
		1				APSDQKRDFLVPHGADSAMAK
		<u> </u>	L			HGGSHRAVLPQGW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29862	60230	Α	30045	1	2142	
29863	60231	Α	30046	1	2463	
29864	60232	Α	30047	1	1066	
29865	60233	В	30048	790	820	
29866	60234	Α	30049	3	126	
29867	60235	Α	30050	1853	2257	
29868	60236	Α	30051	90	411	
29869	60237	Α	30052	1375	3174	
29870	60238	Α	30053	5	206	
29871	60239	Α	30054	1	1986	
29872	60240	Α	30055	339	596	PPYKRRKRRESVSDGMRNTG KTRRTR*IINLLGRS*NRNFVSV PSGQNYP*ISLDHGRENYGGYS TIQNRLLRLPLSRSGCILQ
29873	60241	A	30056	634	924	
29874	60242	Α	30057	42	665	KYGVNPGPYGGTT\RKLYEKK LLKLREQGTESRSSTPLPTISSSA ENTRQNGSSDSDRYSDNEEDSK IELKLEKREPLKGRAKTPVTLK QRRVEHNQSYSQAGITETEWTS GSSKGGPLQALTRESTRGSRRT PRKRVETSEHFRIDGPVISESTPI AETIMASSNESLVVNRVTGNFK HASPILPITEFSDIPRRAPKKPLT RAEVG
29875	60243	Α	30058	1822	4791	
29876	60244	Α	30059	310	1275	
29877	60245	A	30060	52	390	
29878	60246	Α	30061	250	1530	
29879	60247	Α	30062	1	1641	
29880	60248	Α	30063	1009	1140	
29881	60249	Α	30064	913	1218	
29882	60250	Α	30065	900	999	
29883	60251	Α	30066	2282	2741	
29884	60252	A	30067	1	2199	
29885	60253	Α	30068	1	2229	
29886	60254	Α	30069	441	608	
29887	60255	A	30070	122	517	CTIVIRSRCFWWKTAWAQKMN LLPMARLTTTIALATYANISAQ WAKRLQTAFR*WATPHGAVLI *FPALRVK*ANATALSLLTVTT QATGRLRARQRKTATPRTIRPG ESTSSSPRSSGSLSAPACSVPWM

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:		Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, -possible nucleotide insertion)
				sequence		
29888	60256	Α	30071	498	1155	KQPSAVSGTGAAGEANLHAVR
						TAEQTAVVYRHRQRVR\YLLR
						YGILDWSPTYLKEVKHFALDKS
		1				SWAYFLYEYAGIPGTLLCGWM
						SDKVFRGNRGATGVFFMTLVTI
						ATIVYWMNPAGNPTVDMICMI
						VIGFLIYGPVMLIGLHALELAPK
į						KAAGTAAGFTGLFGYLGGSVA
	:					ASAIVGYTVDFFGWDVGFMLS
						HELWESEFTKLKYEYNNSCPAS
						VSGWL
29889	60257	l _A	30072	670	1100	NCRKTSPKRRFSFDDPKSDRAK
						DFLAKILH*SLWRAYPIARHLTL
		1				YRFAPRICYILALPLSQRSTQQG
		1				ATMALPILLDCDPGHDDAIAIV
						LALASPELDVKAITSSAGNQTP
						EKTLRNVLRMLTLLNRTDIPVA
						GGRGKTVNA
29890	60258	В	30073	861	935	
29891	60259	Α	30074	1	2510	
29892	60260	Α	30075	3	119	NALRKSASSCSGRNRYPGS*PS
				:		RPDCQRSCSHKHAGYG
29893	60261	Α	30076	3	227	GGEGRASCSADTGWLPSDPPGC
						AAGALGGGGWAVAGAAAGGP
						CA*SAGGIGVHAPKAQHPATFS
						GPAEGVIPPQ
29894	60262	Α	30077	1	2277	
29895	60263	A	30078	1	2187	
29896	60264	Α	30079	1	3666	
29897	60265	Α	30080	1	699	
29898	60266	Α	30081	513	1019	TGGVCCWCARYVDALVVFAD
						QLFVAEVLASAHSPSRLYAHAH
						GDTPQRLRLNGRQALSP*FCCN
						HRAALQRHQPVRPLPARQSRQ
						MRRCNLLYQKASAQRSQRDSS
						*RSLFFRSVDADGG*R*SHGYA
						FRHGRFQCHRPHGLPGTGPPRH
						ADSAFSRRLIYPACRWRL
29899	60267	A	30082	389	462	
29900	60268	Α	30083	1	278	MGVNDAVLEMHGLGNDFMVV
		1				DAGFDQLLVVEPPYDLELDFHY
						RMFNADGS/DSGAVRQRCALLC
		ŀ				PFCASERTDQ*A*YPRQHRQRA
		ļ				DGSDRHR
29901	60269	A	30084	1240	4914	
29902	60270	A	30085	1	1308	LATINGS A DTA CLASOCKYODED
29903	60271	Α	30086	30	164	VTWW*RAPTAGLMQC*YCRNR
						RARLRLTYGHAPAHRRNGPDV
	1	<u>L_</u>	<u> </u>		I	PS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
29904	60272	Α	30087	3	264	TLRPANRF*HIPDAAGVIPVGY
						AL*RGTSVSAVHRW/CSTVFGV
						NWATLATKLMVAGIRRSGAAS
		1				RISRASPPSFSVPACSVGRKKVI
29905	60273	Α	30088	1	3639	The state of the s
29906	60274	A	30089	1	957	MGFRRTMPHIVISALVGGLLLV
	į					FADCLAWTCRHDKLDDISDVA
						KITGLTSKAIRFYEEKGLVTPPM
						RSENGYRTYTQQHLNELTLLRQ
						ARQVGFNLEESGELVNLFNDPQ
						RHSADVKRRTLEKVAEIERHIE
				İ		ELQSMRDQLLALANACPGDDS
						ADCPIIENLSGCCHHRAGKYVG
						LIRRVKRRIRHRCWPIKTLSQRA
		1				-
		1				VSEFQRLIQPNHQYQSYTRQCA
	1					PETDNHADNSYNAGLFIVNSLY
						TAEGVMDKHSLWQRYVPLMR
ŀ						HEALRLQVRLPASVELDDLLQA
		ĺ				GGIGLLNAVERYDALQGTAFTT
						YAVQRIR\GAMLD
29907	60275	Α	30090	1	699	
29908	60276	Α	30091	430	660	HQTHFIVEHRRIMQRTARQNIG
						RHYQIQLSAVQRIRGAMLDELR
						SRDWVPRS\RRNAREVAQAIGQ
						MSLPMLQVALS
29909	60277	В	30092	1	1575	
29910	60278	Α	30092	1	289	MISANRPIINLDLDLLRTFVAVA
						DLNTFAAAAAAVCRTQSAVSQ
						QMQRLEQ\PLGKNCSLVTVATN
į						C*LNMAFNFLVTPGKSCVLMM
						RSCIQPNSD
29911	60279	Α	30094	1	1095	
29912	60280	Α	30095	1037	1297	LILRCPWSYSRCIRILIAPSSS*Q
						TEAKPFASRASRTSDDCQWANI
						SSVMPVKPNSTTPSILRRFSTPK
						CSATNCGEN*LSIMIGS
29913	60281	A	30096	905	2042	
29914	60282	Α	30097	87	760	
29915	60283	Α	30098	1	2793	
29916	60284	Α	30099	308	485	KSLNAICYRNTRTSMACY*PA*
						VRWPKHSAGLMTISPVLHVISP
						RHWRLECATRVGRLG
29917	60285	Α	30100	1	2784	
29918	60286	A	30101	453	1975	
29919	60287	A	30102	3	470	
29920	60288	Α	30103	1447	1773	QFAFTEHHQTQEHHHQRSYDC
						PQRDPRHIDAQVSDQRPCPDSG
						LREPLHCAQPDSGG*ADNSADH
1		1				IRRNGGDGAFQRKRNRTLTDPH
		<u> </u>				KRQEHGGLTLRIKLSVEQAFAG
29921	60289	Α	30104	1	449	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29922	60290	A	30105	188	1508	
29923	60291	A	30106	171	410	
29924	60292	A	30107	3080	3232	
29925	60293	A	30108	1	1272	
29926	60294	A	30109	438	617	
29927	60295	A	30110	259	392	
29928	60296	A	30111	905	1545	RLTTPSLSVCWRPAAKRPILPRS LKQLKKIASRKVTP*/SLGNAW NNLEKQRAYLSMMAQKRVDG LLVMCSEYPEPLLAMLEEYRHI PMVVMDWGEAKADFTDAVID NAFEGGYMAGRYLIERGHREIG
						VIPGPLERNTGAGPPCRFYEGD GRSDDQVDGDIQFFFSTNTITGR GHFRTMVDGICPCKDGNLRFN RILEHREPFYPQIPATFAYA
29929	60297	A	30112	3	466	AIVKFKRNVHQDGGYCSVQIQ QCRFALIFKDFCRMRHNGLIRR TISQQSVGRIRCVSIASGRVYYC FFALEGKKPSSSISAAPTQMAVS ARLKVAKCQSPT*KSIISTTKPC HRRSNRLPSAPPIISATRVHRQM RYSTSSGAAALLSITVTPS
29930	60298	Α	30113	1	1562	
29931	60299	A	30114	706	857	PMRELISKGVSPFAISNSGLLTS LLTSVV*IDAIDGIRFSFLSWAS GKGP
29932	60300	A	30115	966	1142	SLEETEKYRNVNEMCFPVKRR RREREKTSERTPAPV*VKITTRK LYPAEERTGRIFEA
29933	60301	A	30116	1	3095	MDKFLNTYTLPRLNREEVESLN RPVTASGLEVIINSLPIKKSPGPD GFTAAFYQRYKEDAGEREGEG GNQQVAVRGKRKTTERKKKLG EDVKVKESKNSGAYEVKQHRF FRSLDWNSLLRQKAEFIPQLESE DDTSYFDTRSEKYHHMETEEE DDTNDEDFNVEIRQFSSCSHRFS KAAEVSTRLLSTRVTEIEGWLI VQRNQKLLQSNLKQRSGEPLIL DDDSHVPPELRAGYRLLKNAG CLPPELEQRREAIQ
29934	60302	Α	30117	1	2583	
29935	60303	Α	30118	1	3141	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	1	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29936	60304	A	30119		1037	MRVVILGSGVVGVASAWYLNQ AGHEVTVIDREPGAALETSAAN AGQISPGYAAPWAAPGVPLKAI KWMFQRHAPLAVRLDGTQFQL KWMWQMLRNCDTSHYMENK GRCFELPVAVYAGGQAVLVKQ CKAIGGPDRAPDTLNTMPIFKA CTPDNRRAVWRHRAQTSPESR LLDMTAAWIEIANHHLQRFTTR LQQLGIKTNNLRHSGKTNAVIV YMIQSISLVDEMSCHLVLTTGG TGPARRDVTPDATLAVADREM PGFGEQMRQISLHFVPTAILSRQ VGVIRKQALILNLPGQPKSIKET LEGVKDA/EGVPYCIQLLEGPY
2007	60205		20100	0.6	711	VETAPEVVAAFRPKSARRDVSE
29937	60305	A	30120	96	711	
29938	60306	C	30121	128	628	
29939	60307	A	30122	1024	1128	LOGRANIA DO DA LA VIDADA VIDA VI
29940	60308	A	30123	193	372	IQTESNPQDIL*NPSPPVFISKHS PNNSYCYAQSREKNKSHFHVF ATTCNRALSIWYLMN
29941	60309	С	30124	202	321	
29942	60310	С	30125	150	491	
29943	60311	A	30126	1163	1257	
29944	60312	Α	30127	929	1023	
29945	60313	A	30128	3	765	TARAWLLLGPVWPCVSERWSK KPSPRGGRDPSDRDPAAFAARS TVPPRISAYERPVPWPGEWNDP RGPGRRASAVVSPREGNWGVL RDPRLQARKPRMVRSRQMCNT NMSVPTDGAVTTSQIPASEQET LVRQESEDYSQP*LLVALFIAA KKM*KSLKGKKPKTKKRVWN LVCPLMPLNLV*FVKVDLKMV ALSMAKQDILWPALH/DAKKL KKRNKPCPVCRQ/HNSNDCANL FPLVDLSIRELYISNYITLGI
29946	60314	Α	30129	2	430	
29947	60315	A	30130	3	1088	
29948	60316	A	30131	303	529	GTGQCANTKMSVPTDGA\VTTS QIPS/SPEQETRVR\PKPLL\LKLL KSVG\AQKDTYYYGKRFLFNLG QYIYGLNDYY
29949	60317	Α	30132	3	619	
29950	60318	Α	30133	123	385	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	1	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29951	60319	A	30134	66	413	HQSEQMYQSSESCLLGTTAKA
	00315	` `				RGHQLRTASACHFPSTPPFWSL
						TLESQREGRFKQPTLISCF/CLF
						MSVPVVSAPPFSSSSSSSSSSSSS
						SRPWFPDQEAR*LTSPVERPCR
						GLRPA
29952	60320	A	30135	257	465	VPTSPASLESKQSCPHVLCPVW
2,,,,,	100320	` `		1237		EVEGHSV*TGKPDRPPRRKLLT
						LLLPVPWVPGQLAIKQEGQEPK
						KRH
29953	60321	Α	30136	1564	1857	
29954	60322	Α	30137	33	265	
29955	60323	Α	30138	114	560	
29956	60324	В	30139	70	555	
29957	60325	Α	30140	650	1045	
29958	60326	Α	30141	374	575	
29959	60327	Α	30142	1	1095	
29960	60328	Α	30143	1	981	
29961	60329	Α	30144	28	698	TACRIRHGHAGRLCCSPCLLVIP
						LKSSQHI\LRVLNPPNLDGRRKI
						A\FAHHCPFKGVG\RRYA\HVVL
						RKAD\IDLTKEGGENSLEDEVE
						RVITH/ILQNPRQYK\IP\DWFLN
						KTRRM*KDGTYSPGP*PIGLGQ
						QAPVKDLGAD*KKIRAH*/RGL
		İ				RHFLGAFRVRGQAHQEPLGRR
						GRHPSGVSKEEIRSVGPCLVNKI
						VYIPKKKKKKKKVDAAANLVV
						VVVVGGR
29962	60330	Α	30145	107	340	
29963	60331	Α	30146	428	934	
29964	60332	Α	30147	1	1533	
29965	60333	В	30148	1	2652	
29966	60334	Α	30149	205	450	
29967	60335	Α	30150	1	879	
29968	60336	Α	30151	139	1029	
29969	60337	Α	30152	237	422	WFETPAQYTNRSPESGTHYRRA
						RSRARWHGCMECVCRRRKSPR
20070	(0220	<u> </u>	20152	1	1124	ANKPRRLPPVR*RCPPRA
29970 29971	60338	A	30153 30154	136	1134	
29971	60340	A	30155	1	3345	
29973	60341	A	30156	194	475	TPATVRRGWRPAVRVFRWWK
[1003-1	``		' '	1	PLTVPPRRKGPLSRGTGCRPVPL
						TTPSTGTVMRAGICAVKMLIVQ
						KSPCMPPC*HRQWTMTGLWQA
						PAAIRPV
29974	60342	A	30157	1	2988	
29975	60343	C	30158	1	3939	
					<u> </u>	L
29976	60344	Α	30159	308	749	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29978	60346	A	30161		4342	MTRDNPVIPRFIHRREVVFIGQE NGGIQNARFIAALFFQHGVNLC QRVGGLLKGIGVEVFRYTSVVE RVVVDYYIRPAGFSIDTNDRGS VTDDFAPDGQLAKAIPGFKPRE PQRQMAVAVTQAIEKGQPLVV EAGTGTGKTYAYLAPALRAKK KVIISTGSKALQDQLYSRDLPTV SKALKYTGNVALLKGRSNYLC LERLEQQALAGGDLPVQILSDV ILLRSWSNQTVDGDISTCVSVA EDSQAWPLVTSTND
29979	60347	A	30162	1	1023	LDSQXWIE VISIND
29980	60348	A	30163		679	MFRVTWSSGRTGLGKRLFRTP YDNDDTGPYAFNKTHPKDNYT CTVLFIDDMSASGQSLDKAQD NYRQAMKKLSSGRGNVLAQAE AFRGLGVEIKREINPDLAEQAIR LQDCVFDTQETMTTTFTGTVSS ANSGNYYTIFNTDTGAAFNNVS LAIGNYVVLAFSAS/VGA/DMK MVNSTITASGSKRSTTVLRQGL SQRWLLSAGARNLLQHYSFRE TCANWNMLFIGR
29981	60349	A	30164	114	685	
29982	60350	Α	30165	1	1353	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
29983	60351	Α	30166	1	1661	MRGEVLLAGVPRHVAEREIATL
1						AGSFSLHEQNIHNLPRDQGPGN
						TVSLEVESENITERFFVVGEKRV
Ì					ļ	SAEVVAAQLVKEVKRYLASTA
						AVGEYLADQLVLPMALAGAGE
						FTVAHPSCHLLTNIAVVERFLP
						VRFSLIETDGVTRQLLGVSYRIL
						AMGHAEFLIQIADMRNDGGWR
						DFQFSGNLVMDEPNRSAQTYIK
						LVKSRLGTTKRYNHKDDCPRC
						RWIAAMIDNPPRIRKPTKSASV
						WHATATSASPERQMSTTVIMS
						ARFISCWVMTPFCMPRSGPMRF
						VHLPCRFRDAFNTGVGKLDQL
						GPSMSTRIRQRFTTLCPMTLSSS
						STEFENVSDCRPSRARSCLRFRL
		ŀ				CRSIRCVYRLADYVQRSLQAGF
		İ				IQRPAIRHPYHHVKGAFTEYVR
						NNRLPETVIRVLQPALARFSPDI
						APLFSPFPLHDDDVTARLYAPS
						LMPKLRLIGLTLLALSATAVSH
						AEETRYVSDELNTWVRSGPGD
	ł	ŀ				HYRLVGTVNAGEEVTLLQTDA
						NTNYAQVKDSSGRTAWI/HVET
						T*H*AKPALPCARSGKSGQNPD
						R*THQYR
29984	60352	Α	30167	254	496	RASRLKTCGDGCCSLSAVVSVG
						ASPFASRVKSSRRWV*S*VGPSS
						WPPGMSL*TAEIRRSRRIPVVSS
						GSLTASFANVVR
29985	60353	Α	30168	1	984	
29986	60354	Α	30169	1	429	
29987	60355	Α	30170	1	523	
29988	60356	Α	30171	1	702	
29989	60357	A	30172	302	421	
29990	60358	A	30173	308	2468	
29991	60359	A	30174	612	671	
29992	60360	С	30175	1	2649	
29993	60361	Α	30176	501	754	
29994	60362	A	30177	1030	1327	
29995	60363	A	30178	3	108	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
29996	60364	A	30179	404	1347	DVTILARAVLQALLKILYH/KCE FNDEMLTEGVIREKMGFNPQTL REVLQACQQQGCVANNLDLDV VMIIIDGAFSGIVQNWLMNMA GYDLYKQAPALVDNRTGMER ASNGGPWQVQSLPARSYRQLD SYYGEAMAIGERALVALLDFSG PSPSGDWRYQTHHTFPPTGWR RQATLVKMRACIEAVKAVGEE LCPALGLTIPVGKDSMSMKTR WQEGNEEREMTSPLSLVISAFA RVEDVRHTITPQLSTEDNALLLI DLGKGNNALGATALAQVYRQL GDKPADVRDVAQLKGFYDAIQ ALVAQRKLLAYHDRLI
29997	60365	Α	30180	494	1433	
29998	60366	A	30181	1092	1347	
29999	60367	A	30182	315	600	STPIEKTVSKAFSAGSCSILTVT NARASARSACIISITAAVSGSCA PTP*EVSSAFARSLICRSIRKPGL KLRSITIGALASKTVLPASPPRIA
30000	60368	Α	30183	535	661	
30001	60369	Λ	30184	1	1491	
30002	60370	Α	30185	1400	1852	
30003	60371	Α	30186	199	534	
30004	60372	Α	30187	2	539	
30005	60373	Α	30188	1	690	
30006	60374	Α	30189	127	939	
30007	60375	Α	30190	1	665	
30008	60376	A	30191	1287	1548	SSCVLVRWRETADCRWRKLCL TDERTRR\NNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERS DEIPEAAKEIMREMGINPETWE Y
30009	60377	A	30192	242	709	NYMHYHADRCITRCHGNACTV NYAGLRSVPTSTVWTGLNLLT KRIKYLMAEWSGE/YISGPCVEP GKKSDQSKKITVSIPLKVLKILT DERTRRQVNNLRHATNSELLCE AFLHAFTGQPLPDDADLRKERT AE\IPEAAKREHA*HGGLTPET WEY
30010	60378	A	30193	1	897	
30011	60379	A	30194	1030	1263	
30012	60380	A	30195	263		PAHFSVAHSHLWQNINPLSSVQ CRQNHQAIPCRIFELLNVMRH/ VTRDSSSGLGCSWRLTASVNAR RFVDPVQILVMAMSGRRSR
30013	60381	Α	30196	1	1995	
30014	60382	Α	30197	141	229	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30015	60383	Α	30198	1	702	
30016	60384	A	30199	36	144	DGLLLMDERNISPLLQKRMPT* QAV*VWWWKDYGV
30017	60385	A	30200	462	646	QWVPIARPNMPACHVQRRTSSL ERRQPVMLMVMLRILWYIYCSI HVLG*WICRLYYKTLLK
30018	60386	Α	30201	107	1200	
30019	60387	Α	30202	366	500	
30020	60388	A	30203		1193	LADCSRYNGLEMTLSCCAGAS T\DAVGGIERGGLKSPEASEGEI APRLLLDGEPLALSGDKWRISP WLLVTDDTATITAFLQMIQEGK AITLRDGDQTISLSGLKAALLFI DAQQKRVGSETAWIKKGDEPP LSVPPAPALKEVAVVNPTPTPL SLEERNDLLDYGNWRMNGLRC SLDPLRREVNVTALTDDKALM MISSQIFNGHMVHIIKDLVFTDH APDKGISFGSDTGMDRPARGD HRLLVMHHDMTRFLRLPHHVE NAGVIIHIEIEINFHPALVGVTRH GVPLVTRSQLRQPHTRLAGFQY IRDQIFVNRATVTGEEIAYAELF TNFPANGNRFSYRHNAANNNS VNVAVNHGVLIGDKYLFNQKFI AQPLGIQRFCVRTVDALSYVHI
30021	60389	A	30204	3	1057	
30022	60390	Α	30205	1	955	
30023	60391	Α	30206	1281	1370	
30024 30025	60392 60393	B A	30207 30208	1	2199 589	MLKKREQTVFTHEKSVFQGLD RGNRELGPPKTFGVKGAQKGN LQIFSEDKNFGPGGSGEIWGHR GPKWDIPRGKRETLGKPHFFW KPSQEFGRKGLGSFGPWERVSG NKNSGKRIYPWGPVDGINCRW REPRNVDVAEYRRDCGSRFRSL RHFYRSLFSLHRPASTRHQKAQ SSAVT\VLQTNAQHGRRQRWQ
30026	60394	A	30209	1118	1460	FQASTTQPRTCCAPLSSVWRCR PPRSSPWPASWRSVPSSMGLRR TPWCPELLSSRGSTGFLWAEMT SSQARPKSSPCLWTSSLAPASRP CPS*\LQPPGQQRWGEPIGAIAV PL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, ∖=possible nucleotide insertion)
30027	60395	Α	30210	61	641	RHKHRRRIPGRWDQIRPAPNR
						WQTGFQWFALPVTGVRLISGY
						TELLPRL/PAQKNLPYTIHPAWR
			ļ			FVAHQGRESALECRYVPLPVRH
						*RNCRWREPRNVDVAEYRRDC
ŀ						GSRFRSLRHFYRSLFSLHRPAST
						RHPGAQTGAVTGFADECPARK
		1				AAALAKASVNKVVFHSTNATV
						CHRPDRSRRASGSFRRYWRQE
30028	60396	Α	30211	214	462	
30029	60397	A	30212	116	283	KKIKRHSLSVINSLANSKNKRR
						WRKNIKLR*SSLLK*TESPLPMA
						ILVLTSLTAI
30030	60398	Α	30213	451	834	IWTGKKVDSARALIARGWGLH
						VILRRTDDWMDGRRSRHTDDT
						DVLLRIHHVIGELPTYGYRRVW
ľ						ASSQTGRT**FKVQNRYFPPVLS
:						DFEHLQEPYEYFGKLR*PWLPA
						TGEFHAEIYRSVDFCKHPV
30031	60399	Α	30214	1180	2547	
30032	60400	Α	30215	341	505	
30033	60401	Α	30216	293	4221	KPFSPCCRKGRWLFRNHSSARR
						PTVLYYRRSTMR*NSW*PNLRR
						QRGNPANRS/RQSMLELSGVKD
						GELIPAKLFNHLVTWLQARQTL
1						SQQNTPRPGGGEIPPWCSSVLA
				:		ESERKKRGRKKQRGIDSPDVGA
						LLLVRATFYIWQQPPVNKIALGI
						EYAASKYYGWQRQNEVRSVQ
						EKLEKALSQVANEPITVFCAGR
						TDAGVHGTGQVVHFETTALRK
					:	DAAWTLGVNANLPGDIAVRW
		:				VKTVPDDFHARFSATAR
30034	60402	Α	30217	1	1362	
30035	60403	Α	30218	1	1440	
30036	60404	A	30219	389	503	YESARLSGLHRQSDDRWRR*SP QYARHTRKRTSAGCSA
30037	60405	Α	30220	1160	2385	
30038	60406	Α	30221	290	373	
30039	60407	Α	30222	1	627	
30040	60408	A	30223	3	862	
30041	60409	Α	30224	1	469	
30042	60410	Α	30225	241	615	
30043	60411	Α	30226	1	1428	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	:			sequence		
30044	60412	A	30227	862	1453	SFLLVSPSQACHHYYAP/KIFDL/
		` `				SGYTSTTEQMWGTVIVGLTNV
						LATFIAIGLVDRLGFLAMPAGM
	1					GVLGTMMHIGIHSPSAQYFAIA
						MLLMFIVGFAMSAGPLIWVLCS
						EIQPLKGRDFGITCSTATNWIAN
						MIVGATFLTMLNTLGNANTFW
						VYAALNVLFILLTLWLVPETKH
		ļ				VSLEHI/ERNLMKGRKLREIGAH
						D
30045	60413	A	30228	1	987	
30046	60414	A	30229	767	1472	CMSRQCCTAYVPPVRSCCPPVS
30010		ľ.	5022)	1,0,	12	VHFFHSRLCRDALNEAFHPSG
1						FQVVKCCDIARIHRNRYGDLLF
						AIGVVHIANVNAIHRNATFHQR
i e						QEIGGCFTNQQDFLSIGGAMNV
						VDNFLQRPETYGDPFCQYHFH
						QVLLYRIFGNLIVGYQHQICPR
						KSDPLNADLTVNQAFINPA*NN
						-
						IWHSVFLFVLLIGLHRLCGMRQ
						DVLNMVDNEFPWRWLQLAGA
	10.11	ļ. <u>. </u>	2222	0.550	2015	NFHVLQRQILADQRQRNW
30047	60415	A	30230	2553	3845 656	
30048	60416	A	30231 30232	3	228	
30049 30050	60417	A A	30232	185	206	ATVDPPFITEPGDILAGGFA*PL
30030	100418	^	30233	103	200	SWFAGFALEHHNLPWATGDLH
						SLRA
30051	60419	A	30234	12	155	SLKA
30052	60420	A	30235	698	2684	
30053	60421	A	30236	1	2004	
30054	60422	A	30237	1	811	
30055	60423	В	30238	11	7521	
30056	60424	В	30239	52	1023	
30057	60425	A	30240	2	163	LTPTWWRKPWNRKPVLSVIP*K
30057	00423	' '	30240	1	103	WKLKGPVALKTAYPAKRLPLPI
						TSFSLPGVA
30058	60426	A	30241	1	2067	
30059	60427	В	30242	1	2787	
30060	60428	A	30243	101	947	
30061	60429	Α	30244	1	1917	
30062	60430	Α	30245	239	469	KRVSISSRRRFSAQKASASALA
					1	RWWRSAVNIYVFAI*TTAQRV*
						QLRMTNCVRTTITACHSR*RITL
		1				SLSPVKPAS
30063	60431	Α	30246	1	4348	
		+	20215	11141	2244	
30064	60432	A	30247	1141	2244	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30066	60434	A	30249	418	930	PRVIENFLFQLTFLPGGITQSHQ YVRRLFIGAERFQHIAGSGHYR VV*NANAGSKIGGRSMQNKPAI FSQRTAEHNRFIQTD*FITRLRR DLQLFQNPFNFEIFQRLVDDDP HCTIGIMFANVDHGTTENRIRK LCFNLTNTGTQRKGHANISGPE TFRIYHRNAHAPLTI
30067	60435	Α	30250	1	526	
30068	60436	Α	30251	442	684	
30069	60437	Α	30252	1	3144	
30070	60438	A	30253	59	340	LLPQRQAKAPVLPLPLPTENVP AARAGKKDAVIFSSAQFEQIAL AANGAFTGG*YQNRQ*NMRCY ASGESVTDRPRLAIRDATIGISG FCSLA
30071	60439	Α	30254	62	298	
30072	60440	Α	30255	904	1530	-
30073	60441	A	30256	701	1329	HRLSMCRGRCSRWWSARTNVI SMLVFALSFASWRIVSPRTM/D ALTFAAESALPGSPTHISTDHQG QFVFVGSYNAGNVSVTRLEDG LTMLHEELSSHMMKEEQILFPM IKQGMGSQAMGPISVMESEHD EAGELLEVIKHTTNNVTPPPEA CTTNKQPAQPQRDKPQRGNQQ RLASVIFQCQQHDHEHKERHTY PAHQLAERHLVDRLLM
30074	60442	Α	30257	8	382	
30075	60443	В	30258	1	2655	
30076	60444	A	30259	1109	1531	TFLHSIPAAKTQGPPPRNTLVDT PQHL*HQQRRTRQPQLALSLRT *VFLNRILRGALFAPKACLKPD LVISPRGPPQGLGVTRVQVSAH TNPRTTHRNTPHYTRNTQTRPE STPRRDTTTPQQRHTPPPHTGK RRGTPET
30078	60446	A	30261	1025	1252	SSTVFSNLDRSDSPISQSKMKIIA SITTIRMEP*AIATPYSPSSTRLR M*AVATRVSGVTRNTMALTVV MARTKL
30079	60447	A	30262	2114	2380	LPGLAKLTVKDLPRLSLAFERE VRDSPISQSKMKIIASITTIRMEP *AIATPYSPSSTRLRM*AVATRV SGVTRNTMALTVVMARTKL
30080	60448	A	30263	3026	3217	LPQCKWDPYGVTISPQVSIRSR ANPSCTSPFFV*SATKGLLYQQ TRIPALDIPPSSNRRNSHG

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30081	60449	A	30264	1403	1799	YGHEWRWMPGNRPHYGRWPQ HDFPPFKKLRPQSVTSRIQPGSD VIVCAEMDEQWGYVGAKSRQ RWLFYAYDSLRKTVVAHVFGE RSLFTGP*RERFATQIEVGKLFA AAVDMVLWLSGKAQPDTVVV KVVVL
30082	60450	Α	30265	3174	4135	
30083	60451	Α	30266	1	2771	
30084	60452	Α	30267	1	1281	
30085	60453	A	30268	10	233	LRIQASDPEINSRRESGIHLPYTT DKAPSPLTVDGAK*EVSRSSI/R QNSQVQHPPDAAKYPSGCHKS FRGFRRA
30086	60454	A	30269	300	564	SANSTLKRTQVNRRPLTVKLSA RKLPMLKVNTRNSLVVVVSMV MLLSTCTRWSRVQTRKATSSST TLKVV*SLANTSRPLIKVSRNS
30087	60455	Α	30270	5259	8003	
30088	60456	Α	30271	1	819	
30089	60457	Α	30272	1173	1369	
30090	60458	Α	30273	1	4767	
30091	60459	Α	30274	905	1162	FSSVVMCSSIIVSEQEITSRLKAT VASQVADSAGLNSRKITSCRSS AFLSALIRHPTGGIFNKL*LSGT LNPALLSFITSHGILL
30092	60460	Α	30275	1164	1582	
30093	60461	A	30276	1	1785	
30094	60462	A	30277	1	168	LEHLSPCDSIRHSRTRATAAIRS RCYSKYAQ*IRDHRVNGDGVS RLYAANQHRTCQ
30095	60463	В	30278	1	954	
30096	60464	A	30279	108	530	SIRQTHVQIVRRSCLAIRHQVPS TAIRVGIVKGNFAS*AGAQPSK TLR*HRCTTRALTSGVLAVRLS AGCNFPELVHRRLTLWRAGRT YPPASGHHHDNRNAPSLSDQTR TDPPIRAHASRYQRQKPDWLTP PFPAGQRC
30097	60465	Α	30280	1	1389	-
30098	60466	A	30281	1	380	
30099	60467	Α	30282	1	3255	
30100	60468	A	30283	569	2547	
30101	60469	Ā	30284	1	585	
30102	60470	A	30285	1376	1693	CPMADTPAT*PIPKRLMLCYST GLPACYITVKPP*TLGSVQGSLG PSSGPKTAGAPSSRPPSPSARRP RTTETRWTLLRSKDYWLITRKV
						GLGNLQDGGRAGSLS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30103	60471	A	30286	737	1088	NMLMNVCNLPVVCVPMMSRK RGCVTITWALICGLSWGCRMS GGLRKPAPRPQKWRCLPIIVGR RKSGGSKIRANVCSLPIFPSGI\G R*TTGESKRLCRSYHDAAGNDS *WRDLVIG
30104	60472	A	30287	3	209	VQHSCRMCGTHSQKCPSHRQK LRPHGHLVA*CLCAGSREWEA NPLFPGRGHCTDSPPETRPHQL VQRV
30105	60473	A	30288	2366	2768	STRSGGNCRGAGAGV*SGPVA GR*SQSGDRAEST\SPLAMVGD GINDAPAMKAAAIGIAMGSGT DVALETADAALTHNHLRGLVQ MIELARATHANIRQNITIALGLK GIFLVTTLLGMTGLWLAVLAD TGATVL
30106	60474	Α	30289	714	881	
30107	60475	A	30290	791	1618	NTISIRPIKLRS*L/CDPGFAGQPF IPEMLDKLAELKAWREREGLE YEIEVDGSCNQATYEKLMAAG ADVFIVGTSGLFNHAENIDEAW RVMTAQILAAKSEQWGQQVY AIVQNTDQAQAVMPYGPKCLY VLAQNDALQRTENYAESIAALL KDKHPAMLLLAATKRVLFAIV DTYVTTNASLAGIALNSMDLSP GGRVAVKESNQRWCSDGFEFC CDNGERLRVTFALDCCDREAL HWAVTTGGFNSETVQDVMLG AVETPLRQRSSVVSSGVADG
30108	60476	A	30291	364	1305	
30109	60477	A	30292	105	609	CGGCPQSRHRPAPALRYPQLQ MPHWRRSICTSLHRQR*WTPSG SV
30110	60478	A	30293	159	438	CASVPRSRGGSQAIAARKSGRA LIKSASLS*FK*LLKPAINAG*Q AS*WRASASKPCSASPDCAGDN CASIVSAASALALGCSKRISAPR TAP
30111	60479	Α	30294	1246	1300	
30112	60480	С	30295	1	1374	
30113	60481	A	30296	231	413	SPRCTRPCNAGSDVRRGSASF* AGGAGY*TPRPGVW*SVGYGE RQQRAPPADWSQRCGVD
30114	60482	В	30297	1	3081	
30115	60483	A	30298	345	505	TNAACNRQSGLINQWMKQTVK ME/VTASGTVISVINPVATKLRR *RVFPAPCCG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
30116	60484	Α	30299	3	421	QRRATGDLRLPTR*TARRGGRC
						DS*SSRRWHRAFTGACREISRQ
						QNRRHRQRPAGGVALVGSE*T
						SGILAGQRHYRVYRAGYRRSPP
						AGYAPD*SD*RPVDGRHECGRR
					:	PVWRRENVPATGGQIGARHET
						GGGLPRTVY
30117	60485	Α	30300	1	3202	
30118	60486	Α	30301	317	554	
30119	60487	Α	30302	474	599	TTSVQRTFLPDTY*APTPVLLPA
			-			RKATAARKLHRFSGRQDR
30120	60488	Α	30303	212	569	TSLKVVTPALRSMPSVPINNLS
						KVKCSKAFSASCP*NEADFLRN
						VPPGIRIVCSLSSSDSALTICRLL
						VITVMLLKRESRGTICKTVLPAS
						RMIESPSWIKLTAASAISSFLWV
						LMSVL
30121	60489	Α	30304	1	160	WSKMSRAVRPSDWESWTQTRE
						VVRQTVRCRPDPPSAAVCLTAS
						SPANCGIPIG**MLAEILA*RAV
						RPSDWESWTQTREVVRQTVRC
						RPDPPSAAVCLTASSPANCGIPI
	1					G
30122	60490	Α	30305	1	975	
30123	60491	Α	30306	1	762	
30124	60492	A	30307	1	733	
30125	60493	A	30308	493	948	LGAIFLAGALFAAAWLADFRL
						GLGARLYRYGADWFCADGGM
						SAEELKFISENGAVVDMDHKKP
						GSAAASGPKLHYIKQLLSNRM
		1				MLGVFFGQYFINTITWFFLTWF
		1			,	PIYIGNVVSDNR*YVAQITFITW
						IKTYGRCPSFQRDGDGFVNRCL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30126	60494	A	30309	153	2031	RRNYQRQKKRGSEGAGRPDR RSRISAAYSPRSEFNNAAVTEH Y*NRF*T/LVPRSR/HANADTVT REAVNQVIALLDSGALRVAEKI DGLPTNQMQASRRAKEEEVHL TGQPSRVQSPPRRCEEKQYMVL MIVSGRSGSGKSVALRALEDM GFYCVDNLPVVLLPDLARTLA DREISAAVSIDVRNMPESPEIFE QAMSNLPDAFSPQLLFLDADRN TLIRRYSDTRRLHPLSSKNLSLE SAIDKESDLLEPLHGFPDYDTV GFSCKRRIDYVCRIKHSRRIRQV VLLNFAKSGAFSTTRGTDDKTR RSLLVTLVRIFCVRVIFAYDIRD GIHVRIIQINSKSGKVGSKHNSG YSAAKFGGVGLTQSLALDLAE YGITVHSLMLGNLLKSPMFQSL LPQYATKLGIKPDQVEQYYIDK VPFKRGCDYQDVLNMLLFYAS PKAVVLAPDSRSMSPAVSGRFK PRVVVAIALDDQQRIVDTLFMK GLTVFARPQKIPAITGRHSGATL QKQGKCSVEELAQYFDTTGTT MRKDLVILEHAGTVIRTSGGVV PDSPPHTRRDPRRFSMAFPWFD NIRSAEFHHVTTLLAEIPRQQND IHRPAHAAAAPKVETRSGDETN
30127	60495	A	30310	720	872	RRWNRPAQHLFA EKVPVSIGPGGMQELPMQSPDR RSAGKPGPASRAGR*TGGGAFS
30128	60496	A	30311	1967	2452	TKRDYR SRRCSASINQRPRPGHEKMVSV RIAPASNVPTCRPITVTTGSIALR SAWTIITRMRVSPLARAVRM*S SPSTSSIEERVIRTMTASGIVPST MAGKIIWATASIKLPSSPQMAV SISIKPVNGLESSRNTISLTRPET GVRFQCTETSMISIMPHQKIGIE
30129	60497	A	30312	1912	3960	
30130	60498	A	30313	2	250	LIRKVST*SVLMKAFLRIA*KDC ERLGLKCFWSGSEKGCPLVNT NAFGGHCEHHQWVSSVSRVRV SQSAGGCPLFNILLNTV
30131	60499	Α	30314	1	300	SVFSH*AKKIWKGVSQRALGQ NSRGSGSGCQASWTIRFPVGFH TDGTRLRRNPGMQAFLGPVAR FLALEARSLDCAFSSSLLFKRKL SGRWGRASRGTKL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	i	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30132	60500	Α	30315	1	468	MTEKVKQQPAPVTASDEIDIGR
						LVGTVIEARWWVIGITTVFALC
						AVVYTFFATPIYSADALVQIEQ
						NSGNSLVQDIGSALANKPPASD
					:	AEIQLIRSRLVLGKTVDDLDLDI
						AVSKNTFPIFGAGWDRLMGRQ
						NETRRGFSARGTGQMLKKEGV
						TLMVEAIHASPGSEFTVTKYST
					•	LGMINQLHNSLTVTENGKDAG
						VLSLTYTGEDRYTNHAGVVNT
						MIIIAATHNLVFENNSCEYAHP
						MGNAPAGLTEYQNVFYKHDRI
						QGHYVWEWRDHGIQAQDDHG
						NVWYKFGGDYGDYPNNYNFC
						LDGLIYSDQTPGPGLKEYKQVI
						APVKIHARDLTRGELKVENKL
						WFTTLDDYTLHAEVRAEGETL
						ATQQIKLRDVAPNSEAPLQITLP
						QLDAREAFLNITVTKDSRTRYS
						EAGHPIATYQFPLKENTAQPVP
						FAPNNARPLTLEDDRLSCTVRG
						YNFAITFSKMSGKPTSWQVNGE
						SLLTREPKINFFKPMIDNHKQEY
						EGLWQPNHLQIMQEHLRDFAV
						EQSDGEVLIISRTVKPRGPARCP
						DSSVGTTYCTENNPPFDNGLLN
						AQLLQQAKPFVDERQSK*FGCH
						SPSYSCLWLSIIGLKKLIFGSRVS
						SDSPFTCQDVGLPLIFEKVIAKL
30133	60501	A	30316	1	524	
30134	60502	A	30317	1669	4421	
30135	60503	Α	30318	2	349	SMAKCPLRKNQGPVRSCGAWS
						GCLWLPSPSGTPWRSSLWILLL
						F/SQISQLLSLLHQGQFQPKPNH
		1				RGNKYLAKPGGSRSAIPDTDGP
						SARAGGQTDPEQEEGPLDPEED
0015	(0.50)		20216	0.5		LSVKQLL
30136	60504	В	30319	217	368	
30137	60505	Α	30320	1	951	
30138	60506	C	30321	1	3729	
30139	60507	Α	30323	1	2437	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30140	60508	A	30324	1005	1815	PDLHCQKKHPTLCSGYWPTFRT PVHYAAFS**/HALGHLAFS/EA SLHSHRGTQALTTQKKSPAKSP TAATTETRVMRKISHGTRDPPG FASL\MQ*MHYGKLCAFQSELL FQSLQRSHWTQSWWLCWPHW RLCWTQNWWQCWPHWTLCW TQSWWLCWPHWRSCWTQRW WLCWPHWTLCWTQSWWLCW SHWRSCWTQSWWLCWPHWRL CWTQSWWLCWPHWRSCWTQS WWLCWPHWRLCWSQSWWLC WPHWRLYWTQSWWLCWPHW RVCWTQN
30141	60509	A	30325	2436	3678	KMPPWPPGSPGPLGCSAWAEA PPAHCPDVLLHLHPACPHIQAP CGTGAPGTGLAAAADSEPLGSS APPAGRPCPQAAAACGLAPPLP RGWCPPPTSSWMGRRLQSLSA HPTSPAPLLAAPTAVCSCSRCSA PRSRCVARPAARTGLPTPAPAS SPAPATSPAPAESPAATASHPV AEASPAPGAPPPRPAASPSPAAS PAPPAASPVLTASPPLPAASPAL AASPVHTASPPVHVASPPVHVAS PPVSCSGDSTSDCFPPQPGAVFP HSL/VSFLRWLVSSCSCSTLDGP AGGCGARGSAVWFLSLNKLLP/ MLLYQMYLMLLLLRCANQ*I DVFSELTDYCGA*IQGYC*FLV LAIPR*VVTTRSGCVRATAIDFL FPVSSCWNARALPLPICF
30142	60510	Α	30326	929	2910	T V S S C W W M C V E M C M
30143	60511	Α	30327	1	1488	
30144	60512	Α	30328	203	701	
30145	60513	A	30329	493	924	SDPGFRHGKARITDPRGQPGRR LQGGSSEGNGSDMKAARKVSG NKHSTSSHQHAVWCPGVPS*SG KAWAADQRFVPRILGKGRGHV DAA*LSWKCRNHLSSVSLNGE NQRFVGDARYRTRLQRGSANL FKRQRCGTLHQNLELL
30146	60514	Α	30330	1	2193	
30147	60515	Α	30331	1	2990	
30148	60516	A	30332	2512	2560	FALRYRQPVRHRW*FHLVQRH GRFSRASGATWPASAAAFAWP LLVCAPLSAASAAPLARL
30149	60517	Α	30333	1	2820	
30150	60518	С	30334	194	418	
30151	60519	Α	30335	25	458	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30152	60520	A	30336	860	1209	IPGNCRDSSGVGIKERETNAGS QHMH/IKNSSVHGYPRLCVEDE DAYKKQFSQYIKNSVTPDMME EMYKKAHAAVPENPVYEKKPK KEVKKKRWNRSKMSLAQKKD WVAQKKASFLRA
30153	60521	Α	30337	1	1440	
30154	60522	A	30338	138	512	
30155	60523	Α	30339	1723	1845	
30156	60524	A	30340	6	983	RRWACRSLSSSGRRSLFRRMGF VKVVKNKAYFKRYQVKFRRRR EGKTDYYARKRLVIQDKNKYN TPKYRMIV\RVTNRDIICQIAYA RIEGDMIVCATYAH\ELPKYGV KVGLTNYAAAYCTGLLLARRF L\NRFG\MDKIYEGQV\ELTGDE YNVESIDGQPGAFTCYLDAGLA RTTTGNKVFGALKGAVDGGLS YPLTVPKRFPWF/DDS*KPRNLI AEVHRKPHPWAQNVARLHAPT LMEED\EDA\YKKQFVRQYVKN SVT\PDMM\EEMY\KKAHAAIRE ESSSMEKKAQGKKFKKKRWNR P\KMSLAQKKDRVAQKKASFL RAQERGC
30157	60525	В	30341	1	2043	
30158	60526	Α	30342	390	1180	
30159	60527	Α	30343	2	649	
30160	60528	Α	30344	1	1929	
30161	60529	Α	30345	1	773	
30162	60530	А	30346	3	484	NSSCRDPGY/CPIIVSLNSS*GSL LQDMPGPSKVISEILATRGAVNI TTVAYKSAVILSFTTASAVSLSS RNVIGPLFASQPSFTIHFSLFSHN GSAPLNAPDMANCFGLTALTSS LDERLFSRNSAGSCCGIRNCFIS TLPPNTSTLTSVNSKGSSSVHG
30163	60531	В	30347	1	2775	
30164	60532	A	30348	1	1386	
30165	60533	Α	30349	439	555	
30166	60534	Α	30350	1	1785	
30167	60535	A	30351	100	488	IALASSHCTANARFRITRCRTK/ EQRYALSQAKSIADELMTGCTN FAFSGKPGTGKNHLAALSGIAC WKTFLMNLASARDEKRAVVLH QIVDRRTASMRSVGMLTNLNY EAMKTLLGERIMDRMTMNGG RW
30168	60536	Α	30352	1	786	
30169	60537	Α	30353	1	288	
30170	60538	A	30354	711	953	

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30171	60539	С	30355	1	2355	
30172	60540	A	30356	1035	1152	SPDSVDAQRGDADKPEL*GHE NIARRADYGSHDHERRAM
30173	60541	Α	30357	1	420	
30174	60542	Α	30358	1115	1561	
30175	60543	В	30359	501	555	
30176	60544	Α	30360	441	602	SPPASWR**IPPAGFFT
30177	60545	Α	30361	386	1647	
30178	60546	Α	30362	1	1179	
30179	60547	Α	30363	1	1215	
30180	60548	Α	30364	1282	1657	
30181	60549	Α	30365	388	804	
30182	60550	Α	30366	1328	1978	
30183	60551	Α	30367	455	1000	
30184	60552	A	30368	291	303	RVRRMMYTVTLYSFSTNKNTY I*E*E*G*GWRHHIFLG*MKCFS SRVILVLTSHDSSQSSLQTVSLL LLSSFALDPSSTMLTTEESVE
30185	60553	A	30369	284	433	RVRRMMYTVTLYSFSANKNTY I*E*E*GLGWRHHIFRGYM/RQH FND*SWP
30186	60554	A	30370	290	425	RVRRMMYTVTLSSFSANKNTYI *E*E*GLGWRHHIFLG*IQHFNR
30187	60555	A	30371	842	905	
30188	60556	Α	30372	784	3453	
30189	60557	Α	30373	1	209	
30190	60558	A	30374	36	412	ESEVLGPRSLPTWVPSPSGSLGP RGGRGGCILRPSRGGRGRHGPT KAGPWSPESRGR*DWKARGPP APSRGSPSRARARRGGSGGGPA DEPGLQGRTRRPALSSRTSAPD PGRVVERSGRFRSES
30191	60559	Α	30375	1	340	
30192	60560	Α	30376	2	3336	
30193	60561	Α	30377	22	419	
30194	60562	Α	30378	1	13683	
30195	60563	A	30379	220	403	CLSTVFFLCITLVSECWSLF*SH MHVLLPRNRKEKLIEIFRTQTY DVNAYKASAHRNSGPG
30196	60564	С	30380	169	415	
30197	60565	A	30381	3	1324	
30198	60566	A	30382	2	3455	
30199	60567	A	30383	85	2695	
30200	60568	Α	30384	69	303	
30201	60569	Α	30385	1	951	
30202	60570	Α	30386	1	4749	
30203	60571	A	30387	176	1553	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30204	60572	Α	30388	1	425	MDQIISLFGRPDHVAYDIRSLRN
						KANPDDTFEAQLFYGDLKAIVK
1						TSHLVKIDYPKFIVHGKKGSFIK
						YGIDQQETSLKANIMPGEPGFA
						ADDSVGVLEYVNDEGVTVREE
		l				MKPEMGDYG/PRL*CVVSNHHP
			ļ			RCAKLRQGI
30205	60573	Α	30389	3	1890	PSQPLLWFAGRPRGRDTGCPRC
		l				KQNSTCIAAVKMEGPLSVFGDR
		l			İ	STGETIRSQNDKESFNEQKTCRI
						*RKRLV*LYEVAEHEIVMAAAS
						IANIVKSSLGPVGLDKML\VDDI
		į				GDVTITNDGATILKLLEVEHPA
		l				AKVLCELADLQDKEVGDGTTS
		1				VVIIAAELLKNADELVKQEIHPT
						SVISGY\RLA\CKEAVR\YINENP
		l				NLLTQDELGRDCLINAAKTSMS
		ł	ł			S\QIIGINGDFFANMVVDAVLAI
						KYTDIRGQPRYPVNSVNILKAH
	•	İ				GRSQMESML\ISGYALNCVVGS
		İ				QGMPKRIVNAKIACLDFSLQKT
						KMKLGVQVVITDPEKLDQIRQR
						ESDITKERIQKILATGANVILTT
						GGIDDMCLKYFVEAGAMAVRR
						VLKRDLKRIAKASGATILST\LA\
						NLEGEETFEAAMLGQA\EEVVQ
		İ				ERICDDELILIKSTKA\RTSASIIS
		ŀ				RVPIDSMCDEMERSL\HDALC\V
						VK\RVLESK\SVVPR\GGAVEAA
						LSIY\LENYA\TSMGSREQLAIAR
						VCKITLWLFPNTLSS*CLPRDST
		ŀ				DLVLQNLRAF\HNEAQV\NPER\
						KNLKWIGLDLSNGTPRDNKQA
		ł				GVFEPTIVKVRGLNFATEAAIT\1
						LRIDDLIKLHPESKDDKH/G/GS
		<u> </u>				YEDAVHSGALND
30206	60574	В	30390	1	975	
30207	60575	В	30391	1	2577	
30208	60576	В	30392	1	3126	
30209	60577	В	30393	1	1134	
30210	60578	В	30394	1	2082	
30211	60579	В	30395	1	915	
30212	60580	В	30396	1	2658	
30213	60581	В	30397	1	2412	
30214	60582	В	30398	1	2454	
30215	60583	В	30399	89	2533	
30216	60584	В	30400	1	4083	
30217	60585	В	30401	1	1725	
30218	60586	С	30402	127	345	
30219	60587	Α	30403	1	597	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30220	60588	Α	30404	3	3386	MPATASAGVPATVSEKQEFYQ
		1	:			LLKNLINPSCMVRRQAEEIYENI
:						PGLCKTTFLLDAVRNRRAGYE
						VRQMAAALLRRLLSSGFEEVYP
						NLPADVQRDVKIELILAVKLET
				1		HASMRKKLCDIFAVLA\RNLID
						EDGTNHWPEGLKFLIDSIYSTN
						VALWEVALHVFWHFPGIFGTQ
						ERHDLDIIKRLLDQCIQDQDHP
						AIKTLSARAAAAFVLANENNIA
						LFKDFADLLPGILQAVNDSCYQ
						DDDSVLESLVEIADT
30221	60589	A	30405	1	1695	
30222	60590	Α	30406	1126	1355	
30223	60591	Α	30407	1	1610	MGSRCLNPPPPAHSDTTGKDSF
						GNIRGAETGQGASACSVTSARV
				ŀ		TCGAGSEPHSHRNPGISAQVGL
						APSYGAARGRRRPLALQQSPQE
						RRHVGWNSTRGLLPASLPGTAS
						SQSASATASAALPLKVTGPLAR
						NPTPPWTAAAALATRGQRPEK
		i				GLFPGPAPFSLGKRKRGRGRTW
						ERRRVSIETSTCFRPGCERLGA
						AAGANLSQLASSQRPLRERWV
		İ				LYTIIMAAAGAPDGMEEPGMD
						TEAETVATEAPARPVNCLEAEA
						AAGAAAEDSGAARGSLQPAPA
						QPPGDPAAQASVSNGEDAGGG
						AGRELVDLKIIWNKTKHDVKFP
ŀ			:			LDSTGSELKQKIHSITGLPPAMQ
						KVMYKGLVPEDKTLREIKVTS
1		1				GAKIMVVGSTINDVLAVNTPK
						DAAQQDAKAEENKKEPLCRQK
						QHRKVLDKGKPEDVMPSVKGA
						QERLPTVPLSGMYNKSGGKVR
						LTFKLEQDQLWIGTKERTEKLP
						MGSIK\NVV\SDPI\EGHEDYHN
						DGRFQLAPTEA\SYYWVYWVP
						TQYVDAIK\DTVLGKWQYF
30224	60592	Α	30408	71	415	WLFPPNPPVFRGQHPRQGLGPP
						SAAGRRAMKKKLVVLCLLAVV
						LVLVIVGLCLW/LPSASKEPDN
						HVYTRATVAADAKQCSEIGRK\
						AEVINAREVAPSVAFASMFNSS
		<u></u>				EQSQKAL
30225	60593	Α	30409	562	2376	

SEQ ID	_		SEQ ID NO:	Nucleotide	•	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
30226	60594	Α	30410	604	2475	RQREVTRSPPERSGLRVLQLFPP
						NPPVFRGQHPRQGLGPPSAAGR
						RAMKKKLVVLGLLAVVLVLVI
						VGLCLWLPSASKEPDNHVYTR
						AAVAADAKQCSKIGRDALRDG
						GSAVDAAIAALLCVGLMNAHS
						MGIGGGLFLTIYNSTTRKAEVIN
						AREVAPRLAFATMFNSSEQSQK
						GGLSVAVPGEIEGYELAHQRHG
						RLPWARLFQPSIQLARQGFPVG
						KGLAAALENKRTVIEQQPVLCE
						VFCRDRKVLREGERLTLPQLAD
						TYETLAIEGAQAFYNGSLTAQI
						VKDIQAAGGIVTAEDLNNYRA
						ELIEHPLNISLGDAVLYMPSAPL
						SGPVLALILNILKGYNFSRESVE
						SPEQKGLTYHRIVEAFRFAYAK
]						RTLLGDPKFVDVTEASSGVSA\
1						VVRNMTSEFFAAQLRAQISDDT
]		j		ļ		THPISYYKPEFYTPDDGGTAHL
						SVVAEDGSAVSATSTINLYFGS
						KVRSPVSGILFNNEMDDFSSPSI
]				TNEFGVPPSPANFIQPGKQPLSS
1						MCPTIMVGQDGQVRMVVGAA
						GGTQITTATALAIIYNLWFGYD
						VKRAVEEPRLHNQLLPNVTTVE
						RNIDQAVTAALETRHHHTQIAS
						TFIAVVQAIVRTAGGWAAASDS
						RKGGEPAGY
30227	60595	Α	30411	63	342	GRTLVPHGGLPHHYLVQCEWL
						PGTS*AEFPVVHLPAFVARARG
1				1		ADRQHHGPFLPLCHLHPARPRR
						EDLHRKSPGEPNPIEHHRSSGPG
2222	60.506	ļ	20412		010	CRRI
30228	60596	Α	30412	1	910	MLFRPALGSRQVVRNMTSEFF
						AAQLRAQISDDTTHPISYYKPEF
						YTPVDGGTAHLSVVAEDGSAV STTSTINLYFGSKVRSPVSEILFN
						DEMDDFSSPNITNEFGVPPSPAN
						FIQPGMGWR\KQPLSSMCPTIM
						VGQDGQVRMVVGAAGGTQITT ATALICVTAFLPGRAHPAQPPS
						HADHTPMPQAIIYNLWFGYDV
		İ				`
						KRAVEEPRLHNQLLPNVTTVER
						NIDQAVTAALETRHHHTQIAST
						FIAVVQAIVHTAGGWAAASDS
						RKGGAYRILSALQEDKADKQS RDKILTRTRKGTLGDWLPM
	L	<u> </u>				RUNILIKIKKUILUUWLPM

SEQ ID	SEQ ID NO:		SEQ ID NO:	t .	18:	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
30229	60597	Α	30413	110	868	DLCPLPTLPPHLLRPALGSRQV
						VRNMTSEFFSAQLRAQISDDTT
						HPISYYKPEFYMPDDGGTAHLS
						VVAEDGSAVSATSTINLYFGSK
						VRSPVSGILLNNEMDDFSSTSIT
						NE\LGVPPSPANFIQPGKQPLSS
						MCPTIMVGQDGQVRMVVGAA
						GGTQITMATALAIIYQPSWFGY
						DVKRAVEEPRLHNQL\LPNVTT
						VERNIDQAVTAAL\ETRHHHTQ
						IASTFIAVVQAIVRTAGGWAAA
			İ			SDSRKGGEPAGY
30230	60598	Α	30414	1	1626	
30231	60599	Α	30415	171	2097	PSGEREGCLIRESLKKILWLQAS
		ŀ]	AECEGDPGYFLSYFHQILLSFV
						ANTPRQGLGPPSAAGRRAMKK
	:					KLVVLGLLAVVLELVIVGLCL
						WLPSASKEPDNHVYTRAAVAA
		l				DAN\LCSKIGRDALRDGGSAVD
=		1				AAIAALLCVGLMNAHSMGIGG
		l				GLFLTIYNSTTRK\AEVINAREV
		İ				APRLAFATMFNSSEQSQKGGLS
		ŀ				VAVPGEIRG\YELAHQRHGRLP
						WARLFQPSIQLARQGFPVGKGL
						AAALENKRTVIEQQPVLCEVFC
						RDRKVLREGERLTLPQLADTYE
						TLAIEGAQAFYNGSLTAQIVKDI
						QAAGGIVTAEDLNNYRAELIEH
						PLNISLGDAVLYMPSAPLSGPV
		İ	:			LAL\ILNILKGYNFSRESVESPEQ
						KGLTYHRI\VEVFRFAYAKRTL
						LGDPKFVDVTEASSGVSA\VVR
						NMTSEFFAAQLRAQISDDTTHPI
		ŀ				SYYKPEFYTPDDGGTAHLSVV
						AEDGSAVSATS\TINLYFGSKVR
		ŀ				SPVSG\ILFNNEMGDLSSPSI\TN
						EFGAPPSPANFIQPGKQPLLSMC
						LTIMVGQDGQVRMVVGAAGG
						TQITTDTALAIIYN\LCFGYDVK
						RAVEEPRLHNKLLPNVTTVERN
						IDQAVTAALETRHHHTQIASTFI
						AVVQAIVRTAGGWAAASDSRK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
30232	60600	A	30416	645	2571	GRPRLFPQLFPPNPPVFRGQHPR
						QGLGPPSAAGRRAMKKKLVVL
						GLLAVVLVLVIVGLCLWLPSAS
						KEPDNHVYT\RAAVAADAKQC
						SEIGRVLVGGPAYLLLLGKAEV
						INAREVAPRLAFASMFNSSEQS
						QKGGLSVAVPGEIRGYELAHQ
						RHGRLPWARLFQPSIQLARQGF
ļ						PVGKGLAAVLENKRTVIEQQPV
						LWYVCGKVLREGERLTLPRLA
						DTYEMLAIEGAQAFYNGSLMA
					-	QIVKDIQAAGGIVTAEDLNNYR
						AELIEHPLNISLGDAVLYMPSA
						RLSGPVLALILNILKGYNFSRES
						VETPEQKGLTYHRIVEAFRFAY
						AKRTLLGDPKFVDVTENSIAGL
						LCARMDSPALGSRQVVRNMTS
						EFFAAQLRSQISDHTTHPISYYK
						PEFYTPDDGGTAHLSVVAEDGS
						AVSATSTINLYFGSKVCSPVSGI
						LFNNEMDDFSS\PAFTNEFGAPP
						SPANFIQPGKQPLLSMCLTIMV
						GQDGQVRMVVGAAGGTQITTD
						TALPPSHADHTPMPQAIIYNLW
						FGYDVKRAVEEPRLHNKLLPN
						VTTVERNIDQAVTAALETRHH
						HTQIASTFIAVVQAIVRTAGGW
						AAALDSRKVPTPGAGFWEGLV
						EVGWWEAVITAQHLDITRGTG
30233	60601	A	30417	5	439	
30234	60602	Α	30418	1	423	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30235	60603	A	30419	97	2012	WADEETWLCLPHLPVFSPTAHL
30233	00005	ľ`	30412	,	2012	PLLSSTPFSSLLPFISTPHPRGFA
						LPLPPSARLYLELRKLPATLPWS
						SVTDTGSYLSGRRERGGEGEGP
		ļ				GRRVRVADHGFALPRTGPQGS
						EEELANMQGL\VERLERAVSRL
		Ī				ESL\SAESHRPPGN\CGEVNGVI
l						A\GVAPSRGKPLHKLMDSMVA
						EF\LKNSRILSGDVETLAEIVHS
						AFQAQRAFLLMASQYQQPHEN
						DV\AALLKP\ISEKI\KEIQTFQRE
						/RTRGSNMFNHLSAVSE*IPCPL
						DGIAVSPKPG\PY\VKEMND\AA
						TFYT\NRVLKD*KQSDLRHVDW
						VKSYLNIWSELQAYIKEHHTTG
						LTWE/SKTGPV\ASTVS\AFSVLS
		İ				SGAWGFPPPPPPLPPPG\PPSTFS
ĺ		İ				EEWKGKKEESSPSR\SALFAQL
						N/QGEKAITKGLRHVT\DDQKT
			:			YKNPSLRAQGGQTQSPTKSHTP
						SPTSPKSYPSQKHAPVLELEGK
		İ				KWRVEYQEDRIDLVISETELKQ
İ						VAYIFKCEKSTIQIKGKVNSIIID
						NCKKLGLVFDNVVGIVEVINSQ
						DIQIQVMG\RVPTISI\NKTEGCH
						IYLSEDALDCEI\VSAKSIWKWN
						ILYPPQGWVD\YREFPHFP\EQF
						KTS/AWDGS\KLITEP\AEIMALT
-						SLRDRTPSPESPSIKTNKKAAVK
30236	60604	В	30420	1	499	
30237	60605	В	30421	390	851	
30238	60606	В	30422	136	603	
30239	60607	В	30423	1	2190	
30240	60608	Α	30424	82	242	
30241	60609	Α	30425	1	330	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30242	60610	Α	30426	215	1984	LLLVVTMSNNGLDIQDKPPAPP
						MRNTSTMIGAGSKDAGTLNHG
						SKPLPPNPEEKKKKDRFYRSILP
						GDKTNKKKEKERPEISLPSDFE
						HTIHVGFDAVTGEFTGMPEQW
						ARLLQTSNITKSEQKKNPQAVL
						DVLEFYNSKKTSNSQKYMSFTS
ŀ		i				GDKSAHGYIAAHPSSTKTASEP
						PLAPPVSEEEDEEEEEEDENEP
						PPVIAPRPEHTKSIYTRSVVESIA
						SPAVPNKEVTPPSAENANSSTL
						YRNTDRQRKKSKMTDEEILEKL
						RSIVSVGDPKKKYTRFEKIGQG
1						P\SGTVYTAMDVATGQEVAIKQ
					İ	MNLQQQPKKELIINEILVMREN
						KNPNIVNYLDSYLVGDELWVV
		1				MEYLAGGSLTDVVTETCMDEG
						QIAAVCRECLQALEFLHSNQVI
ŀ		ł				HRDIKSD\NILLGMDGSVKLTDF
		l				GFCAQITPEQSKLSTHG*GTPY
		ļ				W\M\APEVVDTERAYGPK/VLDI
						W\SLGIMAIEMIEGEPPYLNENP
	1					LRALYLIATNGTPELQNPEKL\S
						AIFR\DFL\NRCLEMDVEKRGFS/
						SKELLQHQFLKIGQAPSPSLTPH
						*LLQPKEATKEQSPKTHTHPQP
ŀ	•					HCAQAFCEINAHFRNSNS
30243	60611	A	30427	2	337	HEAQAFEEINAHFRISIS
30244	60612	A	30428	1	1644	
30245	60613	A	30429	1	330	
30246	60614	A	30430	169	440	
30247	60615	A	30431	1	1689	
30248	60616	A	30432	17	283	GHAWQLASIWLLCLLWPAVPL
30210	00070	1	30.52	'		NCLSSYGWTLWWRIALVGA*R
l						SLAPSRGSWSTQARPLKQRRTK
Ì		l				WCGKSWCLSGTSEPLSHWPRL
		l				RSW
30249	60617	Α	30433	16	346	RTDTYHLEDSKEQSGNRAGSG
		ľ``		1.]- ``	GWL*SCAE/GRRVALKSWPGRT
				1		GMSGTRRVTASSRGTSWYCGG
					1	SAGRSSTPPTGRACSPGSFSSPE
						PQPPGPSAAGSSVSGQLGPCGG
30250	60618	A	30434	1	1772	1 Q11 01 011 1000 Y BUQLUI CUU
30230	100018	$\Gamma_{\mathbf{U}}$	30434	1.	11/12	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30251	60619	A	30436	1	2607	MLTMSVTLSPLRSQDLDPMAT
						DASPMAINMTPTVEQGEGEEA
						MKDMDSDQQYEKPPPLHTGAD
	•					WKIVLHLPEIETWLRMTSERVR
						DLTYSVQQDSDSKHVDVHLVQ
						LKDICEDISDHVEQIHALLETEF
						SLKLLSYSVNVIVDIHAVQLLW
						HQLRVSVLVLRERILQGLQDAN
						GNYTRQTDILQAFSEETKEGRL
						DSLTEVDDSGQLTIKCSQNYLS
			ŀ			LDCGITAFELSDYSPSEDLLSGL
						GDMTSSQVKTKPFDSWSYSEM
						EKEFPELIRSVGLLTVAADSIST
				,		NGSEAVTEEVSQVSLSVDDKG
						GCEEDNASAVEEQPGLTLGVSS
						SSGEALTNAAQPSSETVQQESS
						SSSHHDAKNQQPVPCENATPKR
						TIRDCFNYNEDSPTQPTLPKRGL
						FLKEETFKNDLKGNGGKRQMV
						DLKPEMSRSTPSLVDPPDRSKL
						CLVLQSSYPNSPSAASQSYECL
						HKVGNGNLENTVKFHIKEISSS
						LGRLNDCYKEKSRLKKPHKTSE
						EVPPCRTPKRGTGSGKQAKNT
						KSSAVPNGELSYTSKAIEGPQT
						NSASTSSLEPCNQRSWNAKLQL
						QSETSSSPAFTQSSESSVGSDNI
						MSPVPLLSKHKSKKGQASSPSH
						VTRNGEVVEAWYGSDEYLALP
						SHLKQTEVLALKLENLTKLLPQ
						KPRGETIQNIDDWELSEMNSDS
						EIYPTYHVKKKHTRLGRVSPSS
30252	60620	A	30437	1	1983	
30253	60621	В	30438	1	702	
30254	60622	В	30439	1	936	
30255	60623	В	30440	1	1494	
30256	60624	В	30441	1	921	
30257	60625	В	30442	1	3342 1072	
30258	60626	В	30443	1	3711	<u></u>
30259	60627	В	30444	1 15	674	
30260 30261	60628	B B	30445 30446	15	2127	
			30446	1	3132	
30262	60630	B B	30447	103	438	
30263 30264	60632	В	30448	+	3042	
30265	60633		30449	1	1425	
30265	60634	В	30450	84	1954	
30267	60635	В	30451	1	1419	
30268	60636	В	30452	130	1615	
30269	60637	В	30454	1	1794	
30269	60638	В	30455	1	3255	
202/0	100030	ъ.	120422	11	13233	<u>l</u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first)	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30271	60639	В	30456	l l	945	
30272	60640	В	30457	1	7437	
30273	60641	В	30458	1	1122	
30274	60642	В	30459	317	1630	
30275	60643	В	30460	1	1716	-
30276	60644	В	30461	46	915	
30277	60645	В	30462	1	624	
30278	60646	В	30463	244	2988	
30279	60647	В	30464	1	804	
30280	60648	В	30465	1	1455	
30281	60649	В	30466	1	732	
30282	60650	В	30467	340	777	
30283	60651	В	30468	1	714	
30284	60652	В	30469	166	1337	
30285	60653	В	30470	72	617	
30286	60654	В	30471	1	1002	
30287	60655	В	30472	1	4173	
30288	60656	В	30473	1	4488	
30289	60657	В	30474	1	3822	
30290	60658	В	30475	1	1866	
30291	60659	В	30476	1	1002	
30292	60660	В	30477	1	1407	
30293	60661	В	30478	99	1046	
30294	60662	В	30479	122	1113	
30295	60663	В	30480	302	4145	
30296	60664	В	30481	1	669	
30297	60665	В	30482	1	933	
30298	60666	В	30483	1	2136	- · · · ·
30299	60667	В	30484	1	4017	
30300	60668	В	30485	1	1335	
30301	60669	В	30486	i	1095	
30302	60670	В	30487	1	2895	
30303	60671	В	30488	1	1215	
30304	60672	В	30489	1	2001	
30305	60673	В	30490	1	1281	
30306	60674	В	30491	1	780	
30307	60675	В	30492	1	858	
30308	60676	В	30493	1	699	
30309	60677	В	30494	i	1624	
30310	60678	В	30495	1	2958	
30311	60679	В	30496	30	658	
30311	60680	В	30497	1	1755	· · · · · ·
30313	60681	В	30498	1	631	
30314	60682	В	30499	1	1528	
30315	60683	В	30500	1	1056	
30316	60684	В	30501	1	2305	
30317	60685	В	30502	1	723	
30317	60686	В	30503	1	2691	
30318	60687	В	30504	1	2322	
	60688	В	30505	401	2677	
30320				. mm 1 / 1		

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	• • •
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30322	60690	В	30507	1	906	
30323	60691	В	30508	1	2865	
30324	60692	В	30509	45	820	
30325	60693	В	30510	1	783	
30326	60694	С	30511	18	410	
30327	60695	В	30512	1	840	
30328	60696	В	30513	1	945	
30329	60697	В	30514	1	2108	
30330	60698	В	30515	1	2457	
30331	60699	В	30516	1	1156	
30332	60700	В	30517	43	4677	
30333	60701	В	30518	80	964	
30334	60702	В	30519	1	4521	
30335	60703	В	30520	1	2460	
30336	60704	В	30521	1	1854	
30337	60705	В	30522	1	1367	
30338	60706	В	30523	273	419	
30339	60707	В	30524	1	1786	
30340	60708	В	30525	1169	1443	
30341	60709	В	30526	1	486	
30342	60710	В	30527	13	1260	
30343	60711	В	30528	270	723	
30344	60712	В	30529	1	834	
30345	60713	В	30530	i -	1632	
30346	60714	В	30531	1	4831	
30347	60715	В	30532	184	1593	
30348	60716	В	30533	1	615	
30349	60717	В	30534	1	3513	
30350	60718	В	30535	113	1666	
30351	60719	В	30536	101	2667	
30352	60720	В	30537	1	1692	
30353	60721	В	30538	51	142	
30354	60722	В	30539	1	3198	
30355	60723	В	30540	251	1207	
30356	60724	В	30541	1	1491	
30357	60725	В	30542	1	4024	
30358	60726	В	30543	1	3316	
30359	60727	В	30544	1	1342	
30360	60728	В	30545	91	810	
30361	60729	В	30546	17	489	
30362	60730	Ā	30547	1	504	MGGSNRSAEAWKLANGINIIVA
10002	30,30	`	30011	1		TSGRLLDHMQNTPGFMYKNLQ
						CLVIDEADRILDVGFEEELKQII
						KLLLTHRQTMLFSATQTQKVE
	-					DLARISLKKEP/LYVGDDDDNA
						NETVFG\TLLCTDVAARGLDITE
						VDCIVQYDPPDDPKEYIHSVGR
						TARGLNGRENWVFFAT
20262	60731	_	30548	1	2676	I AROLINOREIN W VEFA I
30363 30364	60732	A B	30548	1	1071	
		-	30549	<u> </u>	348	
30365	60733	A	30330	1	J40	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	l .	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
30366	60734	Α	30551	1	711	MAEIQHKTIRPLLEGRDLLAAV
i						KTGSGKTLAVLIPAIELVVKLKF
						MPRNGTGVLILSPTRQLAMQTF
		ŀ]		GVLKELMTHHVHTYGLIIGGSN
			ŀ			RSAEAQKLANGINIIVVTPGRLL
						DHTQNTPGFMYKNLQVEDLAR
						ISPKKEPLYVGVDEDKANATVD
			•			GLEQGHFVCPSEKRYLLLFTFL
						KKNQKKKLMVFFSACMSVKYP
						YGLLKYIDL/PVLAIHGKQKQN
						KHTTTFF*YCNADSGTLL
30367	60735	Α	30552	661	987	VTFYSSEHSNPCHKNLRKARRK
	00,00				, ,	DTKRIILKW*HTLV*GRDI*N*NI
						IITRNTRYSLLCPWATKKLKAC
						FISQK*KRDVIERNSAQCLQPKS
						IYTLVR*VQILKSTKILL
30368	60736	A	30553	188	2188	KFQGASNLTLSETQNGDVSEET
	00,00					MGSRKVKKSKQKPMNVGLSET
						QNGGMSQEAVGNIKVTKSPQK
						STVLTNGEAAMQSSNSESKGK
		1				MKKKRKMVNDAEPDTKKAKT
				·		ENKGKSEEESAETTKETENNVE
						KPDNDEDESEVPSLPLGLTGAF
		İ				EDTSFASLCNLVNENTLKAIKE
		1				MGFTNMTEIQHKSIRPLLEGRD
		l				LLAAAKTGSGKTLAFLIPAVELI
İ		1	•			\VKLRFMPRNGTGVLILSP\TRE
						LAMQTFGVLKELMTHHVHTYG
		l				LIMGGSNRSAEAQKLGNGINIIV
						ATPGRLLDHMQNTPGFMYKNL
						QCLVIDEADRILDVGFEEELKQI
		Ì				IKLLPTRRQTMLFSATQTRKVE
						DLARISLKKEPLYVGVDDDKA
						NATVDGLEQGYV\VCPSEKRFL
						LLFTFLKKNRKKKLMVFFSSCM
		1				SVKYHYELLNYIDLPVLAIHGK
				ļ		QKQNKRTT\TFFQFCNADSG\TL
}						LCT\DV\AARGLDIPEVDWIVQY
				İ		DPPDDPKEYI\HRVG*EQPEGLN
						GEEGHALASFLRPRKDLGFFFR
						LL*KHSKGFPLSGIWTFSW/SLK
						ISDIQFSAWRNWIGKVITFLHKS
						A\QEAYKSYITEPMDSPFL*NRS
		1				FN\VNNLNLASGLLCQFGFK\VP
						PFVDLNVNSNEGKQKKRGGGG
						GFGLPRKTQEKLEKS\KIF*TH*
						ARKSSGQAGQFSH
Ц		Ц	l	l	L	

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, and complementary sequences thereof.

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- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
 - 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
 - 6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
 - 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
 - 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-30368.
 - 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

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- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
 - 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
 - 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
 - a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
 - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
 - 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

- b) detecting the complex by detecting reporter gene sequence expression, so
 that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
 - 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-30368, a mature protein coding portion of SEQ ID NO: 1-30368, an active domain of SEQ ID NO: 1-30368, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-30368, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).
 - 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 30369-60736, the mature protein portion thereof, or the active domain thereof.

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- 21 The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-30368.
- 25 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
 - 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 30 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
 - 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

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27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

IPC(7) US CL	SSIFICATION OF SUBJECT MATTER : C12N 15/00, 15/12 : 536/23.1, 23.5; 435/6, 320.1, 325								
	cording to International Patent Classification (IPC) or to both national classification and IPC FIELDS SEARCHED								
	cumentation searched (classification system followed 36/23.1, 23.5; 435/6, 320.1, 325	by classification symbols)							
Documentati NONE	tation searched other than minimum documentation to the extent that such documents are included in the fields searched								
Electronic da NONE	ata base consulted during the international search (nat	me of data base and, where practicable,	search terms used)						
C. DOC	UMENTS CONSIDERED TO BE RELEVANT								
Category *	Citation of document, with indication, where a	<u>``</u>	Relevant to claim No.						
X, P	Database Genbank, Accession No. AL135937, 15	March 2001 (15.03.2001),	1-8						
Α	particularly nucleotides 29925 through 30325.		9, 19						
х	Database Genbank, Accession No. AA004350, HI	LLIER et al., Generation and	1-8						
 A	analyhsis of 280,000 Human Expressed Sequence T (07.05.1997), Vol. 6, No. 9, pages 807-828,	Cags. Genome Res. 07 May 1997	9, 19						
		,							
Further	documents are listed in the continuation of Box C.	See patent family annex.							
"A" document	pecial categories of cited documents: defining the general state of the art which is not considered to be lar relevance	"T" later document published after the int date and not in conflict with the appli principle or theory underlying the inv	cation but cited to understand the ention						
"E" earlier ap	plication or patent published on or after the international filing date	"X" document of particular relevance; the considered novel or cannot be considered novel or cann							
establish specified)	combined with one or more other such documents, such combination								
	referring to an oral disclosure, use, exhibition or other means	being obvious to a person skilled in the	}						
priority d	published prior to the international filing date but later than the late claimed	"&" document member of the same patent							
	actual completion of the international search 2001 (23.10.2001)	Date of mailing of the international sea 0 2 JAN 2002	arch report						
Name and m	ailing address of the ISA/US	Austorize officer	· · · · · · · · · · · · · · · · · · ·						
Con Box	PCT shington, D.C. 20231	Marianne P. Allen	ureace for						
	o. (703)305-3230	Telephone No. 703-308-0196							

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows: Please See Continuation Sheet
 As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9 and 19 with respect to SEQ ID NO: 1
Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08631

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-9 and 19, drawn to polynucleotides.

Group II, claim(s) 10-11, drawn to polypeptides.

Group III, claim(s) 12, drawn to antibodies.

Group IV, claim(s) 13-15, drawn to methods of detecting polynucleotides.

Group V, claim(s) 16, drawn to methods of detecting polypeptides.

Group VI, claim(s) 17, drawn to a first method of identifying compounds that bind.

Group VII, claim(s) 18, drawn to a second method of identifying compounds that bind.

Group VIII, claim(s) 20-21, drawn to polypeptide arrays.

Group IX, claim(s) 22-26, drawn to polynucleotide arrays.

Group X, claim(s) 27, drawn to a method of treatment using a polypeptide.

Group XI, claim(s) 28, drawn to a method of treatment using an antibody.

In addition, each of the SEQ ID NOS. named in the groups is considered to be a separate invention and applicant must elect a single SEQ ID NO. or for Groups VIII and IX a specific combination of SEQ ID NOS. for searching. Due to the burden of search for sequences, only a single SEQ ID NO. or specific combination of SEQ ID NOS. for Groups VIII and IX is considered to meet unity of invention.

The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the products of Groups I-III, VIII, and IX differ structurally and functionally and thus lack the same or corresponding special technical feature. Each of the methods of Groups IV-VII, X and XI have different starting materials, method steps, and goals and thus lack the same or corresponding special technical feature.

As each SEQ ID NO. does not appear to share a common core structure, they are considered to be structurally and functionally distinct invention.

The number of inventions has been determined as follows: Each of groups I-XI is directed to 30368 SEQ ID NOS. As such, 30368 SEQ ID NOS. X 11 groups results in 334048 inventions.

If no additional fees are paid, Group I, claims 1-9 and 19, will be scarched with respect to SEQ ID NO: 1. If Group VIII is elected, the default polypeptide array is considered to be an array comprising all of SEQ ID NOS: 30369-60736. If Group IX is elected, the default polynucleotide array is considered to be an array comprising all of SEQ ID NOS: 1-30368. Applicant is advised that they should specifically identify each additional group and each additional SEQ ID NO. being paid for. With respect to Groups VIII and IX, applicant should specifically identify each subset of SEQ ID NOS. present on the arrays if additional combinations are to be searched.